Annexures

Annexure 01: Fold change (FC >2) differences across different growth conditions (Experiment P1)

(1a)Protein FC >2 Tween 80 Vs control P1

Protein names	Functional Class	Gene	Gene locu	Protein IDs	-Log t-test p-value	t-test difference	Fold change
Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	ADH2	BN194_08400	K0N307	4.39533	4.46995	22.16098
Probable dipeptidase (EC 3.4.-.-)	Amino acid-related metabolism		BN194_23190	K0MXA1	0.847866	2.71144	6.549751
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	pycB	BN194_20290	K0MWI8	3.91589	2.453	5.475535
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	citF	BN194_20310	K0N607	3.09828	2.11955	4.345584
Autoinducer-2 (AI-2) kinase	General prediction only		BN194_27880	K0NB06	4.79712	1.87068	3.657049
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	yacO	BN194_24420	K0NC34	0.348556	1.67058	3.183425
>tr|K0N6D0|K0N6D0_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_20650 PE=4 SV=1	Unknown/uncharacterized	K0N6D0		K0N6D0	1.32144	1.59629	3.023648
Cold shock protein 1	Transcription-associated proteins	csp	BN194_06990	K0MT67	1.25878	1.48889	2.806729
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	yfeX	BN194_07170	K0N8U9	3.6789	1.48108	2.791576
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	citX	BN194_20300	K0N6A3	1.30726	1.47315	2.776274
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	fruA_4	BN194_27690	K0MY77	3.34175	1.42903	2.692656
Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	rpiA_2, ripA	BN194_28600	K0N8W9	0.678894	1.41042	2.658145
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	fruK_2	BN194_27700	K0N8P7	2.09742	1.33116	2.516049
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	citE	BN194_20320	K0NBF4	1.08958	1.30862	2.477045
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	msmK	BN194_11180	K0N747	0.950875	1.22574	2.338754
Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	plsX	BN194_17940	K0MW37	0.543333	1.21709	2.324773
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	citD	BN194_20330	K0N9Q5	0.819627	1.19286	2.286055
Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	0.57742	1.09194	2.131605
UPF0342 protein yheA	Unknown/uncharacterized	yheA	BN194_19080	K0N9F7	1.76945	1.08652	2.123612

Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	3.48745	1.05097	2.071922
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	Posttranslational modification	citC	BN194_20340	K0MWJ1	2.21605	1.015	2.020903

(1b)Protein FC<2 Tween 80 Vs control P1

Protein names	Functional Class	Gene	Gene locus	Protein IDs	-Log t-test p-value	t-test Difference	Fold change
Biotin carboxyl carrier protein	Tricarboxylic acid pathway	bcc	BN194_20370	K0NBF7	2.14	1.00	1.99
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	pflB	BN194_16080	K0N8I5	1.91	0.84	1.79
UPF0092 membrane protein yrbF	Protein export	yrbF	BN194_08390	K0MTL6	0.36	0.83	1.78
Cold shock-like protein CspLA	Transcription-associated proteins	cspLA	BN194_12460	K0N438	0.50	0.82	1.77
>tr|K0N518|K0N518_LACCA IolA protein OS=Lactobacillus casei W56 GN=iolA PE=3 SV=1	Carbohydrate-related metabolism	iolA		K0N518	0.90	0.80	1.75
>tr|K0N1K5|K0N1K5_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_01360 PE=4 SV=1	Unknown/uncharacterized	K0N1K5		K0N1K5	0.30	0.77	1.70
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	HBN1	BN194_16550	K0N597	1.58	0.75	1.68
Protein hit	tRNA aminoacyl synthesis	hit	BN194_19040	K0MWA8	1.74	0.74	1.67
50S ribosomal protein L7/L12	Ribosomal proteins	rplL	BN194_24080	K0NA98	4.79	0.72	1.65
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	mtlF	BN194_30410	K0N8N0	1.78	0.71	1.63
Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	bceA_2	BN194_21230	K0N9X1	0.57	0.70	1.62
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	Cell wall biogenesis	glmS	BN194_11560	K0N3V9	1.27	0.68	1.60
>tr|K0N7I1|K0N7I1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02220 PE=4 SV=1	Unknown/uncharacterized	K0N7I1		K0N7I1	1.01	0.68	1.60
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		BN194_01410	K0N1L0	0.85	0.67	1.59
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	asnS	BN194_16760	K0N569	1.47	0.66	1.58
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	tpiA	BN194_11030	K0N736	2.32	0.64	1.55

Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		BN194_08960	K0N387	1.30	0.63	1.55
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	1.19	0.60	1.51
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	mtlD_3mtlD	BN194_30400	K0N9C8	1.86	0.58	1.50
>tr|K0N9X8|K0N9X8_LACCA SpsK protein OS=Lactobacillus casei W56 GN=spsK PE=4 SV=1;>tr|K0N6D6|K0N6D6_LACCA SpsK_2 protein OS=Lactobacillus casei W56 GN=spsK_2 PE=4 SV=1	Cell wall biogenesis	spsK_2		K0N9X8;K0N6D6	1.92	0.57	1.49
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC_2,deoC	BN194_02790	K0MSB5	2.50	0.55	1.46
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	ddl	BN194_01390	K0MRY4	0.73	0.55	1.46
Uncharacterized protein yueI	Unknown/uncharacterized	yueI	BN194_13920	K0NAC7	0.79	0.54	1.45
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	helD	BN194_21130	K0N9W3	0.80	0.53	1.45
FMN-binding domain protein	General prediction only		BN194_24320	K0NC29	0.85	0.53	1.45
Probable L-ascorbate-6-phosphate lactonase ulaG (EC 3.1.1.-)	Carbohydrate-related metabolism	ulaG	BN194_28590	K0MYF8	0.25	0.53	1.45
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	mtnN	BN194_14890	K0MV90	1.82	0.53	1.44
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	dltA	BN194_08590	K0MTN0	1.37	0.53	1.44
Uncharacterized protein MJ0282	Cofactor-related metabolism		BN194_03700	K0N1T2	0.56	0.52	1.43
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	pepO_2	BN194_16630	K0N8Q0	1.68	0.50	1.42
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	apbE_3	BN194_21550	K0N6S8	1.37	0.50	1.41
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	yqjQ(K0N8A1)	BN194_15480	K0N8A1	0.76	0.50	1.41
Uncharacterized protein	Unknown/uncharacterized		BN194_27530	K0NAX5	0.31	0.47	1.39
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	pgk	BN194_11020	K0N9R1	0.86	0.46	1.37
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	luxS	BN194_08330	K0N6J0	0.26	0.45	1.37
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	BN194_21350	BN194_21780	K0N6Q5	2.95	0.45	1.36
Penicillin acylase (EC 3.5.1.11)	Cell defense/detoxification		BN194_04910	K0N2B8	0.82	0.44	1.36
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	serS	BN194_20080	K0N9N4	1.70	0.44	1.35
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	deoB	BN194_02800	K0N1N0	2.67	0.43	1.35

GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	obg	BN194_15440	K0MVD3	1.39	0.42	1.34
>tr|K0N2Q1|K0N2Q1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_06460 PE=4 SV=1;>tr|K0MXJ1|K0MXJ1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_24990 PE=4 SV=1	Unknown/uncharacterized	K0N2Q1		K0N2Q1;K0MXJ1	1.61	0.41	1.33
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	pmi	BN194_02920	K0N7U2	0.75	0.41	1.32
Uncharacterized protein ynbB	Cell defense/detoxification	ynbB	BN194_18380	K0N9B7	1.61	0.41	1.32
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	rmlB	BN194_21340	K0MWS0	1.28	0.41	1.32
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	0.60	0.40	1.32
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	pepV	BN194_08800	K0N324	3.00	0.40	1.32
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	1.22	0.39	1.31
Elongation factor P	Protein translation (elongation)	efp	BN194_18240	K0MW57	1.22	0.39	1.31
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	deoD	BN194_02810	K0N1Z0	1.11	0.38	1.30
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	nagB	BN194_30440	K0MYW0	2.96	0.37	1.29
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	1.74	0.37	1.29
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	mco	BN194_25410	K0N7A4	2.22	0.36	1.28
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	mnmA	BN194_14930	K0N844	1.97	0.35	1.28
UPF0337 protein lp_1708	General prediction only		BN194_05810	K0N2J8	0.35	0.35	1.27
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	treA	BN194_06930	K0N662	1.08	0.34	1.27
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	ileS	BN194_14810	K0N4L9	0.80	0.34	1.26
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	pncB	BN194_19860	K0N5X0	1.28	0.33	1.26
Uncharacterized protein	Unknown/uncharacterized		BN194_01870	K0N7D4	0.24	0.33	1.26
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshB	BN194_08460	K0N356	1.06	0.33	1.26
ABC-type uncharacterized transport system, ATPase component	ABC-type transporter systems		BN194_07730	K0N6C9	0.83	0.33	1.26
Uncharacterized protein	Unknown/uncharacterized		BN194_11770	K0N9Y6	0.79	0.33	1.25
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	purB	BN194_12520	K0NA41	0.95	0.33	1.25
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	dhaM	BN194_04960	K0N2C2	0.91	0.33	1.25
Uncharacterized protein ykuJ	Unknown/uncharacterized	ykuJ	BN194_09100	K0N348	0.74	0.31	1.24

Predicted hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	0.43	0.31	1.24
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	1.37	0.31	1.24
Response regulator ArlR	Signal transduction	arlR	BN194_18650	K0N5X3	0.53	0.31	1.24
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	ycnE	BN194_13230	K0N7R3	0.79	0.30	1.23
Oligoendopeptidase, pepF/M3 family	Amino acid-related metabolism		BN194_11580	K0N779	0.55	0.30	1.23
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	lysS	BN194_26380	K0NAN7	0.64	0.29	1.22
Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	fba_2	BN194_05060	K0N2C9	1.02	0.29	1.22
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	ykpA	BN194_07220	K0N8V6	1.19	0.29	1.22
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	glnA_2	BN194_18340	K0MW64	0.97	0.29	1.22
Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	rp2	BN194_17060	K0N598	0.68	0.29	1.22
50S ribosomal protein L16	Ribosomal proteins	rplP	BN194_26150	K0N863	0.61	0.28	1.21
Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	leuS	BN194_09210	K0N3A9	1.02	0.27	1.21
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	dhaK_2	BN194_04980	K0N5Q3	0.60	0.27	1.21
Transcription termination/antitermination protein NusG	Transcription-associated proteins	nusG	BN194_24260	K0N730	0.77	0.27	1.20
Mannose permease IID component	Phosphotransferase systems	manZ_9	BN194_29700	K0N954	0.66	0.26	1.20
Uncharacterized protein SE_0534	tRNA/Ribosome assembly/processing		BN194_10150	K0N3F2	0.78	0.26	1.20
30S ribosomal protein S16	Ribosomal proteins	rpsP	BN194_17810	K0N5H1	0.24	0.26	1.20
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	pepDB	BN194_21110	K0N678	0.78	0.26	1.20
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	ptsH	BN194_19430	K0N9I2	0.26	0.25	1.19
Aspartate racemase (EC 5.1.1.13)	Amino acid-related metabolism		BN194_02170	K0N7H2	0.67	0.25	1.19
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	murC	BN194_18950	K0N600	0.66	0.25	1.19
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	guaA	BN194_21070	K0NBJ2	1.39	0.24	1.18
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	pyc	BN194_15170	K0NAI2	1.57	0.24	1.18
Uncharacterized protein	Unknown/uncharacterized		BN194_28350	K0N8V3	0.46	0.24	1.18
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	0.61	0.23	1.18
Glutamine-binding periplasmic protein	ABC-type transporter systems	glnH_2	BN194_29910	K0N8I1	0.33	0.23	1.17
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	yqeL,rsfS	BN194_18710	K0N5N6	1.52	0.22	1.17

Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	rpoE	BN194_26810	K0N7L4	1.11	0.22	1.17
5-dehydro-2-deoxygluconokinase (EC 2.7.1.92) (2-deoxy-5-keto-D-gluconate kinase)	Carbohydrate-related metabolism	iolC	BN194_02250	K0N1H4	0.17	0.22	1.16
Elongation factor G (EF-G)	Protein translation (elongation)	fusA	BN194_26270	K0NCN8	2.11	0.22	1.16
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		BN194_11600	K0N3Z3	0.38	0.21	1.16
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE_3	BN194_04780	K0N5N9	0.37	0.21	1.16
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	pepN	BN194_05410	K0N2F5	2.31	0.21	1.16
30S ribosomal protein S17	Ribosomal proteins	rpsQ	BN194_26130	K0NAL6	0.25	0.21	1.16
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	0.66	0.21	1.16
Translation initiation factor IF-1	Protein translation (initiation)	infA	BN194_26000	K0N847	0.40	0.20	1.15
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	pepQ	BN194_08740	K0MTP0	0.81	0.20	1.15
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		BN194_21400	K0N6R1	0.44	0.20	1.15
Thioredoxin-like protein ytpP	Posttranslational modification	ytpP	BN194_18980	K0N9F1	1.49	0.20	1.15
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_3	BN194_21440	K0MWS9	0.36	0.20	1.15
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	galE	BN194_07350	K0N2R3	0.63	0.20	1.15
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	patA_2	BN194_22950	K0N7F8	0.38	0.20	1.15
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	proS	BN194_17610	K0N5E2	1.12	0.19	1.14
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	yabR	BN194_26500	K0N8A7	0.41	0.18	1.14
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	glyr1	BN194_30100	K0N992	0.40	0.18	1.13
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	lacA	BN194_07500	K0N2T4	0.52	0.18	1.13
Acetyltransferase	General prediction only		BN194_08200	K0N2Z8	0.62	0.18	1.13
3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase (THcHDO hydrolase) (EC 3.7.1.22)	Carbohydrate-related metabolism	iolD	BN194_02260	K0N1T3	0.08	0.18	1.13
Uncharacterized protein yghZ	General prediction only	yghZ	BN194_27510	K0N7U8	0.35	0.18	1.13
Probable dipeptidase (EC 3.4.-.-)	Amino acid-related metabolism		BN194_13380	K0N7S0	0.78	0.18	1.13
Histidinol-phosphatase	General prediction only		BN194_14010	K0N4F8	0.34	0.17	1.13
Uncharacterized protein yutG	Lipid-related metabolism	yutG	BN194_08940	K0MTQ3	0.73	0.17	1.13
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	asd	BN194_01060	K0N1I5	0.57	0.17	1.12

Mannose permease IID component	Phosphotransferase systems	manZ	BN194_02990	K0MSE1	0.06	0.17	1.12
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	0.68	0.17	1.12
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	murF	BN194_26720	K0NCU5	0.29	0.16	1.12
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	cysS	BN194_24430	K0NAB2	0.38	0.16	1.12
>tr|K0N3R3|K0N3R3_LACCA Gap protein OS=Lactobacillus casei W56 GN=gap PE=3 SV=1	Central glycolytic/intermediary pathways	gap		K0N3R3;K0N4X1	0.34	0.16	1.12
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	groS,grES	BN194_23760	K0N700	0.16	0.16	1.12
>tr|K0N7B1|K0N7B1_LACCA Acetate kinase OS=Lactobacillus casei W56 GN=ackA PE=3 SV=1	Central glycolytic/intermediary pathways	ackA		K0N7B1;K0N6W4	0.32	0.16	1.12
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_4	BN194_29900	K0N971	0.47	0.16	1.11
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	hisS	BN194_17110	K0N5A0	0.49	0.15	1.11
50S ribosomal protein L19	Ribosomal proteins	rplS	BN194_17770	K0NB12	0.75	0.15	1.11
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	tuf	BN194_15310	K0N4R1	0.77	0.15	1.11
Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	nfo	BN194_17070	K0NAW5	0.15	0.14	1.10
Predicted hydrolase of the HAD superfamily	General prediction only	mtlD	BN194_30450	K0N9D4	0.61	0.14	1.10
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	dut	BN194_24640	K0MXG3	0.58	0.14	1.10
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	nadE	BN194_19840	K0MWF6	0.79	0.14	1.10
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	yjlD	BN194_24330	K0NAA7	0.26	0.14	1.10
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	ppaC	BN194_16110	K0N4Z4	0.60	0.13	1.10
UPF0659 protein YMR090W	General prediction only	ylbE	BN194_07030	K0N671	0.38	0.13	1.09
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	rpe	BN194_18000	K0N5T1	0.42	0.13	1.09
30S ribosomal protein S2	Ribosomal proteins	rpsB	BN194_17680	K0N936	0.59	0.13	1.09
>tr|K0N5T2|K0N5T2_LACCA Phosphoenolpyruvate-protein phosphotransferase OS=Lactobacillus casei W56 GN=ptsI PE=3 SV=1	Phosphotransferase systems	ptsI		K0N5T2	0.60	0.13	1.09
Single-stranded DNA-binding protein (SSB)	DNA replication-related	ssb	BN194_00110	K0N1C2	0.30	0.12	1.09
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	manD	BN194_02950	K0N1P4	0.39	0.12	1.09
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	eno	BN194_11040	K0MU67	0.99	0.12	1.09
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	greA	BN194_18520	K0NB62	0.63	0.12	1.09

Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatC	BN194_11950	K0N436	0.70	0.12	1.09
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC	BN194_00080	K0N486	0.37	0.12	1.08
50S ribosomal protein L18	Ribosomal proteins	rplR	BN194_26060	K0N7F4	0.29	0.12	1.08
30S ribosomal protein S3	Ribosomal proteins	rpsC	BN194_26160	K0N7G5	0.29	0.11	1.08
Transcription termination/antitermination protein NusA	Transcription-associated proteins	nusA	BN194_17580	K0N927	1.64	0.11	1.08
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	purA	BN194_01160	K0N1J0	0.79	0.11	1.08
Thioredoxin	Posttranslational modification	trxA_2	BN194_08570	K0N975	0.27	0.11	1.08
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	0.25	0.11	1.08
DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	0.48	0.10	1.07
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	cmk	BN194_15710	K0N4V1	0.40	0.10	1.07
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	ldh	BN194_26560	K0N7J5	0.30	0.10	1.07
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	yutF	BN194_08910	K0N383	0.30	0.10	1.07
Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (Guanine insertion enzyme) (tRNA-guanine transglycosylase)	tRNA/Ribosome assembly/processing	tgt	BN194_08380	K0N6J4	0.05	0.10	1.07
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	glyS	BN194_16950	K0N5D3	0.52	0.10	1.07
>tr|K0N8X1|K0N8X1_LACCA Galactose-1-phosphate uridylyltransferase OS=Lactobacillus casei W56 GN=galT PE=3 SV=1	Carbohydrate-related metabolism	K0N8X1		K0N8X1	0.44	0.10	1.07
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	mhqD	BN194_18770	K0NB71	0.28	0.09	1.07
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	coaD	BN194_15200	K0N4X3	0.67	0.09	1.07
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	thiD_2	BN194_07650	K0N2U9	0.43	0.09	1.07
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	hslO	BN194_26400	K0N893	0.87	0.09	1.07
30S ribosomal protein S6	Ribosomal proteins	rpsF	BN194_00100	K0N0Z1	0.30	0.09	1.07
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	zwf	BN194_08420	K0N966	0.11	0.09	1.07
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	ykwC	BN194_02520	K0N7M3	0.15	0.09	1.06
Non-specific ribonucleoside hydrolase rihC (EC 3.2.-.-)	Nucleic acid/nucleotide metabolism	rihC	BN194_03870	K0N803	0.07	0.09	1.06
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	iscS1	BN194_14900	K0N4U8	0.10	0.09	1.06

Nucleoid-associated protein BN194_23980	General prediction only		BN194_23980	K0NA95	0.19	0.09	1.06
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	ung	BN194_11330	K0N758	0.03	0.08	1.06
Aldose 1-epimerase (EC 5.1.3.3)	Central glycolytic/intermediary pathways		BN194_07390	K0MTA8	0.42	0.08	1.06
Probable flavodoxin-1	Membrane bioenergetics	ykuN_2	BN194_12220	K0NA19	0.25	0.08	1.06
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	yuxL	BN194_19910	K0N5X4	0.57	0.08	1.05
50S ribosomal protein L6	Ribosomal proteins	rplF	BN194_26070	K0NCK5	0.31	0.07	1.05
Oligopeptide-binding protein oppA	ABC-type transporter systems	oppA	BN194_17880	K0N983	0.24	0.07	1.05
Probable catabolite control protein A	Transcriptional regulation	ccpA	BN194_08750	K0N323	0.23	0.07	1.05
Uncharacterized protein ylxR	General prediction only	ylxR	BN194_17570	K0NAZ6	0.32	0.07	1.05
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	xpt	BN194_12490	K0MUR6	0.44	0.07	1.05
Protein lacX, plasmid	Carbohydrate-related metabolism	lacX	BN194_27070	K0NCY0	0.21	0.06	1.04
Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	pyk	BN194_15580	K0N8B6	0.35	0.06	1.04
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	gpmA2,gpmA	BN194_22740	K0MX58	0.23	0.06	1.04
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	yqeH	BN194_18740	K0MW90	0.16	0.06	1.04
50S ribosomal protein L22	Ribosomal proteins	rplV	BN194_26170	K0NCM1	0.16	0.06	1.04
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	asnB	BN194_22990	K0MX90	0.10	0.05	1.04
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshA	BN194_26700	K0N8C7	0.44	0.05	1.04
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	uvrA	BN194_10450	K0N3J2	0.20	0.05	1.04
Uncharacterized protein	Unknown/uncharacterized		BN194_01760	K0N1N3	0.08	0.05	1.04
>tr|K0N6A9|K0N6A9_LACCA Tyrosine--tRNA ligase OS=Lactobacillus casei W56 GN=tyrS PE=4 SV=1	tRNA aminoacyl synthesis	tyrS		K0N6A9	0.12	0.05	1.04
50S ribosomal protein L14	Ribosomal proteins	rplN	BN194_26120	K0NCL3	0.25	0.05	1.04
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2_2,lacD	BN194_27060	K0N7P0	0.15	0.05	1.03
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	cysK	BN194_05520	K0N8E6	0.19	0.05	1.03
>tr|K0N7I6|K0N7I6_LACCA Glucose-6-phosphate isomerase OS=Lactobacillus casei W56 GN=pgi PE=3 SV=1	Central glycolytic/intermediary pathways	pgi		K0N7I6;K0N4A6	0.06	0.04	1.03
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	thyA	BN194_15800	K0N522	0.11	0.04	1.03

Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	tig	BN194_15330	K0N884	0.13	0.04	1.03
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	typA	BN194_15150	K0N4W9	0.11	0.04	1.03
Pur operon repressor	Transcriptional regulation	purR_2	BN194_26960	K0N7M9	0.03	0.04	1.03
Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	upp	BN194_13550	K0N4J8	0.15	0.04	1.03
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	aspS	BN194_17100	K0N5F3	0.08	0.03	1.02
50S ribosomal protein L29	Ribosomal proteins	rpmC	BN194_26140	K0MXT6	0.29	0.03	1.02
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdF	BN194_16610	K0N552	0.04	0.03	1.02
UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	0.04	0.03	1.02
Uncharacterized protein YwcC	Carbohydrate-related metabolism	ywcC	BN194_09930	K0N6V0	0.06	0.03	1.02
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	rnr	BN194_11100	K0N3S4	0.07	0.03	1.02
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	gltX	BN194_24470	K0NC38	0.09	0.03	1.02
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	0.11	0.03	1.02
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	def	BN194_15060	K0N4N6	0.05	0.02	1.02
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	11E,P100	BN194_02180	K0N513	0.05	0.02	1.02
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	rbfA	BN194_17540	K0MVV7	0.06	0.02	1.01
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	gnd	BN194_18660	K0N5N2	0.05	0.02	1.01
UPF0478 protein SAOUHSC_01855	Signal transduction		BN194_08710	K0N365	0.04	0.02	1.01
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	0.04	0.02	1.01
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	pyrC	BN194_16470	K0NAS6	0.01	0.02	1.01
Uncharacterized protein	Unknown/uncharacterized		BN194_08190	K0MTK3	0.04	0.01	1.01
Glycosyl transferase family protein	Cell wall biogenesis		BN194_02420	K0N7L2	0.01	0.01	1.01
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	tsf	BN194_17670	K0NB01	0.05	0.01	1.01
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	argS	BN194_19120	K0NB86	0.03	0.01	1.01
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	oppD	BN194_17920	K0NB35	0.08	0.01	1.01
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	valS	BN194_14510	K0N4J6	0.09	0.01	1.01
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	gatA	BN194_11960	K0N3Z6	0.04	0.01	1.01

PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	bglP	BN194_06940	K0MT60	0.01	0.01	1.01
50S ribosomal protein L13	Ribosomal proteins	rplM	BN194_25850	K0N828	0.02	0.01	1.00
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	rpoB	BN194_26340	K0MXV4	0.02	0.01	1.00
Uncharacterized protein ypuA	Unknown/uncharacterized	ypuA	BN194_27250	K0N8I3	0.01	0.01	1.00
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	pyrDA, pyrD	BN194_19150	K0N623	0.02	0.00	1.00
Transcriptional regulator, xre family	Transcriptional regulation		BN194_23510	K0N6Y7	0.00	0.00	1.00
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	agl	BN194_27950	K0N8T1	0.01	0.00	1.00
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	pta	BN194_11340	K0MU95	0.01	0.00	1.00
>tr|K0N699|K0N699_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA PE=3 SV=1;>tr|K0MWW4|K0MWW4_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA_2 PE=3 SV=1	Cell wall biogenesis	rmlA		K0N699;K0MWW4	0.01	0.00	1.00
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	nrnA	BN194_08450	K0N309	0.00	0.00	1.00
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	gmuB	BN194_23840	K0MXC7	0.00	0.00	1.00
Putative nrdI-like protein	Nucleic acid/nucleotide metabolism		BN194_08250	K0N300	0.01	0.00	1.00
Uncharacterized protein	Central glycolytic/intermediary pathways		BN194_04970	K0N8A3	0.00	0.00	1.00
30S ribosomal protein S14 type Z	Ribosomal proteins	rpsZ,rpsN	BN194_26090	K0MXS9	0.00	0.00	1.00
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	0.01	0.00	1.00
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	thrS	BN194_18860	K0N5P5	0.05	0.00	1.00
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC_2	BN194_24680	K0NAC2	0.01	0.00	1.00
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	0.02	0.00	1.00
Uncharacterized protein	Cofactor-related metabolism		BN194_18720	K0NB69	0.02	-0.01	1.00
50S ribosomal protein L5	Ribosomal proteins	rplE	BN194_26100	K0N859	0.04	-0.01	1.00
Putative tRNA-binding protein ytpR	General prediction only	ytpR	BN194_18970	K0NB80	0.01	-0.01	1.00
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	msrA_2,msrA	BN194_15860	K0N4W6	0.02	-0.01	1.00
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	fabZ	BN194_22520	K0NBS8	6.27	-5.89	-59.2749

Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	fabD	BN194_22570	K0NBT1	6.77	-5.71	-52.4765
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	bkr4	BN194_22550	K0N799	6.45	-5.63	-49.6358
>tr|K0N788|K0N788_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_22500 PE=4 SV=1	Unknown/uncharacterized	K0N788		K0N788	3.68	-4.89	-29.5859
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	fabK	BN194_22580	K0NA38	4.35	-4.85	-28.7893
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)	Lipid-related metabolism	accC	BN194_22510	K0N6M5	4.95	-4.56	-23.65
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	fabF	BN194_22540	K0MX40	4.30	-4.15	-17.71
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	accB	BN194_22530	K0NA35	4.03	-3.94	-15.3963
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	fabG	BN194_22560	K0N6N3	2.30	-3.68	-12.8183
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	fabH	BN194_22600	K0N7B0	5.00	-3.46	-11.0326
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	alsS	BN194_20150	K0N695	2.24	-3.20	-9.21376
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	fabZ_2	BN194_22620	K0NBT3	1.26	-2.95	-7.73612
>tr|K0NAP8|K0NAP8_LACCA ParC protein OS=Lactobacillus casei W56 GN=parC PE=4 SV=1	Phosphotransferase systems	K0NAP8		K0NAP8	0.48	-2.66	-6.31775
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	glpK	BN194_07280	K0N694	2.41	-2.62	-6.15061
Acyl carrier protein (ACP)	Lipid-related metabolism	acpP_2, acpP	BN194_22590	K0MX45	1.56	-2.37	-5.15417
PspC domain-containing protein	Unknown/uncharacterized	ythC	BN194_10300	K0N3H5	6.26	-2.18	-4.53194
Tautomerase (EC 5.3.2.-)	General prediction only		BN194_16890	K0MVQ1	0.43	-2.16	-4.47293
>tr|K0N2V4|K0N2V4_LACCA GlpO protein OS=Lactobacillus casei W56 GN=glpO PE=4 SV=1	Carbohydrate-related metabolism	glpO		K0N2V4	1.81	-2.15	-4.42955
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	accA	BN194_22470	K0NBS6	4.14	-2.13	-4.37493
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	pdhD	BN194_15110	K0N4P1	4.72	-2.00	-3.99914
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	pdhC	BN194_15100	K0N4W5	3.47	-1.93	-3.81097
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	pdhA	BN194_15080	K0N860	3.26	-1.84	-3.58696
Uncharacterized protein	Unknown/uncharacterized		BN194_29450	K0N932	2.77	-1.72	-3.29404
Lactaldehyde dehydrogenase (EC 1.2.1.21) (EC 1.2.1.22)	Cell defense/detoxification	aldA	BN194_25470	K0NCB9	2.70	-1.71	-3.2754
Uncharacterized oxidoreductase YrbE (EC 1.-.-.-)	Carbohydrate-related metabolism	yrbE	BN194_02280	K0N524	1.57	-1.67	-3.17659
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	rex_2,rex	BN194_23820	K0NBZ5	0.70	-1.64	-3.11027

Transcriptional regulatory protein spaR	Signal transduction	spaR	BN194_05330	K0N5S9	0.67	-1.56	-2.9512
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	pdhB	BN194_15090	K0MVA7	4.48	-1.56	-2.94272
UPF0337 protein yhjA	General prediction only	yhjA	BN194_24800	K0N7S1	1.79	-1.32	-2.49115
GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	0.47	-1.21	-2.31392
ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit) (F-ATPase epsilon subunit)	Membrane bioenergetics	atpC	BN194_13630	K0N7T2	0.79	-1.18	-2.27315
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	npr	BN194_04740	K0MSP8	2.95	-1.12	-2.17214
Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	0.33	-1.09	-2.13308
PTS system IIB component, Gat family	Phosphotransferase systems		BN194_07430	K0N6A5	2.57	-1.07	-2.09841
Uncharacterized protein ycaC	General prediction only	ycaC	BN194_29650	K0N948	3.67	-1.04	-2.05877
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	maa	BN194_30010	K0N8I9	0.59	-1.04	-2.05102
ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	atpF	BN194_13580	K0N7S9	1.15	-1.01	-2.01432
Pyruvate, phosphate dikinase (EC 2.7.9.1)	Central glycolytic/intermediary pathways	ppdK	BN194_24730	K0NAC6	0.84	-1.00	-1.99736
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	yabO	BN194_26520	K0NCR8	1.07	-0.97	-1.96302
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	nox_2	BN194_02850	K0N1N9	2.70	-0.96	-1.93966
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	rny	BN194_10100	K0N3E5	0.61	-0.90	-1.8653
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	tpx	BN194_08090	K0MTJ5	2.03	-0.90	-1.85979
Uncharacterized protein YxeH	General prediction only	yxeH	BN194_04750	K0N1Y7	1.21	-0.89	-1.85909
Glucitol operon repressor	Transcriptional regulation	srlR	BN194_28690	K0MYG3	0.38	-0.89	-1.84709
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	pcp	BN194_01980	K0N4Y4	2.00	-0.87	-1.82423
Chaperone protein ClpB	Protein folding/turnover	clpB_2	BN194_26350	K0N887	1.99	-0.84	-1.79076
50S ribosomal protein L32	Ribosomal proteins	rpmF	BN194_15510	K0N4T0	0.41	-0.83	-1.78175
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	yqeC	BN194_02330	K0N532	2.35	-0.83	-1.77488
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	murA2,murA	BN194_26780	K0NAR9	0.57	-0.80	-1.74004
Uncharacterized protein	Unknown/uncharacterized		BN194_20380	K0N9Q9	0.89	-0.75	-1.68594
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	ysgA	BN194_18610	K0N5M8	0.43	-0.75	-1.68395

Protein translocase subunit SecA	Protein export	secA	BN194_10170	K0N9J2	1.61	-0.74	-1.66707
DegV domain-containing protein CA_C1624	Unknown/uncharacterized		BN194_14170	K0NAD8	0.47	-0.73	-1.65906
Nucleic acid-binding protein	Unknown/uncharacterized		BN194_18680	K0N9D5	0.47	-0.73	-1.65559
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	lplJ	BN194_16640	K0MVN0	1.83	-0.73	-1.65477
Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	pox5	BN194_19670	K0NBB6	2.64	-0.73	-1.65432
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	1.28	-0.73	-1.65321
Protein LemA	Unknown/uncharacterized	lemA	BN194_27350	K0N8J7	4.18	-0.71	-1.6373
PTS system IIB component, L-Asc family	Phosphotransferase systems		BN194_28560	K0N861	0.10	-0.71	-1.63166
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	ispA	BN194_18180	K0N9A2	0.71	-0.70	-1.62589
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	phoU	BN194_10290	K0MTZ9	1.83	-0.70	-1.62485
Cell division protein FtsA	Cytokinesis	ftsA	BN194_14750	K0N4T3	1.85	-0.69	-1.61717
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	oppF	BN194_17910	K0N5I3	0.37	-0.69	-1.6157
>tr|K0N1M9|K0N1M9_LACCA Probable phosphoketolase OS=Lactobacillus casei W56 GN=xpkA PE=3 SV=1	Central glycolytic/intermediary pathways	xpkA		K0N1M9;K0N8X7	2.86	-0.69	-1.60917
UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	1.72	-0.66	-1.58098
Chaperone protein DnaJ	Protein folding/turnover	dnaJ	BN194_17450	K0N5J4	2.70	-0.64	-1.55781
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	carB	BN194_16450	K0N587	0.53	-0.63	-1.54538
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	act	BN194_16090	K0MVI3	1.38	-0.61	-1.52535
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	ohrR	BN194_10500	K0N3J7	1.50	-0.61	-1.52289
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	yhaA	BN194_30550	K0N9E4	0.84	-0.60	-1.51519
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	cap4C	BN194_12280	K0N7E3	2.31	-0.59	-1.5096
Transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	1.90	-0.59	-1.50601
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdE2	BN194_16600	K0N5A1	2.49	-0.59	-1.50059
>tr|K0NB98|K0NB98_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_19420 PE=4 SV=1	Unknown/uncharacterized	K0NB98		K0NB98	0.61	-0.58	-1.49608
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	frr	BN194_17650	K0N5M3	2.83	-0.57	-1.48867
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	dkgB	BN194_08260	K0N347	1.69	-0.54	-1.45523
Bifunctional protein GlmU	Cell wall biogenesis	glmU	BN194_26940	K0MY10	1.03	-0.51	-1.42784
ABC-type phosphate/phosphonate transport system,periplasmic component	ABC-type transporter systems		BN194_25680	K0NAI1	1.63	-0.51	-1.42587

Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	fhs	BN194_16520	K0NAT0	1.69	-0.51	-1.42441
Aldose 1-epimerase	Central glycolytic/intermediary pathways		BN194_16020	K0NAP4	1.58	-0.51	-1.42175
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	nusB	BN194_18220	K0NB49	0.50	-0.50	-1.41297
Cold shock protein CspA	Transcription-associated proteins	cspA	BN194_14820	K0NAH0	0.26	-0.50	-1.4117
Transcriptional regulator lytR	Transcriptional regulation	lytR_3	BN194_21700	K0N6U3	0.59	-0.49	-1.40734
Inososе dehydratase (EC 4.2.1.44) (2-keto-myo-inositol dehydratase)	Carbohydrate-related metabolism	iolE	BN194_02290	K0MS68	0.45	-0.49	-1.40647
Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	aspC	BN194_16770	K0NAU6	0.95	-0.49	-1.40537
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	proC	BN194_19900	K0N677	1.88	-0.49	-1.40012
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	hslV	BN194_16000	K0N542	2.74	-0.49	-1.39997
Uncharacterized protein	Unknown/uncharacterized		BN194_16650	K0N5A4	2.06	-0.48	-1.39406
50S ribosomal protein L35	Ribosomal proteins	rpmI	BN194_18810	K0N5P1	1.17	-0.47	-1.3856
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	atpA	BN194_13600	K0N4K1	1.78	-0.47	-1.38184
Uncharacterized protein	Lipid-related metabolism	YerQ	BN194_11980	K0N7B3	2.76	-0.47	-1.38041
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	manX_5	BN194_29720	K0NDL4	2.87	-0.46	-1.3722
Virulence factor mviM	General prediction only	mviM	BN194_13310	K0N4B2	0.96	-0.45	-1.36839
Protein QmcA	Unknown/uncharacterized	qmcA	BN194_12070	K0NA10	0.52	-0.44	-1.35994
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	clpE	BN194_19450	K0N644	1.95	-0.44	-1.35463
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	hslU	BN194_16010	K0N4Y1	1.98	-0.43	-1.35002
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	1.31	-0.43	-1.34964
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	rluB	BN194_15650	K0N509	1.50	-0.42	-1.33517
Transcriptional regulator, TetR family	Transcriptional regulation		BN194_12190	K0MUM1	2.84	-0.41	-1.33155
Maltose ABC transporter, periplasmic maltose-binding protein	ABC-type transporter systems		BN194_11200	K0N3U4	1.08	-0.41	-1.33135
D-ribose-binding protein	ABC-type transporter systems	rbsB	BN194_03290	K0MSF6	1.16	-0.41	-1.32899
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	metG	BN194_27130	K0NAU5	1.15	-0.41	-1.32472
Protein RecA (Recombinase A)	DNA repair/recombination	recA_2,recA	BN194_27650	K0N8P0	0.72	-0.41	-1.32411
RNA polymerase sigma factor SigA	RNA polymerase	rpoD,sigA	BN194_16920	K0NAV6	0.32	-0.39	-1.31265
Lipoprotein	ABC-type transporter systems	metQ_2	BN194_13740	K0MV23	2.67	-0.39	-1.31218

Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		BN194_08520	K0N972	0.38	-0.38	-1.30454
Cell division ATP-binding protein FtsE	Cytokinesis	ftsE	BN194_10190	K0MTZ2	1.46	-0.38	-1.30158
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	grpE	BN194_17470	K0NAZ2	1.54	-0.38	-1.29833
Sporulation initiation inhibitor protein soj	Cytokinesis	soj	BN194_02040	K0MS45	0.46	-0.38	-1.29802
Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	gntK	BN194_02340	K0MS76	1.39	-0.38	-1.2979
Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	Steap4	BN194_01990	K0MS41	0.89	-0.38	-1.2974
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	glgD	BN194_21590	K0MWU4	0.90	-0.37	-1.29434
Glutathione peroxidase	Cell defense/detoxification	gpo	BN194_09780	K0N6T6	1.22	-0.37	-1.29304
50S ribosomal protein L33	Ribosomal proteins	rpmG	BN194_20200	K0N697	1.01	-0.37	-1.29013
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	ftsH	BN194_26460	K0N7I8	1.98	-0.35	-1.27086
30S ribosomal protein S14	Ribosomal proteins	rpsN	BN194_09950	K0N3D1	0.54	-0.35	-1.27061
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE	BN194_02970	K0N7U7	1.05	-0.34	-1.26774
DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	gyrB	BN194_00060	K0N1B8	1.16	-0.34	-1.26588
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	rnc	BN194_17870	K0NB31	2.35	-0.34	-1.26369
Transcriptional regulator, XRE family	Transcriptional regulation		BN194_30170	K0NDP4	0.52	-0.33	-1.26007
30S ribosomal protein S20	Ribosomal proteins	rpsT	BN194_15250	K0N4X9	0.71	-0.33	-1.25472
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	guaB	BN194_02100	K0N1G3	1.99	-0.32	-1.2499
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	2.73	-0.32	-1.24506
Signal recognition particle protein (Fifty-four homolog)	Protein export	ffh	BN194_17820	K0NB27	0.63	-0.31	-1.24163
Penicillin-binding protein 1A	Cell wall biogenesis	ponA	BN194_16720	K0NAU3	0.40	-0.31	-1.23987
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	1.08	-0.31	-1.23789
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	ldh1,Idh	BN194_06970	K0N8S5	0.84	-0.29	-1.22502
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	glcK	BN194_18420	K0NB57	0.92	-0.29	-1.22426
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	pth	BN194_26550	K0N8B3	0.31	-0.29	-1.22212
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	galK	BN194_07340	K0MTA3	0.33	-0.29	-1.21872
ABC transporter, permease protein	ABC-type transporter systems		BN194_29810	K0N8H4	1.46	-0.28	-1.21725
30S ribosomal protein S11	Ribosomal proteins	rpsK	BN194_25970	K0NCJ0	0.49	-0.28	-1.21486

Cadmium efflux system accessory protein	Other transporter proteins	cadC	BN194_21540	K0MWU0	0.25	-0.28	-1.21252
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	0.53	-0.28	-1.21158
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	gpsB	BN194_16690	K0MVN5	0.90	-0.28	-1.21016
Uncharacterized protein	General prediction only		BN194_17420	K0NAY8	1.51	-0.27	-1.20835
Transcriptional regulatory protein YycF	Signal transduction	yycF_2	BN194_29510	K0N8E4	0.75	-0.27	-1.20646
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	fbp	BN194_21660	K0N6C3	1.20	-0.27	-1.20515
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	atpD	BN194_13620	K0NAB3	1.56	-0.27	-1.20483
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	aldB	BN194_20140	K0MWH5	0.48	-0.27	-1.20206
50S ribosomal protein L9	Ribosomal proteins	rplI	BN194_01130	K0N4K3	1.11	-0.26	-1.1953
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	murE	BN194_02160	K0N1S5	1.26	-0.25	-1.19312
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	der	BN194_15730	K0N8E1	1.45	-0.25	-1.19301
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	atpG	BN194_13610	K0N4D3	0.37	-0.25	-1.19059
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	htrA	BN194_29460	K0N8D9	1.10	-0.25	-1.18928
Dumpy	Cell surface proteins/internalins	dp	BN194_05390	K0MSV0	0.66	-0.25	-1.18912
Transcriptional regulator	Transcriptional regulation		BN194_08230	K0N6I4	0.44	-0.25	-1.18792
>tr|K0N8W1|K0N8W1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07270 PE=4 SV=1	Unknown/uncharacterized	K0N8W1		K0N8W1	0.28	-0.25	-1.18542
Uncharacterized protein	Unknown/uncharacterized		BN194_24010	K0N715	0.85	-0.24	-1.18292
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	potA	BN194_11290	K0MU90	1.56	-0.24	-1.18257
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	glgC	BN194_21600	K0N6T3	1.86	-0.24	-1.18136
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	ssdA	BN194_24140	K0MXE0	2.77	-0.24	-1.18078
2-oxoisovalerate dehydrogenase subunit beta (EC 1.2.4.4)	Lipid-related metabolism	bfmBAB	BN194_16390	K0MVK8	0.97	-0.24	-1.18065
Cellobiose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	celA_5	BN194_29600	K0N945	0.23	-0.24	-1.17919
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	mhqA_3	BN194_18760	K0N5N7	1.19	-0.23	-1.17553
Rod shape-determining protein MreB	Cytokinesis	mreB	BN194_14550	K0N4R7	0.20	-0.23	-1.17552
50S ribosomal protein L30	Ribosomal proteins	rpmD	BN194_26040	K0MXS6	1.91	-0.23	-1.17487

Chaperone protein ClpB	Protein folding/turnover	clpB	BN194_15500	K0N4Z8	1.89	-0.23	-1.1736
Uncharacterized protein YqhY	Unknown/uncharacterized	yqhY	BN194_18230	K0N9A7	0.64	-0.23	-1.17349
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	atpH	BN194_13590	K0MV16	1.38	-0.23	-1.17153
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		BN194_24180	K0NAA2	0.55	-0.23	-1.16952
Translation initiation factor IF-3	Protein translation (initiation)	infC	BN194_18820	K0NB73	0.68	-0.22	-1.16732
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	0.60	-0.22	-1.16678
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	0.46	-0.22	-1.16537
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		BN194_18780	K0N9E0	0.13	-0.22	-1.16508
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	gmk	BN194_18110	K0N5J6	0.37	-0.22	-1.16388
Protein ytsP	Signal transduction	ytsP	BN194_14450	K0N4Q9	0.14	-0.21	-1.16017
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	dacA	BN194_02140	K0MS53	0.62	-0.21	-1.15942
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		BN194_13770	K0NAC0	0.53	-0.21	-1.15614
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	rpoZ	BN194_18100	K0N5T7	0.45	-0.21	-1.1549
>tr|K0NBL8|K0NBL8_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_21520 PE=3 SV=1	Unknown/uncharacterized	K0NBL8		K0NBL8	1.08	-0.21	-1.15369
30S ribosomal protein S15	Ribosomal proteins	rpsO	BN194_15260	K0N4Q6	0.46	-0.21	-1.15369
FeS cluster assembly protein sufB	Cofactor-related metabolism	sufB	BN194_13810	K0N4E5	0.41	-0.20	-1.15264
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	glyA	BN194_13540	K0MV12	0.53	-0.20	-1.14893
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07700	K0N2V5	0.35	-0.20	-1.14845
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	trxB	BN194_10360	K0N3L1	0.60	-0.20	-1.14839
Putative secreted protein	cell wall biogenesis		BN194_02820	K0N7S8	0.17	-0.20	-1.14726
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	1.38	-0.20	-1.14693
30S ribosomal protein S13	Ribosomal proteins	rpsM	BN194_25980	K0NAK3	0.38	-0.20	-1.1459
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism	K0N6M0	BN194_22460	K0N6M0	0.40	-0.20	-1.14582
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07710	K0N2Z3	2.73	-0.19	-1.14472
>tr|K0N4Z7|K0N4Z7_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02080 PE=4 SV=1	Unknown/uncharacterized	K0N4Z7		K0N4Z7	0.42	-0.19	-1.14417
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	clpC	BN194_21680	K0N9Z7	0.19	-0.19	-1.14311

ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	clpX	BN194_15340	K0MVC6	0.75	-0.19	-1.14271
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	apt	BN194_17380	K0N902	0.37	-0.19	-1.14128
Glycerol-3-phosphate ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_11260	K0N3T6	0.63	-0.19	-1.13894
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	0.80	-0.19	-1.13738
2-dehydropantoate 2-reductase (EC 1.1.1.169) (Ketopantoate reductase)	Cofactor-related metabolism		BN194_16370	K0NAS0	0.30	-0.18	-1.13451
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	groL,groEL	BN194_23750	K0N7K7	1.39	-0.18	-1.13196
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	alaS	BN194_08480	K0N6K2	0.63	-0.18	-1.13047
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	hmgCS1	BN194_19680	K0N9K3	1.11	-0.18	-1.13011
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	clpP_2, clpP	BN194_10510	K0N3M4	0.43	-0.17	-1.12606
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	ilvE	BN194_21620	K0NBM4	0.69	-0.17	-1.12453
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	prfB	BN194_10180	K0N6W9	0.61	-0.17	-1.12404
30S ribosomal protein S5	Ribosomal proteins	rpsE	BN194_26050	K0N853	0.47	-0.17	-1.12188
50S ribosomal protein L2	Ribosomal proteins	rplB	BN194_26190	K0MXU1	0.56	-0.17	-1.12186
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	0.66	-0.16	-1.11843
Uncharacterized protein	General prediction only		BN194_21200	K0N6M8	2.10	-0.16	-1.11536
30S ribosomal protein S1 homolog	Ribosomal proteins	ypfD	BN194_15720	K0NAL9	0.28	-0.15	-1.11263
Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	ptp3	BN194_23520	K0NBX6	0.36	-0.15	-1.11147
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	queA	BN194_08370	K0N965	0.37	-0.15	-1.11105
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	ndk	BN194_08160	K0N340	0.06	-0.15	-1.10936
S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	metK	BN194_09150	K0N352	0.47	-0.15	-1.10837
30S ribosomal protein S12	Ribosomal proteins	rpsL	BN194_26290	K0MXV0	0.75	-0.14	-1.10496
30S ribosomal protein S9	Ribosomal proteins	rpsI	BN194_25840	K0MXR0	0.50	-0.14	-1.10469
Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	phoP	BN194_10220	K0N9J6	0.44	-0.14	-1.10292
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	prsA	BN194_19060	K0N5Q8	0.47	-0.14	-1.10241
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	pheS	BN194_18570	K0NB64	0.50	-0.14	-1.10109

Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	0.31	-0.14	-1.10094
50S ribosomal protein L11	Ribosomal proteins	rplK	BN194_24160	K0N724	0.55	-0.14	-1.09957
Translation initiation factor IF-2	Protein translation (initiation)	infB	BN194_17550	K0N5K7	0.53	-0.14	-1.09904
Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	adk	BN194_26010	K0N7F0	0.65	-0.13	-1.09677
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	gpsA	BN194_10350	K0N3I2	0.58	-0.13	-1.09649
50S ribosomal protein L1	Ribosomal proteins	rplA	BN194_24150	K0N7M7	0.80	-0.13	-1.09073
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	ydgI_2	BN194_16210	K0N508	0.22	-0.12	-1.08619
Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		BN194_20000	K0N684	0.56	-0.12	-1.086
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	prfA	BN194_13510	K0N4C6	0.25	-0.12	-1.08501
30S ribosomal protein S19	Ribosomal proteins	rpsS	BN194_26180	K0NAM1	0.38	-0.12	-1.08437
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	pgcA	BN194_10370	K0N9K8	0.53	-0.12	-1.08358
50S ribosomal protein L23	Ribosomal proteins	rplW	BN194_26200	K0N869	0.22	-0.11	-1.08248
50S ribosomal protein L10	Ribosomal proteins	rplJ	BN194_24090	K0MXD8	1.06	-0.11	-1.0823
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	hprK	BN194_10330	K0N6Y3	0.27	-0.11	-1.08137
Cell division protein FtsX	Cytokinesis	ftsX	BN194_10200	K0N3G0	0.07	-0.11	-1.08105
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	garB	BN194_27400	K0N8K3	1.14	-0.11	-1.07703
Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	0.46	-0.10	-1.07387
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	fpaP_3	BN194_21160	K0N682	0.26	-0.10	-1.0724
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	yhfP	BN194_07740	K0MTE1	0.18	-0.10	-1.07154
50S ribosomal protein L17	Ribosomal proteins	rplQ	BN194_25950	K0N841	0.06	-0.10	-1.07118
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	nagA	BN194_19890	K0MWF9	0.16	-0.10	-1.07017
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2,lacD	BN194_07480	K0N6A8	0.36	-0.10	-1.06864
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	hpt	BN194_26470	K0NCR2	0.10	-0.09	-1.06805
50S ribosomal protein L21	Ribosomal proteins	rplU	BN194_18290	K0MW61	0.04	-0.09	-1.06757
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	dnaN	BN194_00020	K0N6S3	0.23	-0.09	-1.06753
30S ribosomal protein S18	Ribosomal proteins	rpsR	BN194_00120	K0N6T2	0.05	-0.09	-1.06593

Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	0.27	-0.09	-1.06518
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	yfmL	BN194_12120	K0NA13	0.27	-0.09	-1.06434
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	trpS	BN194_27360	K0N7S4	0.33	-0.09	-1.06205
Regulatory protein vanR	Signal transduction	vanR	BN194_02120	K0N7G4	0.14	-0.09	-1.06109
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	rpoC	BN194_26330	K0NAN3	0.49	-0.08	-1.06027
GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	relA	BN194_17230	K0N8Y0	0.09	-0.08	-1.0599
>tr|K0N2W3|K0N2W3_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07360 PE=4 SV=1	Unknown/uncharacterized	K0N2W3		K0N2W3	0.29	-0.08	-1.05831
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	0.27	-0.08	-1.05738
Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	rbsK	BN194_03300	K0N1R2	0.16	-0.08	-1.05508
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		BN194_27170	K0NCZ6	0.34	-0.07	-1.05301
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	dnaK	BN194_17460	K0N5C7	0.20	-0.07	-1.05292
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	agaS	BN194_02940	K0MSD9	0.14	-0.07	-1.05174
50S ribosomal protein L31 type B	Ribosomal proteins	rpmE2	BN194_26770	K0NCV4	0.10	-0.07	-1.05095
Stage 0 sporulation protein J	Cytokinesis	spo0J	BN194_02050	K0N1F9	0.27	-0.07	-1.05087
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	prs1,prs	BN194_26930	K0NAT2	0.21	-0.07	-1.05038
50S ribosomal protein L3	Ribosomal proteins	rplC	BN194_26220	K0NCN1	0.38	-0.07	-1.04979
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	pyrG	BN194_26790	K0MXZ1	0.24	-0.07	-1.04862
Elongation factor P	Protein translation (elongation)	efp_2	BN194_22050	K0N712	0.07	-0.07	-1.04859
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		BN194_03130	K0N5D9	0.15	-0.07	-1.04806
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	gyrA	BN194_00070	K0N6S7	0.09	-0.07	-1.04738
50S ribosomal protein L20	Ribosomal proteins	rplT	BN194_18800	K0N5Y4	0.19	-0.07	-1.04637
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	0.40	-0.06	-1.04548
Phosphatase YidA (EC 3.1.3.-)	General prediction only	yidA	BN194_28520	K0NDD5	0.46	-0.06	-1.04223
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	patB_2	BN194_09790	K0MTW3	0.11	-0.06	-1.04163

30S ribosomal protein S7	Ribosomal proteins	rpsG	BN194_26280	K0NAM9	0.36	-0.06	-1.04148
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC	BN194_24670	K0NC50	0.17	-0.06	-1.04026
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	0.11	-0.06	-1.0401
50S ribosomal protein L15	Ribosomal proteins	rplO	BN194_26030	K0NAK7	0.12	-0.06	-1.0397
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	murI	BN194_08640	K0MTN4	0.18	-0.06	-1.03919
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	pfkA	BN194_15570	K0NAK6	0.15	-0.06	-1.0389
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	ftsY	BN194_17850	K0N5R8	0.10	-0.05	-1.03866
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	polA	BN194_18930	K0N9E7	0.09	-0.05	-1.03809
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	murD	BN194_14720	K0NAG5	0.14	-0.05	-1.03746
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	prs1_2	BN194_30370	K0NDQ5	0.17	-0.05	-1.03712
tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	dus1	BN194_26390	K0MXV9	0.24	-0.05	-1.03571
DNA-binding protein HU	DNA replication-related	hup	BN194_15740	K0MVF4	0.08	-0.05	-1.03558
50S ribosomal protein L27	Ribosomal proteins	rpmA	BN194_18270	K0NB51	0.03	-0.05	-1.03362
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	0.07	-0.05	-1.03175
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	rpoA	BN194_25960	K0N7E5	0.10	-0.04	-1.03149
Septum site-determining protein DivIVA	Cytokinesis	divIVA	BN194_14800	K0N4T8	0.03	-0.04	-1.03092
30S ribosomal protein S10	Ribosomal proteins	rpsJ	BN194_26230	K0NAM5	0.22	-0.04	-1.02938
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	0.14	-0.04	-1.02895
50S ribosomal protein L4	Ribosomal proteins	rplD	BN194_26210	K0N7H0	0.13	-0.04	-1.02826
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	yclJ	BN194_11790	K0MUE5	0.11	-0.04	-1.02707
HTH-type transcriptional repressor yvoA	Transcriptional regulation	yvoA_2	BN194_19880	K0N9L8	0.04	-0.04	-1.0263
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	pheT	BN194_18560	K0N5M4	0.10	-0.04	-1.02477
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	lacC	BN194_07470	K0N8Y4	0.12	-0.04	-1.02476
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	pyrH	BN194_17660	K0N5E6	0.05	-0.03	-1.02242

Inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase (EC 1.1.1.18) (EC 1.1.1.369) (Myo-inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase)	Carbohydrate-related metabolism	iolG	BN194_02270	K0N7J1	0.02	-0.03	-1.02081
50S ribosomal protein L24	Ribosomal proteins	rplX	BN194_26110	K0N7F9	0.05	-0.03	-1.01955
30S ribosomal protein S8	Ribosomal proteins	rpsH	BN194_26080	K0NAL1	0.06	-0.03	-1.01754
30S ribosomal protein S4	Ribosomal proteins	rpsD	BN194_14440	K0MV63	0.10	-0.02	-1.01725
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	ybeY	BN194_17010	K0N594	0.10	-0.02	-1.0161
Oligoendopeptidase F	Amino acid-related metabolism	yjbG_2	BN194_08130	K0N6H7	0.14	-0.02	-1.01433
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	glmM	BN194_11550	K0N3Y7	0.09	-0.02	-1.01425
Bifunctional protein FolD	Cofactor-related metabolism	folD	BN194_18210	K0N5K0	0.12	-0.02	-1.0137
Cell division protein FtsZ	Cytokinesis	ftsZ	BN194_14760	K0N4L6	0.05	-0.02	-1.01365
NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	0.08	-0.02	-1.01317
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	pepS	BN194_12180	K0N7D5	0.02	-0.02	-1.01306
30S ribosomal protein S21	Ribosomal proteins	rpsU	BN194_17050	K0N5E5	0.04	-0.02	-1.01229
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	map	BN194_12230	K0N7E0	0.04	-0.02	-1.01198
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	rnjA	BN194_15020	K0NAH6	0.03	-0.01	-1.01011
Ribosome-binding ATPase YchF	Protein translation (peptide release)	engD,ychF	BN194_02070	K0N7F7	0.09	-0.01	-1.00967
MreB-like protein	Cytokinesis	mbl	BN194_13650	K0N4K5	0.04	-0.01	-1.00841
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	lacB	BN194_07490	K0MTB7	0.05	-0.01	-1.00819
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	ywpJ	BN194_11320	K0N9U2	0.03	-0.01	-1.0081
Uncharacterized protein ACIAD3023	Cell defense/detoxification		BN194_07010	K0N2T5	0.02	-0.01	-1.00754
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	sph	BN194_04930	K0N5Q0	0.01	-0.01	-1.00734
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	iolS	BN194_29680	K0NB94	0.02	-0.01	-1.00679
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatB	BN194_11970	K0NA01	0.04	-0.01	-1.00678

(1c) Protein FC >2 Citrate Vs control P1

Protein names	Functional Class	Gene	Gene locu	Protein IDs	-Log t-test p-value	t test Difference	Fold change
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	yacO	BN194_24420	K0NC34	4.6638	5.42286	42.89864
>tr|K0N8W1|K0N8W1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07270 PE=4 SV=1	Unknown/uncharacterized	K0N8W1		K0N8W1	5.02873	5.40597	42.39934
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	pycB	BN194_20290	K0MWI8	6.31014	5.13037	35.02638
Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	ADH2	BN194_08400	K0N307	4.66261	5.06799	33.54417
>tr|K0N7I1|K0N7I1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02220 PE=4 SV=1	Unknown/uncharacterized	K0N7I1		K0N7I1	5.46488	4.62222	24.62787
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	citF	BN194_20310	K0N607	4.22118	4.25077	19.03747
Uncharacterized oxidoreductase YrbE (EC 1.-.-.-)	Carbohydrate-related metabolism	yrbE	BN194_02280	K0N524	4.08326	4.15529	17.81833
>tr|K0N518|K0N518_LACCA IolA protein OS=Lactobacillus casei W56 GN=iolA PE=3 SV=1	Carbohydrate-related metabolism	iolA		K0N518	3.43084	4.02729	16.30554
3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase (THcHDO hydrolase) (EC 3.7.1.22)	Carbohydrate-related metabolism	iolD	BN194_02260	K0N1T3	2.73233	3.91891	15.12549
5-dehydro-2-deoxygluconokinase (EC 2.7.1.92) (2-deoxy-5-keto-D-gluconate kinase)	Carbohydrate-related metabolism	iolC	BN194_02250	K0N1H4	4.35106	3.66084	12.64802
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	citE	BN194_20320	K0NBF4	2.47106	3.49367	11.26418
Uncharacterized protein ACIAD3023	Cell defense/detoxification		BN194_07010	K0N2T5	4.28405	3.43922	10.84697
Biotin carboxyl carrier protein	Tricarboxylic acid pathway	bcc	BN194_20370	K0NBF7	2.81062	3.27419	9.674519
Inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase (EC 1.1.1.18) (EC 1.1.1.369) (Myo-inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase)	Carbohydrate-related metabolism	iolG	BN194_02270	K0N7J1	3.13941	3.23479	9.413884
PTS system IIB component, L-Asc family	Phosphotransferase systems		BN194_28560	K0N861	0.829562	3.07272	8.413581

Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	citD	BN194_20330	K0N9Q5	1.94243	2.99536	7.974312
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	fbp	BN194_21660	K0N6C3	4.87863	2.90072	7.46799
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	pflB	BN194_16080	K0N8I5	5.85455	2.88203	7.371867
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	citX	BN194_20300	K0N6A3	2.58407	2.7275	6.62307
Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	pox5	BN194_19670	K0NBB6	5.38681	2.65123	6.282026
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	ldh1,ldh	BN194_06970	K0N8S5	3.40554	2.63966	6.231848
Aldose 1-epimerase (EC 5.1.3.3)	Central glycolytic/intermediary pathways		BN194_07390	K0MTA8	4.53696	2.60558	6.086361
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	pdhD	BN194_15110	K0N4P1	4.92016	2.56146	5.903048
Uncharacterized protein	Unknown/uncharacterized		BN194_01760	K0N1N3	4.73049	2.50981	5.695451
>tr|K0N2V4|K0N2V4_LACCA GlpO protein OS=Lactobacillus casei W56 GN=glpO PE=4 SV=1	Carbohydrate-related metabolism	glpO		K0N2V4	4.68128	2.46679	5.528124
>tr|K0N7B1|K0N7B1_LACCA Acetate kinase OS=Lactobacillus casei W56 GN=ackA PE=3 SV=1	Central glycolytic/intermediary pathways	ackA		K0N7B1;K0N6W4	3.61925	2.46033	5.503426
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	Posttranslational modification	citC	BN194_20340	K0MWJ1	3.87239	2.36091	5.136943
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	pdhC	BN194_15100	K0N4W5	4.6591	2.29261	4.899417
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	ssdA	BN194_24140	K0MXE0	4.4643	2.24641	4.745006
Pyruvate, phosphate dikinase (EC 2.7.9.1)	Central glycolytic/intermediary pathways	ppdK	BN194_24730	K0NAC6	1.85656	2.23446	4.705865
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		BN194_24180	K0NAA2	3.7252	2.14808	4.432375
Cadmium efflux system accessory protein	Other transporter proteins	cadC	BN194_21540	K0MWU0	2.00075	2.03792	4.10653
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	glpK	BN194_07280	K0N694	4.36535	2.01615	4.045029
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	dhaK_2	BN194_04980	K0N5Q3	3.26987	2.00687	4.019093
Glutathione peroxidase	Cell defense/detoxification	gpo	BN194_09780	K0N6T6	3.8705	2.00059	4.001636

3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	fabG	BN194_22560	K0N6N3	1.90107	1.98872	3.968847
Lactaldehyde dehydrogenase (EC 1.2.1.21) (EC 1.2.1.22)	Cell defense/detoxification	aldA	BN194_25470	K0NCB9	3.91351	1.96694	3.90938
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	ilvE	BN194_21620	K0NBM4	4.53407	1.96402	3.901476
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	Cell wall biogenesis	glmS	BN194_11560	K0N3V9	3.49847	1.96387	3.90107
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	dkgB	BN194_08260	K0N347	4.81605	1.96214	3.896395
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	fabZ_2	BN194_22620	K0NBT3	0.914048	1.95379	3.873909
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	pdhA	BN194_15080	K0N860	4.1409	1.94022	3.837642
Uncharacterized protein yghZ	General prediction only	yghZ	BN194_27510	K0N7U8	3.14055	1.93651	3.827786
Probable dipeptidase (EC 3.4.-.-)	Amino acid-related metabolism		BN194_23190	K0MXA1	0.565819	1.88268	3.687594
Histidinol-phosphatase	General prediction only		BN194_14010	K0N4F8	1.92675	1.85224	3.610604
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	pdhB	BN194_15090	K0MVA7	4.97062	1.8241	3.54086
Uncharacterized protein	Unknown/uncharacterized		BN194_11770	K0N9Y6	3.70971	1.79054	3.459444
Maltose ABC transporter, periplasmic maltose-binding protein	ABC-type transporter systems		BN194_11200	K0N3U4	3.24268	1.77167	3.41449
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	galE	BN194_07350	K0N2R3	4.05789	1.75691	3.379735
Uncharacterized protein	Central glycolytic/intermediary pathways		BN194_04970	K0N8A3	2.63116	1.73997	3.340282
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	dhaM	BN194_04960	K0N2C2	4.00471	1.73428	3.327134
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	mhqA_3	BN194_18760	K0N5N7	3.36079	1.71948	3.293177
Uncharacterized protein	Unknown/uncharacterized		BN194_24010	K0N715	3.34552	1.70341	3.256698
Inosose dehydratase (EC 4.2.1.44) (2-keto-myo-inositol dehydratase)	Carbohydrate-related metabolism	iolE	BN194_02290	K0MS68	4.32207	1.64697	3.131752
>tr|K0N8X1|K0N8X1_LACCA Galactose-1-phosphate uridylyltransferase OS=Lactobacillus casei W56 GN=galT PE=3 SV=1	Carbohydrate-related metabolism	K0N8X1		K0N8X1	4.01992	1.64145	3.119792
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	garB	BN194_27400	K0N8K3	5.2154	1.63852	3.113463

Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	htrA	BN194_29460	K0N8D9	3.37839	1.57539	2.98016
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	pta	BN194_11340	K0MU95	4.30476	1.54154	2.911051
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)	Lipid-related metabolism	accC	BN194_22510	K0N6M5	3.73825	1.53865	2.905225
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	galK	BN194_07340	K0MTA3	1.97677	1.5092	2.846522
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	iolS	BN194_29680	K0NB94	4.41607	1.46029	2.751637
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		BN194_18780	K0N9E0	1.70636	1.44886	2.729923
Probable L-ascorbate-6-phosphate lactonase ulaG (EC 3.1.1.-)	Carbohydrate-related metabolism	ulaG	BN194_28590	K0MYF8	3.59828	1.44355	2.719893
Uncharacterized protein ycaC	General prediction only	ycaC	BN194_29650	K0N948	4.12921	1.43601	2.705715
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	glyr1	BN194_30100	K0N992	3.05455	1.42414	2.683545
Uncharacterized protein	Unknown/uncharacterized		BN194_01870	K0N7D4	1.25286	1.40778	2.653286
>tr|K0N2W3|K0N2W3_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07360 PE=4 SV=1	Unknown/uncharacterized	K0N2W3		K0N2W3	3.56685	1.40776	2.653249
Phosphatase YidA (EC 3.1.3.-)	General prediction only	yidA	BN194_28520	K0NDD5	4.42798	1.39017	2.621096
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	agl	BN194_27950	K0N8T1	3.9277	1.34103	2.533321
Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	fhs	BN194_16520	K0NAT0	3.65659	1.33749	2.527113
Acyl carrier protein (ACP)	Lipid-related metabolism	acpP_2, acpP	BN194_22590	K0MX45	1.24767	1.32768	2.509987
DegV domain-containing protein CA_C1624	Unknown/uncharacterized		BN194_14170	K0NAD8	0.782001	1.32085	2.498133
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	cysK	BN194_05520	K0N8E6	4.15838	1.29397	2.452019
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	ydgI_2	BN194_16210	K0N508	3.46503	1.28699	2.440184
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	glyA	BN194_13540	K0MV12	3.73597	1.27325	2.417054
HTH-type transcriptional repressor yvoA	Transcriptional regulation	yvoA_2	BN194_19880	K0N9L8	1.49921	1.20427	2.304206
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC	BN194_00080	K0N486	2.79376	1.20303	2.302227
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	hslU	BN194_16010	K0N4Y1	4.05445	1.19148	2.283869
UPF0337 protein lp_1708	General prediction only		BN194_05810	K0N2J8	1.47008	1.17584	2.259244
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	thiD_2	BN194_07650	K0N2U9	1.92995	1.16175	2.237286
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	yhfP	BN194_07740	K0MTE1	1.90869	1.1601	2.234729

Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	hmgCS1	BN194_19680	K0N9K3	4.51344	1.15743	2.230597
Uncharacterized protein	Unknown/uncharacterized		BN194_28350	K0N8V3	2.20182	1.14164	2.206317
Penicillin acylase (EC 3.5.1.11)	Cell defense/detoxification		BN194_04910	K0N2B8	2.87616	1.1375	2.199995
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	3.86089	1.07395	2.105189
Transcriptional regulatory protein spaR	Signal transduction	spaR	BN194_05330	K0N5S9	0.488993	1.04032	2.056684
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	mtlF	BN194_30410	K0N8N0	1.84042	1.03178	2.044545
Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	plsX	BN194_17940	K0MW37	0.445643	1.01451	2.020217
Oligoendopeptidase, pepF/M3 family	Amino acid-related metabolism		BN194_11580	K0N779	2.17516	1.01448	2.020175
Elongation factor P	Protein translation (elongation)	efp_2	BN194_22050	K0N712	1.85619	1.00746	2.010369
>tr|K0N788|K0N788_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_22500 PE=4 SV=1	Unknown/uncharacterized	K0N788		K0N788	1.45474	1.00653	2.009073
FMN-binding domain protein	General prediction only		BN194_24320	K0NC29	2.10794	1.00349	2.004844
Uncharacterized protein yueI	Unknown/uncharacterized	yueI	BN194_13920	K0NAC7	1.13824	1.00275	2.003816
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	apbE_3	BN194_21550	K0N6S8	1.89	1.00	2.00

(1d) Protein FC <2 Citrate Vs control P1

Protein names	**Functional Class**	**Gene**	**Gene locu**	**Protein IDs**	**-Log t-test p-value**	**t-test Difference**	**Fold change**
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	nox_2	BN194_02850	K0N1N9	2.67	0.99	1.99
Protein hit	tRNA aminoacyl synthesis	hit	BN194_19040	K0MWA8	2.22	0.97	1.96
UPF0092 membrane protein yrbF	Protein export	yrbF	BN194_08390	K0MTL6	0.42	0.97	1.96
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	phoU	BN194_10290	K0MTZ9	2.63	0.97	1.95

Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	rp2	BN194_17060	K0N598	2.08	0.95	1.93
Predicted hydrolase of the HAD superfamily	General prediction only	mtlD	BN194_30450	K0N9D4	3.09	0.94	1.92
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	pyc	BN194_15170	K0NAI2	2.69	0.94	1.92
Mannose permease IID component	Phosphotransferase systems	manZ	BN194_02990	K0MSE1	0.91	0.93	1.91
Uncharacterized protein	Unknown/uncharacterized		BN194_20380	K0N9Q9	0.88	0.93	1.90
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	11E,P100	BN194_02180	K0N513	2.10	0.92	1.89
Uncharacterized protein ypuA	Unknown/uncharacterized	ypuA	BN194_27250	K0N8I3	2.51	0.91	1.88
>tr|K0N1K5|K0N1K5_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_01360 PE=4 SV=1	Unknown/uncharacterized	K0N1K5		K0N1K5	0.64	0.91	1.88
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	ung	BN194_11330	K0N758	0.61	0.91	1.87
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	sph	BN194_04930	K0N5Q0	1.77	0.90	1.87
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	gnd	BN194_18660	K0N5N2	2.47	0.89	1.85
Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	rpiA_2, ripA	BN194_28600	K0N8W9	0.32	0.88	1.85
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	mhqD	BN194_18770	K0NB71	2.39	0.88	1.84
Transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	2.46	0.88	1.84
Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	bceA_2	BN194_21230	K0N9X1	0.73	0.87	1.83
Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	ptp3	BN194_23520	K0NBX6	2.39	0.87	1.83
Chaperone protein ClpB	Protein folding/turnover	clpB_2	BN194_26350	K0N887	3.04	0.87	1.83
Septum site-determining protein DivIVA	Cytokinesis	divIVA	BN194_14800	K0N4T8	1.62	0.86	1.82
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	fruA_4	BN194_27690	K0MY77	1.84	0.86	1.82
Uncharacterized protein	Unknown/uncharacterized		BN194_08190	K0MTK3	1.98	0.85	1.81
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	yclJ	BN194_11790	K0MUE5	2.46	0.85	1.80
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	1.89	0.84	1.79
Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	0.43	0.84	1.79
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	tpx	BN194_08090	K0MTJ5	2.65	0.84	1.79
Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	Steap4	BN194_01990	K0MS41	1.23	0.84	1.79

Redox-sensing transcriptional repressor Rex	Transcriptional regulation	rex_2,rex	BN194_23820	K0NBZ5	1.30	0.81	1.75
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	deoD	BN194_02810	K0N1Z0	2.37	0.81	1.75
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	alsS	BN194_20150	K0N695	3.45	0.80	1.74
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	asd	BN194_01060	K0N1I5	2.39	0.79	1.73
Protein lacX, plasmid	Carbohydrate-related metabolism	lacX	BN194_27070	K0NCY0	2.85	0.78	1.72
Uncharacterized protein	General prediction only		BN194_17420	K0NAY8	1.93	0.77	1.71
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	thyA	BN194_15800	K0N522	2.96	0.77	1.71
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	lplJ	BN194_16640	K0MVN0	2.32	0.77	1.71
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	2.25	0.75	1.68
Uncharacterized protein YwcC	Carbohydrate-related metabolism	ywcC	BN194_09930	K0N6V0	2.44	0.73	1.66
Cell division ATP-binding protein FtsE	Cytokinesis	ftsE	BN194_10190	K0MTZ2	2.46	0.72	1.64
Thioredoxin	Posttranslational modification	trxA_2	BN194_08570	K0N975	2.04	0.71	1.63
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	polA	BN194_18930	K0N9E7	1.04	0.70	1.63
Sporulation initiation inhibitor protein soj	Cytokinesis	soj	BN194_02040	K0MS45	3.24	0.69	1.61
GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	relA	BN194_17230	K0N8Y0	1.22	0.67	1.59
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdE2	BN194_16600	K0N5A1	2.80	0.65	1.57
UPF0478 protein SAOUHSC_01855	Signal transduction		BN194_08710	K0N365	1.20	0.64	1.56
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	pgcA	BN194_10370	K0N9K8	2.79	0.63	1.55
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	ysgA	BN194_18610	K0N5M8	0.75	0.63	1.55
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	hslV	BN194_16000	K0N542	1.24	0.63	1.54
Transcriptional regulator, xre family	Transcriptional regulation		BN194_23510	K0N6Y7	1.52	0.61	1.53
>tr|K0N2Q1|K0N2Q1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_06460 PE=4 SV=1;>tr|K0MXJ1|K0MXJ1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_24990 PE=4 SV=1	Unknown/uncharacterized	K0N2Q1		K0N2Q1;K0MXJ1	1.43	0.61	1.53

Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	msrA_2,msrA	BN194_15860	K0N4W6	1.46	0.60	1.52
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC_2,deoC	BN194_02790	K0MSB5	1.97	0.60	1.52
Thioredoxin-like protein ytpP	Posttranslational modification	ytpP	BN194_18980	K0N9F1	2.46	0.60	1.51
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	ycnE	BN194_13230	K0N7R3	1.25	0.59	1.51
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	mtlD_3mtlD	BN194_30400	K0N9C8	1.41	0.58	1.50
Mannose permease IID component	Phosphotransferase systems	manZ_9	BN194_29700	K0N954	1.15	0.57	1.49
Aldose 1-epimerase	Central glycolytic/intermediary pathways		BN194_16020	K0NAP4	1.68	0.56	1.47
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	2.11	0.55	1.47
>tr|K0N7I6|K0N7I6_LACCA Glucose-6-phosphate isomerase OS=Lactobacillus casei W56 GN=pgi PE=3 SV=1	Central glycolytic/intermediary pathways	pgi		K0N7I6;K0N4A6	1.91	0.55	1.46
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	1.17	0.55	1.46
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	glgD	BN194_21590	K0MWU4	1.48	0.54	1.46
DNA-binding protein HU	DNA replication-related	hup	BN194_15740	K0MVF4	1.29	0.54	1.45
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	fabZ	BN194_22520	K0NBS8	2.85	0.53	1.44
Uncharacterized protein YxeH	General prediction only	yxeH	BN194_04750	K0N1Y7	1.29	0.52	1.44
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		BN194_13770	K0NAC0	1.03	0.52	1.43
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	pth	BN194_26550	K0N8B3	0.42	0.51	1.42
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	hprK	BN194_10330	K0N6Y3	1.45	0.50	1.42
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	ispA	BN194_18180	K0N9A2	1.16	0.50	1.41
Cell division protein FtsA	Cytokinesis	ftsA	BN194_14750	K0N4T3	1.23	0.50	1.41
Signal recognition particle protein (Fifty-four homolog)	Protein export	ffh	BN194_17820	K0NB27	2.85	0.49	1.40
Bifunctional protein FolD	Cofactor-related metabolism	folD	BN194_18210	K0N5K0	2.04	0.49	1.40
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	coaD	BN194_15200	K0N4X3	3.38	0.48	1.40
Nucleic acid-binding protein	Unknown/uncharacterized		BN194_18680	K0N9D5	0.51	0.48	1.39

30S ribosomal protein S14	Ribosomal proteins	rpsN	BN194_09950	K0N3D1	0.42	0.48	1.39
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		BN194_21400	K0N6R1	1.38	0.48	1.39
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		BN194_27170	K0NCZ6	2.21	0.47	1.39
Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	phoP	BN194_10220	K0N9J6	1.07	0.47	1.39
Virulence factor mviM	General prediction only	mviM	BN194_13310	K0N4B2	1.10	0.47	1.39
Regulatory protein vanR	Signal transduction	vanR	BN194_02120	K0N7G4	1.94	0.47	1.39
Non-specific ribonucleoside hydrolase rihC (EC 3.2.-.-)	Nucleic acid/nucleotide metabolism	rihC	BN194_03870	K0N803	0.46	0.47	1.38
Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (Guanine insertion enzyme) (tRNA-guanine transglycosylase)	tRNA/Ribosome assembly/processing	tgt	BN194_08380	K0N6J4	0.34	0.46	1.38
Glucitol operon repressor	Transcriptional regulation	srlR	BN194_28690	K0MYG3	1.74	0.45	1.37
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	patB_2	BN194_09790	K0MTW3	1.39	0.45	1.36
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	pepV	BN194_08800	K0N324	1.29	0.44	1.35
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	accB	BN194_22530	K0NA35	0.67	0.43	1.35
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	2.28	0.42	1.34
Stage 0 sporulation protein J	Cytokinesis	spo0J	BN194_02050	K0N1F9	1.42	0.42	1.34
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	2.32	0.42	1.34
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	pepS	BN194_12180	K0N7D5	1.00	0.42	1.33
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	ykwC	BN194_02520	K0N7M3	0.69	0.41	1.33
>tr|K0N699|K0N699_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA PE=3 SV=1;>tr|K0MWW4|K0MWW4_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA_2 PE=3 SV=1	Cell wall biogenesis	rmlA		K0N699;K0MWW4	1.17	0.40	1.32
Uncharacterized protein yutG	Lipid-related metabolism	yutG	BN194_08940	K0MTQ3	2.50	0.39	1.31
Predicted hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	0.61	0.38	1.30
Oligoendopeptidase F	Amino acid-related metabolism	yjbG_2	BN194_08130	K0N6H7	1.72	0.38	1.30
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	yuxL	BN194_19910	K0N5X4	2.41	0.38	1.30
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	1.12	0.38	1.30
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	yabO	BN194_26520	K0NCR8	0.61	0.37	1.30

Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	zwf	BN194_08420	K0N966	0.78	0.37	1.30
PspC domain-containing protein	Unknown/uncharacterized	ythC	BN194_10300	K0N3H5	3.35	0.37	1.29
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	fabK	BN194_22580	K0NA38	0.74	0.37	1.29
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	aldB	BN194_20140	K0MWH5	0.65	0.36	1.28
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	pcp	BN194_01980	K0N4Y4	1.93	0.35	1.28
Uncharacterized protein	General prediction only		BN194_21200	K0N6M8	0.64	0.35	1.28
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	rnc	BN194_17870	K0NB31	3.07	0.35	1.27
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	manX_5	BN194_29720	K0NDL4	1.72	0.35	1.27
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	deoB	BN194_02800	K0N1N0	2.32	0.35	1.27
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_3	BN194_21440	K0MWS9	0.61	0.34	1.27
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	agaS	BN194_02940	K0MSD9	1.51	0.34	1.27
Cellobiose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	celA_5	BN194_29600	K0N945	0.26	0.33	1.26
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	purB	BN194_12520	K0NA41	1.26	0.33	1.26
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	1.39	0.33	1.26
Glycerol-3-phosphate ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_11260	K0N3T6	1.38	0.33	1.25
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	rny	BN194_10100	K0N3E5	0.70	0.33	1.25
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	murI	BN194_08640	K0MTN4	0.83	0.32	1.25
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	0.94	0.31	1.24
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	glgC	BN194_21600	K0N6T3	1.23	0.31	1.24
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	carB	BN194_16450	K0N587	1.51	0.30	1.23
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	rpe	BN194_18000	K0N5T1	1.44	0.30	1.23
Rod shape-determining protein MreB	Cytokinesis	mreB	BN194_14550	K0N4R7	0.36	0.30	1.23
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	dut	BN194_24640	K0MXG3	1.19	0.29	1.23

Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	nfo	BN194_17070	K0NAW5	0.27	0.29	1.22
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	0.93	0.29	1.22
Cell division protein FtsX	Cytokinesis	ftsX	BN194_10200	K0N3G0	0.20	0.28	1.22
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	proC	BN194_19900	K0N677	1.09	0.28	1.22
Putative nrdI-like protein	Nucleic acid/nucleotide metabolism		BN194_08250	K0N300	1.37	0.28	1.21
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	fabF	BN194_22540	K0MX40	0.47	0.27	1.21
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	bkr4	BN194_22550	K0N799	1.08	0.26	1.20
UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	1.28	0.26	1.19
Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		BN194_08520	K0N972	0.27	0.25	1.19
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	ddl	BN194_01390	K0MRY4	0.29	0.24	1.18
Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	0.92	0.24	1.18
Protein QmcA	Unknown/uncharacterized	qmcA	BN194_12070	K0NA10	0.39	0.24	1.18
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	cysS	BN194_24430	K0NAB2	1.31	0.23	1.18
Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	1.16	0.23	1.17
Glycosyl transferase family protein	Cell wall biogenesis		BN194_02420	K0N7L2	0.24	0.23	1.17
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	ywpJ	BN194_11320	K0N9U2	0.89	0.23	1.17
Cell division protein FtsZ	Cytokinesis	ftsZ	BN194_14760	K0N4L6	1.69	0.22	1.17
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	1.57	0.22	1.17
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	pmi	BN194_02920	K0N7U2	0.43	0.22	1.17
Single-stranded DNA-binding protein (SSB)	DNA replication-related	ssb	BN194_00110	K0N1C2	0.39	0.22	1.16
Uncharacterized protein ykuJ	Unknown/uncharacterized	ykuJ	BN194_09100	K0N348	0.33	0.21	1.16
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		BN194_08960	K0N387	0.59	0.21	1.16
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	1.06	0.19	1.14
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	pyrC	BN194_16470	K0NAS6	0.09	0.19	1.14
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	manD	BN194_02950	K0N1P4	1.19	0.18	1.14
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	gpsA	BN194_10350	K0N3I2	0.62	0.18	1.13

Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		BN194_20000	K0N684	1.25	0.18	1.13
Cold shock-like protein CspLA	Transcription-associated proteins	cspLA	BN194_12460	K0N438	0.12	0.17	1.12
Probable catabolite control protein A	Transcriptional regulation	ccpA	BN194_08750	K0N323	0.66	0.17	1.12
Protein RecA (Recombinase A)	DNA repair/recombination	recA_2,recA	BN194_27650	K0N8P0	0.19	0.16	1.12
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	0.78	0.16	1.12
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	yhaA	BN194_30550	K0N9E4	0.37	0.16	1.11
50S ribosomal protein L9	Ribosomal proteins	rplI	BN194_01130	K0N4K3	0.46	0.16	1.11
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	murE	BN194_02160	K0N1S5	0.73	0.15	1.11
Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	0.72	0.15	1.11
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		BN194_03130	K0N5D9	0.41	0.14	1.10
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdF	BN194_16610	K0N552	0.34	0.14	1.10
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatB	BN194_11970	K0NA01	0.39	0.13	1.10
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	pncB	BN194_19860	K0N5X0	0.48	0.13	1.10
Acetyltransferase	General prediction only		BN194_08200	K0N2Z8	0.21	0.13	1.09
Aspartate racemase (EC 5.1.1.13)	Amino acid-related metabolism		BN194_02170	K0N7H2	0.27	0.13	1.09
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	yqjQ(K0N8A1)	BN194_15480	K0N8A1	0.06	0.11	1.08
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	0.39	0.10	1.07
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	rluB	BN194_15650	K0N509	0.11	0.10	1.07
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	frr	BN194_17650	K0N5M3	0.36	0.09	1.07
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	glmM	BN194_11550	K0N3Y7	0.48	0.09	1.07
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE	BN194_02970	K0N7U7	0.21	0.09	1.06
Uncharacterized protein YqhY	Unknown/uncharacterized	yqhY	BN194_18230	K0N9A7	0.15	0.08	1.06
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	prs1,prs	BN194_26930	K0NAT2	0.15	0.08	1.06
ABC-type uncharacterized transport system, ATPase component	ABC-type transporter systems		BN194_07730	K0N6C9	0.16	0.08	1.06

DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	rpoZ	BN194_18100	K0N5T7	0.13	0.08	1.06
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	patA_2	BN194_22950	K0N7F8	0.09	0.07	1.05
UPF0342 protein yheA	Unknown/uncharacterized	yheA	BN194_19080	K0N9F7	0.07	0.07	1.05
Transcriptional regulator lytR	Transcriptional regulation	lytR_3	BN194_21700	K0N6U3	0.23	0.07	1.05
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	yfmL	BN194_12120	K0NA13	0.16	0.07	1.05
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	fabH	BN194_22600	K0N7B0	0.48	0.07	1.05
GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	0.03	0.06	1.05
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	rnjA	BN194_15020	K0NAH6	0.39	0.06	1.04
>tr|K0N6D0|K0N6D0_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_20650 PE=4 SV=1	Unknown/uncharacterized	K0N6D0		K0N6D0	0.04	0.05	1.04
ABC-type phosphate/phosphonate transport system,periplasmic component	ABC-type transporter systems		BN194_25680	K0NAI1	0.20	0.05	1.04
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	atpH	BN194_13590	K0MV16	0.18	0.04	1.03
DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	0.09	0.04	1.03
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	xpt	BN194_12490	K0MUR6	0.07	0.04	1.03
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	gpsB	BN194_16690	K0MVN5	0.11	0.03	1.02
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	prs1_2	BN194_30370	K0NDQ5	0.11	0.03	1.02
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	yjlD	BN194_24330	K0NAA7	0.03	0.02	1.02
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	trxB	BN194_10360	K0N3L1	0.09	0.02	1.02
Response regulator ArlR	Signal transduction	arlR	BN194_18650	K0N5X3	0.03	0.02	1.01
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatC	BN194_11950	K0N436	0.07	0.02	1.01
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	fpaP_3	BN194_21160	K0N682	0.06	0.02	1.01
Oligopeptide-binding protein oppA	ABC-type transporter systems	oppA	BN194_17880	K0N983	0.05	0.02	1.01
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	gatA	BN194_11960	K0N3Z6	0.04	0.01	1.01
tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	dus1	BN194_26390	K0MXV9	0.05	0.01	1.01

ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	atpF	BN194_13580	K0N7S9	0.01	0.01	1.01
Cold shock protein CspA	Transcription-associated proteins	cspA	BN194_14820	K0NAH0	0.02	0.01	1.00
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	nadE	BN194_19840	K0MWF6	0.01	0.00	1.00
>tr|K0N9X8|K0N9X8_LACCA SpsK protein OS=Lactobacillus casei W56 GN=spsK PE=4 SV=1;>tr|K0N6D6|K0N6D6_LACCA SpsK_2 protein OS=Lactobacillus casei W56 GN=spsK_2 PE=4 SV=1	Cell wall biogenesis	spsK_2		K0N9X8;K0N6D6	0.01	0.00	1.00
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	nrnA	BN194_08450	K0N309	0.01	0.00	1.00
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	helD	BN194_21130	K0N9W3	0.01	-0.01	1.00
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	ohrR	BN194_10500	K0N3J7	0.02	-0.01	1.00
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	5.24	-7.06	-133.311
>tr|K0NAP8|K0NAP8_LACCA ParC protein OS=Lactobacillus casei W56 GN=parC PE=4 SV=1	Phosphotransferase systems	K0NAP8		K0NAP8	1.08	-5.37	-41.4474
50S ribosomal protein L32	Ribosomal proteins	rpmF	BN194_15510	K0N4T0	1.01	-1.95	-3.87396
2-oxoisovalerate dehydrogenase subunit beta (EC 1.2.4.4)	Lipid-related metabolism	bfmBAB	BN194_16390	K0MVK8	3.74	-1.92	-3.7915
PTS system IIB component, Gat family	Phosphotransferase systems		BN194_07430	K0N6A5	3.42	-1.54	-2.91063
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	treA	BN194_06930	K0N662	3.04	-1.43	-2.70049
2-dehydropantoate 2-reductase (EC 1.1.1.169) (Ketopantoate reductase)	Cofactor-related metabolism		BN194_16370	K0NAS0	1.77	-1.35	-2.552
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE_3	BN194_04780	K0N5N9	2.84	-1.25	-2.38158
30S ribosomal protein S18	Ribosomal proteins	rpsR	BN194_00120	K0N6T2	0.77	-1.20	-2.2977
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	clpC	BN194_21680	K0N9Z7	1.60	-1.17	-2.25258
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	1.22	-1.16	-2.23182
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshA	BN194_26700	K0N8C7	4.49	-1.14	-2.20679
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	bglP	BN194_06940	K0MT60	5.05	-1.12	-2.16792
50S ribosomal protein L17	Ribosomal proteins	rplQ	BN194_25950	K0N841	1.50	-1.09	-2.12317
50S ribosomal protein L21	Ribosomal proteins	rplU	BN194_18290	K0MW61	0.75	-1.04	-2.05194
ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	clpX	BN194_15340	K0MVC6	3.17	-1.01	-2.02015
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	2.49	-1.01	-2.00834

50S ribosomal protein L11	Ribosomal proteins	rplK	BN194_24160	K0N724	2.51	-0.96	-1.95089
30S ribosomal protein S21	Ribosomal proteins	rpsU	BN194_17050	K0N5E5	2.95	-0.96	-1.94602
30S ribosomal protein S8	Ribosomal proteins	rpsH	BN194_26080	K0NAL1	1.96	-0.95	-1.93032
Autoinducer-2 (AI-2) kinase	General prediction only		BN194_27880	K0NB06	2.98	-0.95	-1.92557
30S ribosomal protein S15	Ribosomal proteins	rpsO	BN194_15260	K0N4Q6	2.07	-0.94	-1.92311
30S ribosomal protein S9	Ribosomal proteins	rpsI	BN194_25840	K0MXR0	2.41	-0.94	-1.92046
30S ribosomal protein S11	Ribosomal proteins	rpsK	BN194_25970	K0NCJ0	1.95	-0.94	-1.91263
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	uvrA	BN194_10450	K0N3J2	2.62	-0.92	-1.88895
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	accA	BN194_22470	K0NBS6	2.48	-0.91	-1.88114
50S ribosomal protein L33	Ribosomal proteins	rpmG	BN194_20200	K0N697	2.44	-0.91	-1.87912
Tautomerase (EC 5.3.2.-)	General prediction only		BN194_16890	K0MVQ1	1.15	-0.89	-1.85523
S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	metK	BN194_09150	K0N352	6.41	-0.89	-1.85005
50S ribosomal protein L6	Ribosomal proteins	rplF	BN194_26070	K0NCK5	3.52	-0.89	-1.84977
>tr|K0NB98|K0NB98_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_19420 PE=4 SV=1	Unknown/uncharacterized	K0NB98		K0NB98	0.90	-0.89	-1.84917
Translation initiation factor IF-3	Protein translation (initiation)	infC	BN194_18820	K0NB73	2.38	-0.88	-1.84584
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	typA	BN194_15150	K0N4W9	3.76	-0.87	-1.83057
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	2.39	-0.87	-1.82893
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	pepN	BN194_05410	K0N2F5	2.87	-0.87	-1.82425
50S ribosomal protein L30	Ribosomal proteins	rpmD	BN194_26040	K0MXS6	3.76	-0.86	-1.82054
50S ribosomal protein L23	Ribosomal proteins	rplW	BN194_26200	K0N869	2.40	-0.86	-1.81347
Lipoprotein	ABC-type transporter systems	metQ_2	BN194_13740	K0MV23	3.29	-0.86	-1.81339
50S ribosomal protein L4	Ribosomal proteins	rplD	BN194_26210	K0N7H0	3.36	-0.86	-1.80916
30S ribosomal protein S17	Ribosomal proteins	rpsQ	BN194_26130	K0NAL6	2.61	-0.85	-1.80847
30S ribosomal protein S13	Ribosomal proteins	rpsM	BN194_25980	K0NAK3	1.79	-0.85	-1.80789
50S ribosomal protein L18	Ribosomal proteins	rplR	BN194_26060	K0N7F4	1.66	-0.85	-1.80644
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	groL,groEL	BN194_23750	K0N7K7	3.30	-0.85	-1.80643

Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	yfeX	BN194_07170	K0N8U9	3.15	-0.85	-1.80058
50S ribosomal protein L10	Ribosomal proteins	rplJ	BN194_24090	K0MXD8	3.66	-0.85	-1.80041
Uncharacterized protein ynbB	Cell defense/detoxification	ynbB	BN194_18380	K0N9B7	2.67	-0.85	-1.79843
50S ribosomal protein L35	Ribosomal proteins	rpmI	BN194_18810	K0N5P1	1.99	-0.85	-1.79736
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	hisS	BN194_17110	K0N5A0	2.42	-0.84	-1.79596
50S ribosomal protein L1	Ribosomal proteins	rplA	BN194_24150	K0N7M7	3.09	-0.84	-1.78592
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	pyrG	BN194_26790	K0MXZ1	2.90	-0.82	-1.76516
Elongation factor G (EF-G)	Protein translation (elongation)	fusA	BN194_26270	K0NCN8	4.70	-0.81	-1.75299
50S ribosomal protein L20	Ribosomal proteins	rplT	BN194_18800	K0N5Y4	2.38	-0.81	-1.74977
50S ribosomal protein L5	Ribosomal proteins	rplE	BN194_26100	K0N859	3.36	-0.81	-1.74937
30S ribosomal protein S20	Ribosomal proteins	rpsT	BN194_15250	K0N4X9	2.10	-0.81	-1.74872
30S ribosomal protein S5	Ribosomal proteins	rpsE	BN194_26050	K0N853	2.57	-0.81	-1.74769
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	pfkA	BN194_15570	K0NAK6	2.32	-0.80	-1.74665
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	lacC	BN194_07470	K0N8Y4	2.70	-0.80	-1.74603
50S ribosomal protein L13	Ribosomal proteins	rplM	BN194_25850	K0N828	2.71	-0.80	-1.73702
Dumpy	Cell surface proteins/internalins	dp	BN194_05390	K0MSV0	2.07	-0.79	-1.73037
30S ribosomal protein S12	Ribosomal proteins	rpsL	BN194_26290	K0MXV0	2.41	-0.79	-1.72948
Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	upp	BN194_13550	K0N4J8	2.77	-0.78	-1.71448
Glutamine-binding periplasmic protein	ABC-type transporter systems	glnH_2	BN194_29910	K0N8I1	1.64	-0.78	-1.71437
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	2.26	-0.77	-1.70897
Transcriptional regulatory protein YycF	Signal transduction	yycF_2	BN194_29510	K0N8E4	3.29	-0.77	-1.70342
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	dnaK	BN194_17460	K0N5C7	2.84	-0.77	-1.7016
50S ribosomal protein L16	Ribosomal proteins	rplP	BN194_26150	K0N863	1.69	-0.76	-1.69542
30S ribosomal protein S4	Ribosomal proteins	rpsD	BN194_14440	K0MV63	3.73	-0.75	-1.68567
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	aspS	BN194_17100	K0N5F3	1.91	-0.74	-1.6711

>tr|K0NBL8|K0NBL8_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_21520 PE=3 SV=1	Unknown/uncharacterized	K0NBL8		K0NBL8	1.94	-0.74	-1.66722
50S ribosomal protein L2	Ribosomal proteins	rplB	BN194_26190	K0MXU1	2.99	-0.73	-1.66132
30S ribosomal protein S10	Ribosomal proteins	rpsJ	BN194_26230	K0NAM5	2.52	-0.72	-1.64683
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	msmK	BN194_11180	K0N747	0.93	-0.72	-1.64525
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		BN194_11600	K0N3Z3	1.40	-0.71	-1.64117
Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	pyk	BN194_15580	K0N8B6	3.61	-0.71	-1.6398
Chaperone protein ClpB	Protein folding/turnover	clpB	BN194_15500	K0N4Z8	2.70	-0.71	-1.63579
30S ribosomal protein S19	Ribosomal proteins	rpsS	BN194_26180	K0NAM1	2.29	-0.70	-1.62996
Pur operon repressor	Transcriptional regulation	purR_2	BN194_26960	K0N7M9	0.48	-0.70	-1.62751
50S ribosomal protein L15	Ribosomal proteins	rplO	BN194_26030	K0NAK7	2.22	-0.69	-1.61391
50S ribosomal protein L3	Ribosomal proteins	rplC	BN194_26220	K0NCN1	2.58	-0.69	-1.61059
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	argS	BN194_19120	K0NB86	2.16	-0.69	-1.61006
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	prfB	BN194_10180	K0N6W9	1.76	-0.69	-1.60797
50S ribosomal protein L22	Ribosomal proteins	rplV	BN194_26170	K0NCM1	3.35	-0.68	-1.6056
Translation initiation factor IF-2	Protein translation (initiation)	infB	BN194_17550	K0N5K7	1.93	-0.68	-1.60548
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	yutF	BN194_08910	K0N383	2.04	-0.68	-1.6006
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	grpE	BN194_17470	K0NAZ2	2.22	-0.68	-1.59971
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	2.47	-0.67	-1.5958
Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	fba_2	BN194_05060	K0N2C9	2.37	-0.67	-1.58957
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	gmk	BN194_18110	K0N5J6	1.64	-0.67	-1.58654
FeS cluster assembly protein sufB	Cofactor-related metabolism	sufB	BN194_13810	K0N4E5	1.71	-0.67	-1.58567
>tr|K0N6A9|K0N6A9_LACCA Tyrosine--tRNA ligase OS=Lactobacillus casei W56 GN=tyrS PE=4 SV=1	tRNA aminoacyl synthesis	tyrS		K0N6A9	1.69	-0.65	-1.57193
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	nagB	BN194_30440	K0MYW0	1.98	-0.65	-1.5687
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	gltX	BN194_24470	K0NC38	2.13	-0.65	-1.56694

DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	rpoB	BN194_26340	K0MXV4	4.89	-0.64	-1.55913
50S ribosomal protein L14	Ribosomal proteins	rplN	BN194_26120	K0NCL3	2.35	-0.63	-1.55161
Transcription termination/antitermination protein NusG	Transcription-associated proteins	nusG	BN194_24260	K0N730	1.04	-0.63	-1.54714
30S ribosomal protein S14 type Z	Ribosomal proteins	rpsZ,rpsN	BN194_26090	K0MXS9	0.98	-0.63	-1.54298
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	oppD	BN194_17920	K0NB35	3.46	-0.62	-1.53921
30S ribosomal protein S3	Ribosomal proteins	rpsC	BN194_26160	K0N7G5	1.44	-0.62	-1.53467
50S ribosomal protein L19	Ribosomal proteins	rplS	BN194_17770	K0NB12	2.58	-0.61	-1.531
Protein translocase subunit SecA	Protein export	secA	BN194_10170	K0N9J2	2.63	-0.61	-1.52819
Putative tRNA-binding protein ytpR	General prediction only	ytpR	BN194_18970	K0NB80	1.12	-0.61	-1.52648
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	yqeC	BN194_02330	K0N532	1.95	-0.61	-1.52499
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	ndk	BN194_08160	K0N340	0.52	-0.60	-1.5203
Uncharacterized protein	Unknown/uncharacterized		BN194_27530	K0NAX5	0.39	-0.60	-1.51897
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	yqeL,rsfS	BN194_18710	K0N5N6	3.45	-0.60	-1.51849
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	2.38	-0.60	-1.51477
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC	BN194_24670	K0NC50	1.37	-0.60	-1.5113
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	purA	BN194_01160	K0N1J0	2.55	-0.59	-1.50855
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	rpoC	BN194_26330	K0NAN3	3.10	-0.59	-1.50698
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	glyS	BN194_16950	K0N5D3	2.42	-0.59	-1.50356
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	obg	BN194_15440	K0MVD3	1.86	-0.58	-1.49615
50S ribosomal protein L7/L12	Ribosomal proteins	rplL	BN194_24080	K0NA98	1.73	-0.58	-1.49451
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2,lacD	BN194_07480	K0N6A8	2.54	-0.58	-1.49088
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	atpA	BN194_13600	K0N4K1	2.76	-0.58	-1.4906
30S ribosomal protein S6	Ribosomal proteins	rpsF	BN194_00100	K0N0Z1	2.02	-0.57	-1.4842

Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_4	BN194_29900	K0N971	2.25	-0.57	-1.482
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	glnA_2	BN194_18340	K0MW64	2.41	-0.56	-1.47678
Transcriptional regulator, TetR family	Transcriptional regulation		BN194_12190	K0MUM1	2.68	-0.56	-1.47497
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07700	K0N2V5	0.98	-0.56	-1.47162
30S ribosomal protein S7	Ribosomal proteins	rpsG	BN194_26280	K0NAM9	2.26	-0.55	-1.46629
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	cap4C	BN194_12280	K0N7E3	2.26	-0.55	-1.46568
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	clpE	BN194_19450	K0N644	2.42	-0.55	-1.46286
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	HBN1	BN194_16550	K0N597	1.14	-0.55	-1.45983
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	proS	BN194_17610	K0N5E2	2.20	-0.54	-1.44962
>tr|K0N3R3|K0N3R3_LACCA Gap protein OS=Lactobacillus casei W56 GN=gap PE=3 SV=1	Central glycolytic/intermediary pathways	gap		K0N3R3;K0N4X1	1.58	-0.53	-1.44349
Translation initiation factor IF-1	Protein translation (initiation)	infA	BN194_26000	K0N847	1.41	-0.52	-1.43889
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	thrS	BN194_18860	K0N5P5	4.79	-0.52	-1.43232
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	guaA	BN194_21070	K0NBJ2	2.56	-0.51	-1.42855
RNA polymerase sigma factor SigA	RNA polymerase	rpoD,sigA	BN194_16920	K0NAV6	0.42	-0.51	-1.42702
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	eno	BN194_11040	K0MU67	2.92	-0.51	-1.42627
Probable dipeptidase (EC 3.4.-.-)	Amino acid-related metabolism		BN194_13380	K0N7S0	2.52	-0.51	-1.42595
Bifunctional protein GlmU	Cell wall biogenesis	glmU	BN194_26940	K0MY10	0.74	-0.51	-1.42584
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	mnmA	BN194_14930	K0N844	1.62	-0.51	-1.42013
Transcription termination/antitermination protein NusA	Transcription-associated proteins	nusA	BN194_17580	K0N927	2.35	-0.50	-1.41719
50S ribosomal protein L29	Ribosomal proteins	rpmC	BN194_26140	K0MXT6	2.83	-0.50	-1.41524
30S ribosomal protein S2	Ribosomal proteins	rpsB	BN194_17680	K0N936	2.13	-0.50	-1.40961
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	hpt	BN194_26470	K0NCR2	1.12	-0.49	-1.40387
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		BN194_01410	K0N1L0	0.59	-0.48	-1.39673
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	lacB	BN194_07490	K0MTB7	1.16	-0.48	-1.39636

Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	adk	BN194_26010	K0N7F0	2.08	-0.47	-1.38726
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	tig	BN194_15330	K0N884	2.32	-0.47	-1.38168
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	alaS	BN194_08480	K0N6K2	1.58	-0.45	-1.3706
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	pyrH	BN194_17660	K0N5E6	2.14	-0.43	-1.35167
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism	K0N6M0	BN194_22460	K0N6M0	0.77	-0.42	-1.33525
Ribosome-binding ATPase YchF	Protein translation (peptide release)	engD,ychF	BN194_02070	K0N7F7	2.56	-0.42	-1.33383
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	gyrA	BN194_00070	K0N6S7	0.70	-0.41	-1.33201
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	rpoA	BN194_25960	K0N7E5	2.83	-0.40	-1.32067
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	1.53	-0.40	-1.31871
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	cmk	BN194_15710	K0N4V1	1.92	-0.40	-1.31502
30S ribosomal protein S16	Ribosomal proteins	rpsP	BN194_17810	K0N5H1	0.43	-0.39	-1.31471
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	asnS	BN194_16760	K0N569	0.86	-0.39	-1.31417
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	ileS	BN194_14810	K0N4L9	0.91	-0.39	-1.30878
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	1.53	-0.38	-1.30484
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	ptsH	BN194_19430	K0N9I2	0.45	-0.38	-1.30068
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	rnr	BN194_11100	K0N3S4	1.95	-0.37	-1.29644
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	lacA	BN194_07500	K0N2T4	1.75	-0.37	-1.29425
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	atpG	BN194_13610	K0N4D3	0.85	-0.36	-1.2872
30S ribosomal protein S1 homolog	Ribosomal proteins	ypfD	BN194_15720	K0NAL9	1.47	-0.36	-1.28535
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	greA	BN194_18520	K0NB62	1.60	-0.36	-1.2832
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	maa	BN194_30010	K0N8I9	0.14	-0.36	-1.28216
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	pheS	BN194_18570	K0NB64	1.59	-0.36	-1.27959
50S ribosomal protein L24	Ribosomal proteins	rplX	BN194_26110	K0N7F9	0.91	-0.35	-1.27698
50S ribosomal protein L27	Ribosomal proteins	rpmA	BN194_18270	K0NB51	0.54	-0.35	-1.27479

Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	serS	BN194_20080	K0N9N4	1.54	-0.35	-1.27072
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	ftsH	BN194_26460	K0N7I8	1.05	-0.34	-1.26879
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	atpD	BN194_13620	K0NAB3	2.33	-0.34	-1.26441
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	tsf	BN194_17670	K0NB01	1.44	-0.34	-1.26241
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	asnB	BN194_22990	K0MX90	0.86	-0.32	-1.2478
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	tuf	BN194_15310	K0N4R1	2.34	-0.31	-1.24245
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	queA	BN194_08370	K0N965	0.79	-0.31	-1.24003
Protein LemA	Unknown/uncharacterized	lemA	BN194_27350	K0N8J7	1.26	-0.31	-1.23871
Penicillin-binding protein 1A	Cell wall biogenesis	ponA	BN194_16720	K0NAU3	0.39	-0.31	-1.2376
Uncharacterized protein	Unknown/uncharacterized		BN194_29450	K0N932	0.94	-0.31	-1.23718
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	iscS1	BN194_14900	K0N4U8	0.62	-0.30	-1.2348
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	yqeH	BN194_18740	K0MW90	1.11	-0.30	-1.23222
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	yabR	BN194_26500	K0N8A7	0.86	-0.30	-1.22995
UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	0.62	-0.29	-1.22491
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	ldh	BN194_26560	K0N7J5	1.07	-0.29	-1.22453
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	def	BN194_15060	K0N4N6	1.86	-0.29	-1.22316
Transcriptional regulator	Transcriptional regulation		BN194_08230	K0N6I4	2.48	-0.28	-1.2171
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	metG	BN194_27130	K0NAU5	1.83	-0.28	-1.21553
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	gmuB	BN194_23840	K0MXC7	0.92	-0.28	-1.21425
Uncharacterized protein MJ0282	Cofactor-related metabolism		BN194_03700	K0N1T2	0.46	-0.28	-1.21259
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	murF	BN194_26720	K0NCU5	0.52	-0.27	-1.20902
UPF0337 protein yhjA	General prediction only	yhjA	BN194_24800	K0N7S1	0.29	-0.27	-1.20898
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	pgk	BN194_11020	K0N9R1	0.91	-0.27	-1.20893
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	rpoE	BN194_26810	K0N7L4	0.78	-0.27	-1.20722

ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit) (F-ATPase epsilon subunit)	Membrane bioenergetics	atpC	BN194_13630	K0N7T2	0.15	-0.27	-1.20715
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	der	BN194_15730	K0N8E1	0.98	-0.27	-1.20659
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	lysS	BN194_26380	K0NAN7	0.75	-0.27	-1.20321
Uncharacterized protein SE_0534	tRNA/Ribosome assembly/processing		BN194_10150	K0N3F2	1.19	-0.26	-1.20157
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	valS	BN194_14510	K0N4J6	0.62	-0.26	-1.19877
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	clpP_2, clpP	BN194_10510	K0N3M4	0.74	-0.26	-1.19841
>tr|K0N1M9|K0N1M9_LACCA Probable phosphoketolase OS=Lactobacillus casei W56 GN=xpkA PE=3 SV=1	Central glycolytic/intermediary pathways	xpkA		K0N1M9;K0N8X7	1.23	-0.26	-1.19619
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	dltA	BN194_08590	K0MTN0	0.74	-0.26	-1.19587
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	trpS	BN194_27360	K0N7S4	0.87	-0.25	-1.18955
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	ykpA	BN194_07220	K0N8V6	1.04	-0.25	-1.18596
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	pheT	BN194_18560	K0N5M4	0.88	-0.24	-1.1841
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	guaB	BN194_02100	K0N1G3	1.67	-0.24	-1.17942
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	murD	BN194_14720	K0NAG5	0.78	-0.24	-1.179
50S ribosomal protein L31 type B	Ribosomal proteins	rpmE2	BN194_26770	K0NCV4	0.57	-0.23	-1.17599
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	ybeY	BN194_17010	K0N594	1.55	-0.23	-1.17431
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	act	BN194_16090	K0MVI3	0.19	-0.23	-1.17332
Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	0.70	-0.23	-1.17212
Uncharacterized protein	Cofactor-related metabolism		BN194_18720	K0NB69	2.44	-0.21	-1.16041
Uncharacterized protein ylxR	General prediction only	ylxR	BN194_17570	K0NAZ6	0.66	-0.21	-1.15769
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	dnaN	BN194_00020	K0N6S3	0.71	-0.21	-1.15406
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	mtnN	BN194_14890	K0MV90	0.62	-0.21	-1.15304

Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	glcK	BN194_18420	K0NB57	0.85	-0.20	-1.15235
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	tpiA	BN194_11030	K0N736	0.80	-0.20	-1.15044
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	hslO	BN194_26400	K0N893	0.85	-0.20	-1.14958
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	nusB	BN194_18220	K0NB49	1.26	-0.20	-1.14781
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	mco	BN194_25410	K0N7A4	1.14	-0.20	-1.14681
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	oppF	BN194_17910	K0N5I3	0.58	-0.20	-1.14605
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	npr	BN194_04740	K0MSP8	1.06	-0.19	-1.14447
>tr|K0N4Z7|K0N4Z7_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02080 PE=4 SV=1	Unknown/uncharacterized	K0N4Z7		K0N4Z7	0.87	-0.19	-1.14011
NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	0.53	-0.19	-1.13984
>tr|K0N5T2|K0N5T2_LACCA Phosphoenolpyruvate-protein phosphotransferase OS=Lactobacillus casei W56 GN=ptsI PE=3 SV=1	Phosphotransferase systems	ptsI		K0N5T2	1.11	-0.18	-1.13359
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07710	K0N2Z3	1.92	-0.17	-1.12801
Probable flavodoxin-1	Membrane bioenergetics	ykuN_2	BN194_12220	K0NA19	0.27	-0.17	-1.12211
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	0.38	-0.16	-1.12024
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	prfA	BN194_13510	K0N4C6	0.59	-0.16	-1.11834
Putative secreted protein	cell wall biogenesis		BN194_02820	K0N7S8	0.13	-0.16	-1.11627
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	groS,grES	BN194_23760	K0N700	0.14	-0.16	-1.11496
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	ppaC	BN194_16110	K0N4Z4	2.08	-0.16	-1.11397
Nucleoid-associated protein BN194_23980	General prediction only		BN194_23980	K0NA95	0.60	-0.15	-1.11173
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	rmlB	BN194_21340	K0MWS0	0.29	-0.15	-1.11086
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	1.03	-0.15	-1.10951
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	fruK_2	BN194_27700	K0N8P7	0.25	-0.14	-1.10384
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	1.13	-0.14	-1.09941
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	apt	BN194_17380	K0N902	0.33	-0.13	-1.09779

DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	gyrB	BN194_00060	K0N1B8	0.54	-0.13	-1.09767
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	gpmA2,gpmA	BN194_22740	K0MX58	2.74	-0.13	-1.09323
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	map	BN194_12230	K0N7E0	0.42	-0.13	-1.09291
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	murA2,murA	BN194_26780	K0NAR9	0.24	-0.13	-1.09236
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	ftsY	BN194_17850	K0N5R8	0.43	-0.12	-1.08957
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	0.54	-0.12	-1.088
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshB	BN194_08460	K0N356	0.37	-0.11	-1.08088
Elongation factor P	Protein translation (elongation)	efp	BN194_18240	K0MW57	0.39	-0.11	-1.0798
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	prsA	BN194_19060	K0N5Q8	0.46	-0.11	-1.07801
Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	aspC	BN194_16770	K0NAU6	0.41	-0.11	-1.07627
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	pyrDA, pyrD	BN194_19150	K0N623	0.31	-0.11	-1.07554
Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	0.28	-0.10	-1.07113
Protein ytsP	Signal transduction	ytsP	BN194_14450	K0N4Q9	0.19	-0.10	-1.07069
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	dacA	BN194_02140	K0MS53	0.35	-0.09	-1.06792
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	murC	BN194_18950	K0N600	0.27	-0.09	-1.06765
Uncharacterized protein	Unknown/uncharacterized		BN194_16650	K0N5A4	0.75	-0.09	-1.06464
Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	gntK	BN194_02340	K0MS76	0.21	-0.09	-1.06416
ABC transporter, permease protein	ABC-type transporter systems		BN194_29810	K0N8H4	0.13	-0.09	-1.06123
D-ribose-binding protein	ABC-type transporter systems	rbsB	BN194_03290	K0MSF6	0.38	-0.08	-1.06031
MreB-like protein	Cytokinesis	mbl	BN194_13650	K0N4K5	0.29	-0.08	-1.05673
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	rbfA	BN194_17540	K0MVV7	0.19	-0.08	-1.05462
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	fabD	BN194_22570	K0NBT1	0.27	-0.07	-1.05191
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC_2	BN194_24680	K0NAC2	0.21	-0.07	-1.05006

Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	leuS	BN194_09210	K0N3A9	0.36	-0.06	-1.04468
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	BN194_21350	BN194_21780	K0N6Q5	0.22	-0.06	-1.04398
UPF0659 protein YMR090W	General prediction only	ylbE	BN194_07030	K0N671	0.12	-0.05	-1.03755
Uncharacterized protein	Lipid-related metabolism	YerQ	BN194_11980	K0N7B3	0.14	-0.05	-1.03496
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	pepQ	BN194_08740	K0MTP0	0.42	-0.05	-1.03324
Cold shock protein 1	Transcription-associated proteins	csp	BN194_06990	K0MT67	0.03	-0.05	-1.0329
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	nagA	BN194_19890	K0MWF9	0.14	-0.04	-1.03158
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	luxS	BN194_08330	K0N6J0	0.03	-0.04	-1.03139
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	pepO_2	BN194_16630	K0N8Q0	0.08	-0.03	-1.02206
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	potA	BN194_11290	K0MU90	0.12	-0.03	-1.0214
Chaperone protein DnaJ	Protein folding/turnover	dnaJ	BN194_17450	K0N5J4	0.10	-0.03	-1.02124
Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	rbsK	BN194_03300	K0N1R2	0.05	-0.03	-1.01898
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2_2,lacD	BN194_27060	K0N7P0	0.04	-0.01	-1.00954
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	pepDB	BN194_21110	K0N678	0.06	-0.01	-1.00913
Transcriptional regulator, XRE family	Transcriptional regulation		BN194_30170	K0NDP4	0.02	-0.01	-1.00792

(1e) Protein FC >2 Tween 80 + Citrate Vs control P1

Protein names	Functional Class	Gene	Gene locu	Protein IDs	-Log t-test p-value	t-test Difference	Fold change
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	pycB	BN194_20290	K0MWI8	6.42981	5.54524	46.69642
Citrate lyase acyl carrier protein YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	yacO	BN194_24420	K0NC34	4.74794	5.31625	39.84288
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	citF	BN194_20310	K0N607	5.2615	4.82641	28.37228

Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	ADH2	BN194_08400	K0N307	4.49405	4.74528	26.82079
Pyruvate, phosphate dikinase (EC 2.7.9.1)	Central glycolytic/intermediary pathways	ppdK	BN194_24730	K0NAC6	2.88669	4.20669	18.4646
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	pflB	BN194_16080	K0N8I5	6.002	3.96126	15.57608
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	citE	BN194_20320	K0NBF4	2.65388	3.92938	15.23566
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	citD	BN194_20330	K0N9Q5	2.18159	3.5543	11.74765
Probable dipeptidase (EC 3.4.-.-)	Amino acid-related metabolism		BN194_23190	K0MXA1	1.05479	3.38173	10.42323
Biotin carboxyl carrier protein	Tricarboxylic acid pathway	bcc	BN194_20370	K0NBF7	2.39595	3.21869	9.309412
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	fbp	BN194_21660	K0N6C3	5.64928	3.21506	9.286018
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	citX	BN194_20300	K0N6A3	2.85117	3.18194	9.075266
Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	rpiA_2, ripA	BN194_28600	K0N8W9	2.20047	3.06483	8.367693
Uncharacterized protein ACIAD3023	Cell defense/detoxification		BN194_07010	K0N2T5	3.47841	2.92245	7.581325
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	Cell wall biogenesis	glmS	BN194_11560	K0N3V9	5.24589	2.8748	7.335015
Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	pox5	BN194_19670	K0NBB6	5.46221	2.73866	6.674501
>tr|K0N7B1|K0N7B1_LACCA Acetate kinase OS=Lactobacillus casei W56 GN=ackA PE=3 SV=1	Central glycolytic/intermediary pathways	ackA		K0N7B1;K0N6W4	3.69772	2.68045	6.410558
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	ldh1,Idh	BN194_06970	K0N8S5	3.35843	2.56813	5.930402
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	pdhD	BN194_15110	K0N4P1	7.45479	2.54086	5.819358
Aldose 1-epimerase (EC 5.1.3.3)	Central glycolytic/intermediary pathways		BN194_07390	K0MTA8	4.08234	2.5366	5.8022
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	Posttranslational modification	citC	BN194_20340	K0MWJ1	3.909	2.49009	5.61813
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	pdhC	BN194_15100	K0N4W5	4.85111	2.27443	4.838064
2-oxoisovalerate dehydrogenase subunit beta (EC 1.2.4.4)	Lipid-related metabolism	bfmBAB	BN194_16390	K0MVK8	4.73155	2.22574	4.677508
Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	bceA_2	BN194_21230	K0N9X1	1.69979	2.08306	4.23705
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	pdhB	BN194_15090	K0MVA7	4.33812	2.04351	4.122473

Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	ssdA	BN194_24140	K0MXE0	3.44403	2.04058	4.114109
Uncharacterized protein	Unknown/uncharacterized		BN194_01870	K0N7D4	1.7832	2.02896	4.081105
>tr|K0N8X1|K0N8X1_LACCA Galactose-1-phosphate uridylyltransferase OS=Lactobacillus casei W56 GN=galT PE=3 SV=1	Carbohydrate-related metabolism	K0N8X1		K0N8X1	4.00412	1.96653	3.90827
Uncharacterized protein	Unknown/uncharacterized		BN194_16650	K0N5A4	3.73257	1.95909	3.888167
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	fruA_4	BN194_27690	K0MY77	4.72986	1.93968	3.836205
Uncharacterized protein yghZ	General prediction only	yghZ	BN194_27510	K0N7U8	2.94572	1.93744	3.830254
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	pdhA	BN194_15080	K0N860	3.80233	1.932	3.815838
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	galE	BN194_07350	K0N2R3	3.67814	1.8906	3.707894
Uncharacterized oxidoreductase YrbE (EC 1.-.-.-)	Carbohydrate-related metabolism	yrbE	BN194_02280	K0N524	2.20556	1.8684	3.651274
3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase (THcHDO hydrolase) (EC 3.7.1.22)	Carbohydrate-related metabolism	iolD	BN194_02260	K0N1T3	1.55293	1.86188	3.63481
Uncharacterized protein	Unknown/uncharacterized		BN194_08190	K0MTK3	3.42681	1.85993	3.6299
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	dhaK_2	BN194_04980	K0N5Q3	2.91766	1.83076	3.557244
>tr|K0N8W1|K0N8W1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07270 PE=4 SV=1	Unknown/uncharacterized	K0N8W1		K0N8W1	0.50373	1.81916	3.528757
>tr|K0N2W3|K0N2W3_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07360 PE=4 SV=1	Unknown/uncharacterized	K0N2W3		K0N2W3	4.17282	1.81735	3.524332
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	pta	BN194_11340	K0MU95	3.66788	1.78328	3.442079
Uncharacterized protein	Unknown/uncharacterized		BN194_20380	K0N9Q9	1.3309	1.77434	3.420815
Probable L-ascorbate-6-phosphate lactonase ulaG (EC 3.1.1.-)	Carbohydrate-related metabolism	ulaG	BN194_28590	K0MYF8	2.91103	1.76941	3.409145
Uncharacterized protein	Unknown/uncharacterized		BN194_01760	K0N1N3	4.00301	1.76834	3.406618
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	apbE_3	BN194_21550	K0N6S8	1.86581	1.75378	3.37241
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	dhaM	BN194_04960	K0N2C2	3.39952	1.72163	3.298088
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	galK	BN194_07340	K0MTA3	2.1798	1.71399	3.280669
>tr|K0N518|K0N518_LACCA IolA protein OS=Lactobacillus casei W56 GN=iolA PE=3 SV=1	Carbohydrate-related metabolism	iolA		K0N518	2.04123	1.70904	3.269432
Maltose ABC transporter, periplasmic maltose-binding protein	ABC-type transporter systems		BN194_11200	K0N3U4	2.85671	1.70432	3.258753
Uncharacterized protein	Central glycolytic/intermediary pathways		BN194_04970	K0N8A3	2.47231	1.66708	3.175712

FMN-binding domain protein	General prediction only		BN194_24320	K0NC29	2.62697	1.64462	3.126655
Putative secreted protein	cell wall biogenesis		BN194_02820	K0N7S8	1.23261	1.63947	3.115514
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	yhfP	BN194_07740	K0MTE1	2.48173	1.58522	3.000536
Cell division protein FtsX	Cytokinesis	ftsX	BN194_10200	K0N3G0	1.35261	1.54255	2.913089
>tr|K0N1K5|K0N1K5_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_01360 PE=4 SV=1	Unknown/uncharacterized	K0N1K5		K0N1K5	1.10853	1.54144	2.910849
Glutathione peroxidase	Cell defense/detoxification	gpo	BN194_09780	K0N6T6	3.53603	1.5358	2.899492
Phosphatase YidA (EC 3.1.3.-)	General prediction only	yidA	BN194_28520	K0NDD5	4.52416	1.52775	2.883358
Uncharacterized protein	Unknown/uncharacterized		BN194_28350	K0N8V3	2.54273	1.50266	2.833647
Mannose permease IID component	Phosphotransferase systems	manZ_9	BN194_29700	K0N954	2.51727	1.49595	2.820498
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	4.36906	1.49181	2.812416
Mannose permease IID component	Phosphotransferase systems	manZ	BN194_02990	K0MSE1	1.38793	1.49099	2.810818
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	ydgI_2	BN194_16210	K0N508	3.54272	1.48905	2.807041
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	dkgB	BN194_08260	K0N347	3.63321	1.47919	2.787922
UPF0337 protein lp_1708	General prediction only		BN194_05810	K0N2J8	1.75366	1.47893	2.787419
Histidinol-phosphatase	General prediction only		BN194_14010	K0N4F8	1.38629	1.4782	2.786009
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	agl	BN194_27950	K0N8T1	3.48735	1.4375	2.708511
Cadmium efflux system accessory protein	Other transporter proteins	cadC	BN194_21540	K0MWU0	1.31678	1.4124	2.661796
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	iolS	BN194_29680	K0NB94	3.64644	1.39404	2.628136
Predicted hydrolase of the HAD superfamily	General prediction only	mtlD	BN194_30450	K0N9D4	3.86642	1.37621	2.595855
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	mhqA_3	BN194_18760	K0N5N7	2.87634	1.36497	2.57571
Uncharacterized protein	Unknown/uncharacterized		BN194_24010	K0N715	3.31852	1.30632	2.473099
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	sph	BN194_04930	K0N5Q0	1.99519	1.27907	2.426825
>tr|K0N2Q1|K0N2Q1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_06460 PE=4 SV=1;>tr|K0MXJ1|K0MXJ1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_24990 PE=4 SV=1	Unknown/uncharacterized	K0N2Q1		K0N2Q1;K0MXJ1	3.8323	1.23837	2.359318
ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	atpF	BN194_13580	K0N7S9	1.24892	1.23188	2.348729
Cell division ATP-binding protein FtsE	Cytokinesis	ftsE	BN194_10190	K0MTZ2	3.20791	1.22583	2.3389
Transcriptional regulator lytR	Transcriptional regulation	lytR_3	BN194_21700	K0N6U3	2.64467	1.21384	2.319542

2-dehydropantoate 2-reductase (EC 1.1.1.169) (Ketopantoate reductase)	Cofactor-related metabolism		BN194_16370	K0NAS0	2.64214	1.20767	2.309643
Uncharacterized protein	Unknown/uncharacterized		BN194_11770	K0N9Y6	1.43477	1.19855	2.295089
Protein QmcA	Unknown/uncharacterized	qmcA	BN194_12070	K0NA10	2.1263	1.19717	2.292895
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	yjlD	BN194_24330	K0NAA7	1.24851	1.18565	2.274659
Uncharacterized protein ypuA	Unknown/uncharacterized	ypuA	BN194_27250	K0N8I3	2.63861	1.14424	2.210297
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	mtlF	BN194_30410	K0N8N0	2.49652	1.12676	2.183678
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	garB	BN194_27400	K0N8K3	4.10275	1.08248	2.117673
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	hslU	BN194_16010	K0N4Y1	2.27145	1.07475	2.106357
5-dehydro-2-deoxygluconokinase (EC 2.7.1.92) (2-deoxy-5-keto-D-gluconate kinase)	Carbohydrate-related metabolism	iolC	BN194_02250	K0N1H4	2.16343	1.07346	2.104474
Protein lacX, plasmid	Carbohydrate-related metabolism	lacX	BN194_27070	K0NCY0	2.62181	1.07236	2.10287
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	pyrC	BN194_16470	K0NAS6	0.865273	1.07135	2.101399
Penicillin acylase (EC 3.5.1.11)	Cell defense/detoxification		BN194_04910	K0N2B8	2.51782	1.06515	2.092387
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	glyA	BN194_13540	K0MV12	3.28903	1.05888	2.083314
Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	ptp3	BN194_23520	K0NBX6	3.15726	1.05864	2.082967
UPF0092 membrane protein yrbF	Protein export	yrbF	BN194_08390	K0MTL6	0.47496	1.05819	2.082317
Uncharacterized protein	General prediction only		BN194_17420	K0NAY8	1.55639	1.04508	2.063481
UPF0478 protein SAOUHSC_01855	Signal transduction		BN194_08710	K0N365	2.23372	1.0422	2.059366
Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	fhs	BN194_16520	K0NAT0	2.71104	1.02508	2.035072
Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	rp2	BN194_17060	K0N598	2.00	1.00	2.00
Protein hit	tRNA aminoacyl synthesis	hit	BN194_19040	K0MWA8	1.68	1.00	2.00

(1f) Protein FC <2 Tween 80 + citrate Vs control P1

Protein names	**Functional Class**	**Gene**	**names**	**Protein IDs**	**-Log t-test p-value**	**t-test Difference__**	**Fold change**

Uncharacterized protein yueI	Unknown/uncharacterized	yueI	BN194_13920	K0NAC7	1.14	0.98	1.98
>tr|K0N7I1|K0N7I1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02220 PE=4 SV=1	Unknown/uncharacterized	K0N7I1		K0N7I1	2.27	0.96	1.95
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC	BN194_00080	K0N486	1.90	0.96	1.94
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		BN194_18780	K0N9E0	1.24	0.95	1.93
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	yqjQ	BN194_15480	K0N8A1	2.15	0.94	1.92
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	glgC	BN194_21600	K0N6T3	4.00	0.94	1.92
Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	1.62	0.94	1.92
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	rny	BN194_10100	K0N3E5	3.47	0.92	1.89
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	ilvE	BN194_21620	K0NBM4	2.53	0.91	1.88
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	ung	BN194_11330	K0N758	0.59	0.89	1.85
Elongation factor P	Protein translation (elongation)	efp_2	BN194_22050	K0N712	1.69	0.87	1.83
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	glgD	BN194_21590	K0MWU4	2.29	0.85	1.80
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	manX_5	BN194_29720	K0NDL4	3.14	0.85	1.80
Glycerol-3-phosphate ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_11260	K0N3T6	2.66	0.84	1.80
UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	0.81	0.83	1.78
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	cysK	BN194_05520	K0N8E6	2.78	0.82	1.77
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	hmgCS1	BN194_19680	K0N9K3	3.53	0.80	1.74
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	glyr1	BN194_30100	K0N992	2.18	0.80	1.74
ABC-type uncharacterized transport system, ATPase component	ABC-type transporter systems		BN194_07730	K0N6C9	1.55	0.78	1.72
Glycosyl transferase family protein	Cell wall biogenesis		BN194_02420	K0N7L2	0.92	0.78	1.71
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	deoD	BN194_02810	K0N1Z0	1.62	0.77	1.71
Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	0.38	0.77	1.71
Uncharacterized protein	Unknown/uncharacterized		BN194_27530	K0NAX5	1.18	0.76	1.69
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	polA	BN194_18930	K0N9E7	2.07	0.76	1.69

ABC-type phosphate/phosphonate transport system,periplasmic component	ABC-type transporter systems		BN194_25680	K0NAI1	2.31	0.75	1.69
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	deoB	BN194_02800	K0N1N0	2.44	0.73	1.66
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	2.63	0.73	1.66
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC_2,deoC	BN194_02790	K0MSB5	2.61	0.73	1.66
Stage 0 sporulation protein J	Cytokinesis	spo0J	BN194_02050	K0N1F9	1.94	0.72	1.65
Cold shock protein 1	Transcription-associated proteins	csp	BN194_06990	K0MT67	0.66	0.72	1.65
Inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase (EC 1.1.1.18) (EC 1.1.1.369) (Myo-inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase)	Carbohydrate-related metabolism	iolG	BN194_02270	K0N7J1	0.98	0.72	1.65
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	mtlD_3mtlD	BN194_30400	K0N9C8	1.28	0.72	1.65
>tr|K0N4Z7|K0N4Z7_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02080 PE=4 SV=1	Unknown/uncharacterized	K0N4Z7		K0N4Z7	0.61	0.72	1.64
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	thyA	BN194_15800	K0N522	2.02	0.71	1.63
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	gnd	BN194_18660	K0N5N2	1.90	0.69	1.61
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		BN194_24180	K0NAA2	1.79	0.68	1.60
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	2.03	0.68	1.60
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	act	BN194_16090	K0MVI3	0.62	0.67	1.59
Uncharacterized protein YwcC	Carbohydrate-related metabolism	ywcC	BN194_09930	K0N6V0	2.52	0.66	1.58
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	1.90	0.66	1.58
ABC transporter, permease protein	ABC-type transporter systems		BN194_29810	K0N8H4	2.43	0.65	1.57
Sporulation initiation inhibitor protein soj	Cytokinesis	soj	BN194_02040	K0MS45	0.90	0.63	1.55
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	rex_2,rex	BN194_23820	K0NBZ5	0.81	0.62	1.53
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	0.68	0.61	1.53
Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	plsX	BN194_17940	K0MW37	0.24	0.60	1.51
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	mco	BN194_25410	K0N7A4	1.04	0.59	1.50
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	2.34	0.59	1.50

GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	0.41	0.58	1.50
Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	phoP	BN194_10220	K0N9J6	1.29	0.58	1.50
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	potA	BN194_11290	K0MU90	2.07	0.58	1.49
Rod shape-determining protein MreB	Cytokinesis	mreB	BN194_14550	K0N4R7	0.85	0.58	1.49
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07710	K0N2Z3	2.23	0.57	1.48
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	carB	BN194_16450	K0N587	1.17	0.57	1.48
Septum site-determining protein DivIVA	Cytokinesis	divIVA	BN194_14800	K0N4T8	0.90	0.56	1.48
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	maa	BN194_30010	K0N8I9	0.35	0.56	1.47
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		BN194_21400	K0N6R1	1.42	0.56	1.47
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	pyc	BN194_15170	K0NAI2	2.12	0.56	1.47
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	pgcA	BN194_10370	K0N9K8	2.37	0.53	1.44
DNA-binding protein HU	DNA replication-related	hup	BN194_15740	K0MVF4	1.30	0.53	1.44
>tr|K0N7I6|K0N7I6_LACCA Glucose-6-phosphate isomerase OS=Lactobacillus casei W56 GN=pgi PE=3 SV=1	Central glycolytic/intermediary pathways	pgi		K0N7I6;K0N4A6	1.72	0.52	1.44
Transcriptional regulator, xre family	Transcriptional regulation		BN194_23510	K0N6Y7	1.11	0.52	1.44
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	thiD_2	BN194_07650	K0N2U9	1.53	0.52	1.43
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	prsA	BN194_19060	K0N5Q8	1.17	0.51	1.42
Oligopeptide-binding protein oppA	ABC-type transporter systems	oppA	BN194_17880	K0N983	1.61	0.51	1.42
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	dacA	BN194_02140	K0MS53	2.13	0.49	1.41
Signal recognition particle protein (Fifty-four homolog)	Protein export	ffh	BN194_17820	K0NB27	1.33	0.49	1.41
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	proC	BN194_19900	K0N677	0.87	0.49	1.40
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	fruK_2	BN194_27700	K0N8P7	0.85	0.47	1.39
Autoinducer-2 (AI-2) kinase	General prediction only		BN194_27880	K0NB06	0.81	0.47	1.39
D-ribose-binding protein	ABC-type transporter systems	rbsB	BN194_03290	K0MSF6	1.41	0.47	1.38
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	lplJ	BN194_16640	K0MVN0	1.42	0.47	1.38
Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (Guanine insertion enzyme) (tRNA-guanine transglycosylase)	tRNA/Ribosome assembly/processing	tgt	BN194_08380	K0N6J4	0.35	0.45	1.37
Uncharacterized protein ykuJ	Unknown/uncharacterized	ykuJ	BN194_09100	K0N348	0.94	0.45	1.36

Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	yuxL	BN194_19910	K0N5X4	2.86	0.44	1.36
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	asd	BN194_01060	K0N1I5	1.14	0.44	1.35
Non-specific ribonucleoside hydrolase rihC (EC 3.2.-.-)	Nucleic acid/nucleotide metabolism	rihC	BN194_03870	K0N803	0.39	0.43	1.35
Glucitol operon repressor	Transcriptional regulation	srlR	BN194_28690	K0MYG3	1.55	0.43	1.35
Thioredoxin-like protein ytpP	Posttranslational modification	ytpP	BN194_18980	K0N9F1	1.00	0.43	1.35
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatC	BN194_11950	K0N436	0.88	0.43	1.35
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	luxS	BN194_08330	K0N6J0	0.26	0.42	1.34
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	1.74	0.42	1.34
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	hslV	BN194_16000	K0N542	0.42	0.42	1.34
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	pepO_2	BN194_16630	K0N8Q0	1.43	0.41	1.33
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	11E,P100	BN194_02180	K0N513	1.13	0.41	1.33
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	pmi	BN194_02920	K0N7U2	0.89	0.40	1.32
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	yfmL	BN194_12120	K0NA13	0.64	0.40	1.32
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	ywpJ	BN194_11320	K0N9U2	0.99	0.39	1.31
30S ribosomal protein S14	Ribosomal proteins	rpsN	BN194_09950	K0N3D1	0.53	0.38	1.30
UPF0342 protein yheA	Unknown/uncharacterized	yheA	BN194_19080	K0N9F7	0.28	0.36	1.29
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	yclJ	BN194_11790	K0MUE5	1.64	0.35	1.27
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	msrA_2,msrA	BN194_15860	K0N4W6	0.76	0.33	1.26
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_3	BN194_21440	K0MWS9	0.43	0.33	1.26
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	1.32	0.33	1.26
Uncharacterized protein ycaC	General prediction only	ycaC	BN194_29650	K0N948	1.72	0.32	1.25
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	ispA	BN194_18180	K0N9A2	0.96	0.30	1.24
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	pepV	BN194_08800	K0N324	1.81	0.30	1.23
Nucleic acid-binding protein	Unknown/uncharacterized		BN194_18680	K0N9D5	0.26	0.30	1.23

>tr|K0N699|K0N699_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA PE=3 SV=1;>tr|K0MWW4|K0MWW4_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA_2 PE=3 SV=1	Cell wall biogenesis	rmlA		K0N699;K0MWW4	0.64	0.30	1.23
Probable catabolite control protein A	Transcriptional regulation	ccpA	BN194_08750	K0N323	1.45	0.30	1.23
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	ycnE	BN194_13230	K0N7R3	0.34	0.29	1.22
Aldose 1-epimerase	Central glycolytic/intermediary pathways		BN194_16020	K0NAP4	0.82	0.28	1.22
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	ptsH	BN194_19430	K0N9I2	0.34	0.27	1.21
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE	BN194_02970	K0N7U7	0.86	0.27	1.21
Cold shock-like protein CspLA	Transcription-associated proteins	cspLA	BN194_12460	K0N438	0.27	0.27	1.20
>tr|K0N5T2|K0N5T2_LACCA Phosphoenolpyruvate-protein phosphotransferase OS=Lactobacillus casei W56 GN=ptsI PE=3 SV=1	Phosphotransferase systems	ptsI		K0N5T2	1.49	0.27	1.20
Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	nfo	BN194_17070	K0NAW5	0.25	0.26	1.20
Transcriptional regulator	Transcriptional regulation		BN194_08230	K0N6I4	0.61	0.25	1.19
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	coaD	BN194_15200	K0N4X3	2.20	0.24	1.18
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	pncB	BN194_19860	K0N5X0	0.96	0.24	1.18
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	1.89	0.24	1.18
Penicillin-binding protein 1A	Cell wall biogenesis	ponA	BN194_16720	K0NAU3	0.25	0.24	1.18
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	oppF	BN194_17910	K0N5I3	0.71	0.23	1.17
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	mhqD	BN194_18770	K0NB71	0.18	0.23	1.17
Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	gntK	BN194_02340	K0MS76	0.55	0.22	1.16
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	prs1,prs	BN194_26930	K0NAT2	0.61	0.21	1.16
Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		BN194_08520	K0N972	0.33	0.21	1.16
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	tpx	BN194_08090	K0MTJ5	0.83	0.21	1.16
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	purB	BN194_12520	K0NA41	0.45	0.20	1.15

Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	ysgA	BN194_18610	K0N5M8	0.20	0.20	1.15
Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	0.79	0.20	1.15
Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		BN194_20000	K0N684	1.07	0.20	1.15
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	murE	BN194_02160	K0N1S5	0.65	0.20	1.15
Regulatory protein vanR	Signal transduction	vanR	BN194_02120	K0N7G4	0.69	0.20	1.14
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	cysS	BN194_24430	K0NAB2	0.42	0.19	1.14
Cell division protein FtsZ	Cytokinesis	ftsZ	BN194_14760	K0N4L6	0.83	0.19	1.14
Putative nrdI-like protein	Nucleic acid/nucleotide metabolism		BN194_08250	K0N300	0.60	0.19	1.14
>tr|K0N2V4|K0N2V4_LACCA GlpO protein OS=Lactobacillus casei W56 GN=glpO PE=4 SV=1	Carbohydrate-related metabolism	glpO		K0N2V4	0.58	0.18	1.14
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	0.81	0.18	1.13
Uncharacterized protein YxeH	General prediction only	yxeH	BN194_04750	K0N1Y7	0.68	0.18	1.13
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	0.48	0.18	1.13
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	BN194_21350	BN194_21780	K0N6Q5	1.33	0.18	1.13
Cold shock protein CspA	Transcription-associated proteins	cspA	BN194_14820	K0NAH0	0.43	0.17	1.13
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	prs1_2	BN194_30370	K0NDQ5	0.46	0.17	1.12
Chaperone protein ClpB	Protein folding/turnover	clpB_2	BN194_26350	K0N887	0.39	0.17	1.12
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	tpiA	BN194_11030	K0N736	0.69	0.16	1.12
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	0.33	0.16	1.12
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	rnjA	BN194_15020	K0NAH6	0.56	0.16	1.12
Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	Steap4	BN194_01990	K0MS41	0.31	0.15	1.11
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	dut	BN194_24640	K0MXG3	0.47	0.15	1.11
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		BN194_08960	K0N387	0.40	0.15	1.11
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		BN194_13770	K0NAC0	0.27	0.15	1.11
Oligoendopeptidase, pepF/M3 family	Amino acid-related metabolism		BN194_11580	K0N779	0.28	0.15	1.11
Uncharacterized protein yutG	Lipid-related metabolism	yutG	BN194_08940	K0MTQ3	0.45	0.14	1.10
Transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	0.21	0.14	1.10

Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	pepS	BN194_12180	K0N7D5	0.18	0.13	1.09
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	nox_2	BN194_02850	K0N1N9	0.29	0.12	1.09
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	htrA	BN194_29460	K0N8D9	0.25	0.12	1.09
>tr|K0N9X8|K0N9X8_LACCA SpsK protein OS=Lactobacillus casei W56 GN=spsK PE=4 SV=1;>tr|K0N6D6|K0N6D6_LACCA SpsK_2 protein OS=Lactobacillus casei W56 GN=spsK_2 PE=4 SV=1	Cell wall biogenesis	spsK_2		K0N9X8;K0N6D6	0.39	0.11	1.08
Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	rbsK	BN194_03300	K0N1R2	0.29	0.11	1.08
Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	0.54	0.10	1.07
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	0.25	0.10	1.07
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	patB_2	BN194_09790	K0MTW3	0.28	0.09	1.07
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	phoU	BN194_10290	K0MTZ9	0.16	0.09	1.07
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	agaS	BN194_02940	K0MSD9	0.34	0.09	1.06
Virulence factor mviM	General prediction only	mviM	BN194_13310	K0N4B2	0.12	0.08	1.06
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	nrnA	BN194_08450	K0N309	0.35	0.08	1.06
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	gpsB	BN194_16690	K0MVN5	0.19	0.08	1.06
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2_2,lacD	BN194_27060	K0N7P0	0.19	0.08	1.06
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		BN194_27170	K0NCZ6	0.43	0.07	1.05
Cellobiose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	celA_5	BN194_29600	K0N945	0.11	0.07	1.05
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	pheT	BN194_18560	K0N5M4	0.23	0.07	1.05
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	nusB	BN194_18220	K0NB49	0.15	0.06	1.04
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	0.14	0.06	1.04
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatB	BN194_11970	K0NA01	0.20	0.06	1.04
UPF0659 protein YMR090W	General prediction only	ylbE	BN194_07030	K0N671	0.16	0.06	1.04
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	ftsH	BN194_26460	K0N7I8	0.21	0.06	1.04
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	yqeC	BN194_02330	K0N532	0.14	0.05	1.04

Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	rpe	BN194_18000	K0N5T1	0.11	0.05	1.03
Single-stranded DNA-binding protein (SSB)	DNA replication-related	ssb	BN194_00110	K0N1C2	0.06	0.04	1.03
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	frr	BN194_17650	K0N5M3	0.08	0.04	1.03
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	gpmA2,gpmA	BN194_22740	K0MX58	0.12	0.04	1.03
DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	gyrB	BN194_00060	K0N1B8	0.06	0.04	1.03
PTS system IIB component, Gat family	Phosphotransferase systems		BN194_07430	K0N6A5	0.07	0.03	1.02
Oligoendopeptidase F	Amino acid-related metabolism	yjbG_2	BN194_08130	K0N6H7	0.16	0.03	1.02
Glutamine-binding periplasmic protein	ABC-type transporter systems	glnH_2	BN194_29910	K0N8I1	0.03	0.03	1.02
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	0.07	0.02	1.01
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	ykwC	BN194_02520	K0N7M3	0.02	0.01	1.01
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	glcK	BN194_18420	K0NB57	0.02	0.01	1.01
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	patA_2	BN194_22950	K0N7F8	0.00	0.00	1.00
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	glmM	BN194_11550	K0N3Y7	0.01	0.00	1.00
Cell division protein FtsA	Cytokinesis	ftsA	BN194_14750	K0N4T3	0.00	0.00	1.00
Uncharacterized protein	General prediction only		BN194_21200	K0N6M8	0.01	0.00	1.00
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	dltA	BN194_08590	K0MTN0	0.01	-0.01	1.00
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	5.41	-7.33	-160.783
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	fabD	BN194_22570	K0NBT1	5.68	-6.68	-102.2
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	fabZ	BN194_22520	K0NBS8	6.66	-6.47	-88.4745
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	bkr4	BN194_22550	K0N799	4.16	-5.98	-63.1675
>tr|K0N788|K0N788_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_22500 PE=4 SV=1	Unknown/uncharacterized	K0N788		K0N788	4.21	-5.82	-56.4394
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	fabK	BN194_22580	K0NA38	3.67	-5.35	-40.8689
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)	Lipid-related metabolism	accC	BN194_22510	K0N6M5	4.08	-4.81	-27.9943
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	fabH	BN194_22600	K0N7B0	6.08	-4.52	-22.9207

3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	fabF	BN194_22540	K0MX40	2.02	-4.30	-19.7652
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	accB	BN194_22530	K0NA35	2.92	-3.93	-15.2529
>tr|K0NAP8|K0NAP8_LACCA ParC protein OS=Lactobacillus casei W56 GN=parC PE=4 SV=1	Phosphotransferase systems	K0NAP8		K0NAP8	0.86	-3.23	-9.3543
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	fabG	BN194_22560	K0N6N3	2.29	-3.14	-8.81335
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	fabZ_2	BN194_22620	K0NBT3	1.18	-2.66	-6.32016
Acyl carrier protein (ACP)	Lipid-related metabolism	acpP_2, acpP	BN194_22590	K0MX45	1.99	-2.61	-6.08885
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	accA	BN194_22470	K0NBS6	2.35	-2.51	-5.69056
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	helD	BN194_21130	K0N9W3	1.20	-2.32	-4.99956
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	clpC	BN194_21680	K0N9Z7	2.37	-2.01	-4.03531
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	treA	BN194_06930	K0N662	3.18	-1.82	-3.54027
Tautomerase (EC 5.3.2.-)	General prediction only		BN194_16890	K0MVQ1	0.54	-1.82	-3.53622
PspC domain-containing protein	Unknown/uncharacterized	ythC	BN194_10300	K0N3H5	3.80	-1.41	-2.65516
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism	K0N6M0	BN194_22460	K0N6M0	1.80	-1.36	-2.57323
50S ribosomal protein L32	Ribosomal proteins	rpmF	BN194_15510	K0N4T0	0.70	-1.33	-2.51027
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE_3	BN194_04780	K0N5N9	2.84	-1.31	-2.4857
ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	clpX	BN194_15340	K0MVC6	4.05	-1.31	-2.47169
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	yabO	BN194_26520	K0NCR8	1.00	-1.29	-2.44693
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	uvrA	BN194_10450	K0N3J2	3.17	-1.25	-2.37805
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	pepN	BN194_05410	K0N2F5	4.13	-1.13	-2.18389
Uncharacterized protein	Unknown/uncharacterized		BN194_29450	K0N932	2.16	-1.10	-2.14938
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	guaB	BN194_02100	K0N1G3	2.97	-1.10	-2.14933
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	gmk	BN194_18110	K0N5J6	2.23	-1.07	-2.10006
30S ribosomal protein S14 type Z	Ribosomal proteins	rpsZ,rpsN	BN194_26090	K0MXS9	1.31	-1.06	-2.09052
30S ribosomal protein S18	Ribosomal proteins	rpsR	BN194_00120	K0N6T2	0.58	-1.05	-2.07719
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	1.84	-1.04	-2.05482

Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	msmK	BN194_11180	K0N747	1.40	-1.03	-2.04051
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	npr	BN194_04740	K0MSP8	3.32	-1.02	-2.02467
50S ribosomal protein L17	Ribosomal proteins	rplQ	BN194_25950	K0N841	1.15	-1.00	-1.99362
30S ribosomal protein S11	Ribosomal proteins	rpsK	BN194_25970	K0NCJ0	1.75	-0.99	-1.98136
Translation initiation factor IF-3	Protein translation (initiation)	infC	BN194_18820	K0NB73	2.33	-0.96	-1.94637
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	typA	BN194_15150	K0N4W9	3.56	-0.96	-1.94001
50S ribosomal protein L21	Ribosomal proteins	rplU	BN194_18290	K0MW61	0.81	-0.95	-1.93582
Dumpy	Cell surface proteins/internalins	dp	BN194_05390	K0MSV0	1.58	-0.94	-1.91287
30S ribosomal protein S19	Ribosomal proteins	rpsS	BN194_26180	K0NAM1	1.87	-0.92	-1.8959
50S ribosomal protein L16	Ribosomal proteins	rplP	BN194_26150	K0N863	1.76	-0.92	-1.89099
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshA	BN194_26700	K0N8C7	4.42	-0.91	-1.8789
30S ribosomal protein S5	Ribosomal proteins	rpsE	BN194_26050	K0N853	2.21	-0.89	-1.85007
50S ribosomal protein L30	Ribosomal proteins	rpmD	BN194_26040	K0MXS6	3.25	-0.88	-1.84458
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	yhaA	BN194_30550	K0N9E4	0.68	-0.86	-1.82117
50S ribosomal protein L13	Ribosomal proteins	rplM	BN194_25850	K0N828	2.71	-0.86	-1.81713
30S ribosomal protein S3	Ribosomal proteins	rpsC	BN194_26160	K0N7G5	1.56	-0.85	-1.80093
30S ribosomal protein S13	Ribosomal proteins	rpsM	BN194_25980	K0NAK3	1.81	-0.85	-1.7989
50S ribosomal protein L10	Ribosomal proteins	rplJ	BN194_24090	K0MXD8	3.12	-0.84	-1.79562
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	gyrA	BN194_00070	K0N6S7	2.19	-0.84	-1.7949
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	obg	BN194_15440	K0MVD3	1.78	-0.84	-1.7895
Putative tRNA-binding protein ytpR	General prediction only	ytpR	BN194_18970	K0NB80	1.59	-0.83	-1.78268
30S ribosomal protein S8	Ribosomal proteins	rpsH	BN194_26080	K0NAL1	2.06	-0.82	-1.76167
Pur operon repressor	Transcriptional regulation	purR_2	BN194_26960	K0N7M9	0.57	-0.81	-1.75054
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	pfkA	BN194_15570	K0NAK6	3.16	-0.81	-1.74886
Elongation factor G (EF-G)	Protein translation (elongation)	fusA	BN194_26270	K0NCN8	3.34	-0.80	-1.74515
30S ribosomal protein S17	Ribosomal proteins	rpsQ	BN194_26130	K0NAL6	3.16	-0.80	-1.74172
50S ribosomal protein L4	Ribosomal proteins	rplD	BN194_26210	K0N7H0	2.34	-0.80	-1.73889

50S ribosomal protein L23	Ribosomal proteins	rplW	BN194_26200	K0N869	2.00	-0.79	-1.73457
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	iscS1	BN194_14900	K0N4U8	1.36	-0.76	-1.69748
PTS system IIB component, L-Asc family	Phosphotransferase systems		BN194_28560	K0N861	0.11	-0.76	-1.69254
50S ribosomal protein L6	Ribosomal proteins	rplF	BN194_26070	K0NCK5	3.02	-0.76	-1.69008
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	2.16	-0.75	-1.6864
50S ribosomal protein L5	Ribosomal proteins	rplE	BN194_26100	K0N859	2.85	-0.75	-1.6808
Inosose dehydratase (EC 4.2.1.44) (2-keto-myo-inositol dehydratase)	Carbohydrate-related metabolism	iolE	BN194_02290	K0MS68	1.26	-0.74	-1.67559
Uncharacterized protein ynbB	Cell defense/detoxification	ynbB	BN194_18380	K0N9B7	1.88	-0.74	-1.66802
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	yutF	BN194_08910	K0N383	2.03	-0.74	-1.66521
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdF	BN194_16610	K0N552	1.66	-0.73	-1.66264
50S ribosomal protein L11	Ribosomal proteins	rplK	BN194_24160	K0N724	1.96	-0.73	-1.65809
50S ribosomal protein L18	Ribosomal proteins	rplR	BN194_26060	K0N7F4	1.59	-0.72	-1.6525
30S ribosomal protein S10	Ribosomal proteins	rpsJ	BN194_26230	K0NAM5	2.31	-0.72	-1.64676
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	lacC	BN194_07470	K0N8Y4	3.03	-0.72	-1.64396
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	guaA	BN194_21070	K0NBJ2	2.99	-0.70	-1.62622
Transcriptional regulatory protein YycF	Signal transduction	yycF_2	BN194_29510	K0N8E4	1.80	-0.70	-1.62621
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	1.99	-0.70	-1.62582
50S ribosomal protein L35	Ribosomal proteins	rpmI	BN194_18810	K0N5P1	2.40	-0.70	-1.62318
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	aspS	BN194_17100	K0N5F3	2.02	-0.70	-1.62242
Transcriptional regulator, TetR family	Transcriptional regulation		BN194_12190	K0MUM1	2.88	-0.69	-1.60895
Transcriptional regulatory protein spaR	Signal transduction	spaR	BN194_05330	K0N5S9	0.26	-0.68	-1.60617
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07700	K0N2V5	1.27	-0.68	-1.59993
50S ribosomal protein L19	Ribosomal proteins	rplS	BN194_17770	K0NB12	2.04	-0.68	-1.59974
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	lacB	BN194_07490	K0MTB7	2.25	-0.68	-1.59742
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	prfB	BN194_10180	K0N6W9	1.94	-0.67	-1.58814
30S ribosomal protein S4	Ribosomal proteins	rpsD	BN194_14440	K0MV63	3.14	-0.66	-1.5811

Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	fba_2	BN194_05060	K0N2C9	2.28	-0.66	-1.57892
50S ribosomal protein L14	Ribosomal proteins	rplN	BN194_26120	K0NCL3	2.72	-0.66	-1.57725
50S ribosomal protein L3	Ribosomal proteins	rplC	BN194_26220	K0NCN1	2.36	-0.66	-1.57552
50S ribosomal protein L2	Ribosomal proteins	rplB	BN194_26190	K0MXU1	2.76	-0.65	-1.57433
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	alsS	BN194_20150	K0N695	3.19	-0.65	-1.56868
50S ribosomal protein L22	Ribosomal proteins	rplV	BN194_26170	K0NCM1	2.25	-0.65	-1.56805
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		BN194_01410	K0N1L0	0.75	-0.65	-1.56594
50S ribosomal protein L1	Ribosomal proteins	rplA	BN194_24150	K0N7M7	2.26	-0.64	-1.55637
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	yqeL,rsfS	BN194_18710	K0N5N6	2.40	-0.63	-1.54272
30S ribosomal protein S12	Ribosomal proteins	rpsL	BN194_26290	K0MXV0	1.76	-0.62	-1.54137
30S ribosomal protein S20	Ribosomal proteins	rpsT	BN194_15250	K0N4X9	1.05	-0.62	-1.53632
Transcription termination/antitermination protein NusG	Transcription-associated proteins	nusG	BN194_24260	K0N730	0.95	-0.62	-1.53469
>tr|K0N6D0|K0N6D0_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_20650 PE=4 SV=1	Unknown/uncharacterized	K0N6D0		K0N6D0	0.63	-0.61	-1.52932
30S ribosomal protein S7	Ribosomal proteins	rpsG	BN194_26280	K0NAM9	2.12	-0.60	-1.51808
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	1.86	-0.60	-1.51721
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	rpoC	BN194_26330	K0NAN3	2.99	-0.60	-1.51577
FeS cluster assembly protein sufB	Cofactor-related metabolism	sufB	BN194_13810	K0N4E5	1.40	-0.60	-1.51457
Uncharacterized protein SE_0534	tRNA/Ribosome assembly/processing		BN194_10150	K0N3F2	2.35	-0.59	-1.50512
S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	metK	BN194_09150	K0N352	2.85	-0.59	-1.50126
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	hisS	BN194_17110	K0N5A0	1.78	-0.59	-1.50106
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	clpE	BN194_19450	K0N644	1.64	-0.58	-1.49813
Chaperone protein DnaJ	Protein folding/turnover	dnaJ	BN194_17450	K0N5J4	2.28	-0.58	-1.49807
30S ribosomal protein S9	Ribosomal proteins	rpsI	BN194_25840	K0MXR0	1.08	-0.58	-1.49729
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC	BN194_24670	K0NC50	1.27	-0.57	-1.48895
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	groL,groEL	BN194_23750	K0N7K7	2.70	-0.57	-1.4874

Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	glyS	BN194_16950	K0N5D3	1.86	-0.56	-1.47641
Translation initiation factor IF-2	Protein translation (initiation)	infB	BN194_17550	K0N5K7	1.52	-0.56	-1.47135
50S ribosomal protein L27	Ribosomal proteins	rpmA	BN194_18270	K0NB51	0.79	-0.55	-1.46546
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		BN194_11600	K0N3Z3	0.92	-0.55	-1.4631
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	yqeH	BN194_18740	K0MW90	1.58	-0.55	-1.46303
50S ribosomal protein L20	Ribosomal proteins	rplT	BN194_18800	K0N5Y4	1.86	-0.55	-1.46287
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	1.65	-0.55	-1.46254
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	atpA	BN194_13600	K0N4K1	1.98	-0.55	-1.46057
30S ribosomal protein S2	Ribosomal proteins	rpsB	BN194_17680	K0N936	2.73	-0.55	-1.45992
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	HBN1	BN194_16550	K0N597	0.98	-0.53	-1.4447
50S ribosomal protein L15	Ribosomal proteins	rplO	BN194_26030	K0NAK7	1.69	-0.53	-1.4423
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	mtnN	BN194_14890	K0MV90	0.94	-0.53	-1.44008
Uncharacterized protein	Lipid-related metabolism	YerQ	BN194_11980	K0N7B3	1.82	-0.52	-1.43805
30S ribosomal protein S21	Ribosomal proteins	rpsU	BN194_17050	K0N5E5	1.39	-0.52	-1.43722
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2,lacD	BN194_07480	K0N6A8	1.72	-0.52	-1.4337
50S ribosomal protein L29	Ribosomal proteins	rpmC	BN194_26140	K0MXT6	2.83	-0.51	-1.42622
Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	1.82	-0.51	-1.42432
NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	1.61	-0.51	-1.4239
50S ribosomal protein L31 type B	Ribosomal proteins	rpmE2	BN194_26770	K0NCV4	1.48	-0.51	-1.42273
RNA polymerase sigma factor SigA	RNA polymerase	rpoD,sigA	BN194_16920	K0NAV6	0.43	-0.51	-1.41967
30S ribosomal protein S15	Ribosomal proteins	rpsO	BN194_15260	K0N4Q6	0.99	-0.50	-1.41
Bifunctional protein GlmU	Cell wall biogenesis	glmU	BN194_26940	K0MY10	0.77	-0.49	-1.40849
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	cmk	BN194_15710	K0N4V1	1.22	-0.49	-1.40269
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC_2	BN194_24680	K0NAC2	1.64	-0.48	-1.39811

Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	upp	BN194_13550	K0N4J8	1.76	-0.48	-1.39414
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	hpt	BN194_26470	K0NCR2	0.82	-0.47	-1.38498
Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	pyk	BN194_15580	K0N8B6	2.90	-0.47	-1.38218
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	dnaK	BN194_17460	K0N5C7	1.28	-0.46	-1.37975
50S ribosomal protein L33	Ribosomal proteins	rpmG	BN194_20200	K0N697	0.90	-0.46	-1.37599
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	queA	BN194_08370	K0N965	1.26	-0.45	-1.36565
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	clpP_2, clpP	BN194_10510	K0N3M4	1.47	-0.45	-1.36276
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	apt	BN194_17380	K0N902	0.60	-0.45	-1.36219
30S ribosomal protein S16	Ribosomal proteins	rpsP	BN194_17810	K0N5H1	0.48	-0.44	-1.35953
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	rpoB	BN194_26340	K0MXV4	2.70	-0.44	-1.35894
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	grpE	BN194_17470	K0NAZ2	1.07	-0.44	-1.35491
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	murF	BN194_26720	K0NCU5	0.94	-0.44	-1.354
>tr|K0NBL8|K0NBL8_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_21520 PE=3 SV=1	Unknown/uncharacterized	K0NBL8		K0NBL8	1.33	-0.43	-1.34874
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	cap4C	BN194_12280	K0N7E3	1.78	-0.43	-1.34516
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	atpG	BN194_13610	K0N4D3	0.96	-0.43	-1.34455
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	asnS	BN194_16760	K0N569	0.71	-0.43	-1.34288
Ribosome-binding ATPase YchF	Protein translation (peptide release)	engD,ychF	BN194_02070	K0N7F7	1.99	-0.42	-1.34079
Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	adk	BN194_26010	K0N7F0	1.33	-0.42	-1.33984
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	ykpA	BN194_07220	K0N8V6	1.52	-0.42	-1.33761
DegV domain-containing protein CA_C1624	Unknown/uncharacterized		BN194_14170	K0NAD8	0.25	-0.42	-1.33424
Chaperone protein ClpB	Protein folding/turnover	clpB	BN194_15500	K0N4Z8	0.82	-0.41	-1.33268
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	argS	BN194_19120	K0NB86	1.23	-0.41	-1.33164
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	3.19	-0.41	-1.33139

50S ribosomal protein L24	Ribosomal proteins	rplX	BN194_26110	K0N7F9	0.93	-0.40	-1.32393
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	hslO	BN194_26400	K0N893	1.28	-0.40	-1.32199
Probable dipeptidase (EC 3.4.-.-)	Amino acid-related metabolism		BN194_13380	K0N7S0	1.64	-0.40	-1.31724
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	der	BN194_15730	K0N8E1	1.35	-0.39	-1.30734
Protein translocase subunit SecA	Protein export	secA	BN194_10170	K0N9J2	1.55	-0.38	-1.30477
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	pyrH	BN194_17660	K0N5E6	1.27	-0.38	-1.30212
Transcription termination/antitermination protein NusA	Transcription-associated proteins	nusA	BN194_17580	K0N927	1.67	-0.38	-1.30169
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	ileS	BN194_14810	K0N4L9	0.90	-0.38	-1.29836
30S ribosomal protein S6	Ribosomal proteins	rpsF	BN194_00100	K0N0Z1	1.34	-0.38	-1.29798
Predicted hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	0.52	-0.37	-1.28834
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	pyrG	BN194_26790	K0MXZ1	1.65	-0.36	-1.2852
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	1.36	-0.35	-1.27867
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	1.34	-0.35	-1.27721
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	nagB	BN194_30440	K0MYW0	1.17	-0.35	-1.27607
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	lacA	BN194_07500	K0N2T4	1.68	-0.35	-1.27393
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	ddl	BN194_01390	K0MRY4	0.31	-0.35	-1.27366
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	atpD	BN194_13620	K0NAB3	2.28	-0.35	-1.27086
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	rpoA	BN194_25960	K0N7E5	1.67	-0.34	-1.26896
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	eno	BN194_11040	K0MU67	1.47	-0.34	-1.2689
Lactaldehyde dehydrogenase (EC 1.2.1.21) (EC 1.2.1.22)	Cell defense/detoxification	aldA	BN194_25470	K0NCB9	1.23	-0.34	-1.26553
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	xpt	BN194_12490	K0MUR6	1.74	-0.33	-1.26123
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	ohrR	BN194_10500	K0N3J7	0.40	-0.33	-1.26076
30S ribosomal protein S1 homolog	Ribosomal proteins	ypfD	BN194_15720	K0NAL9	0.87	-0.33	-1.25999
Protein RecA (Recombinase A)	DNA repair/recombination	recA_2,recA	BN194_27650	K0N8P0	0.47	-0.33	-1.25373

Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	pcp	BN194_01980	K0N4Y4	1.79	-0.33	-1.25333
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	gltX	BN194_24470	K0NC38	1.01	-0.32	-1.2522
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	asnB	BN194_22990	K0MX90	0.89	-0.32	-1.2492
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	alaS	BN194_08480	K0N6K2	0.98	-0.32	-1.24728
>tr|K0N3R3|K0N3R3_LACCA Gap protein OS=Lactobacillus casei W56 GN=gap PE=3 SV=1	Central glycolytic/intermediary pathways	gap		K0N3R3;K0N4X1	0.80	-0.31	-1.24157
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	rpoZ	BN194_18100	K0N5T7	0.66	-0.31	-1.23893
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	thrS	BN194_18860	K0N5P5	2.51	-0.31	-1.23884
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	metG	BN194_27130	K0NAU5	1.86	-0.31	-1.23641
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	glnA_2	BN194_18340	K0MW64	0.99	-0.31	-1.23575
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	0.73	-0.30	-1.2272
Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	0.62	-0.29	-1.22647
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	aldB	BN194_20140	K0MWH5	0.43	-0.29	-1.22276
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		BN194_03130	K0N5D9	1.49	-0.29	-1.22157
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	glpK	BN194_07280	K0N694	0.62	-0.29	-1.21983
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	proS	BN194_17610	K0N5E2	1.30	-0.29	-1.21849
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	pgk	BN194_11020	K0N9R1	0.64	-0.28	-1.21663
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	pth	BN194_26550	K0N8B3	0.19	-0.28	-1.21575
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdE2	BN194_16600	K0N5A1	1.14	-0.28	-1.21216
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	rpoE	BN194_26810	K0N7L4	0.80	-0.27	-1.20896
Nucleoid-associated protein BN194_23980	General prediction only		BN194_23980	K0NA95	1.00	-0.27	-1.2082
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	trxB	BN194_10360	K0N3L1	1.27	-0.27	-1.20585
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	yabR	BN194_26500	K0N8A7	0.76	-0.27	-1.20429
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	bglP	BN194_06940	K0MT60	1.06	-0.26	-1.20132

Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	rluB	BN194_15650	K0N509	1.20	-0.26	-1.19889
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	mnmA	BN194_14930	K0N844	1.49	-0.26	-1.1967
Uncharacterized protein MJ0282	Cofactor-related metabolism		BN194_03700	K0N1T2	0.39	-0.25	-1.19038
Protein LemA	Unknown/uncharacterized	lemA	BN194_27350	K0N8J7	0.54	-0.25	-1.18985
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	tuf	BN194_15310	K0N4R1	1.68	-0.25	-1.18897
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	ftsY	BN194_17850	K0N5R8	0.67	-0.25	-1.18816
Protein ytsP	Signal transduction	ytsP	BN194_14450	K0N4Q9	0.22	-0.25	-1.18765
ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit) (F-ATPase epsilon subunit)	Membrane bioenergetics	atpC	BN194_13630	K0N7T2	0.14	-0.25	-1.18653
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	rmlB	BN194_21340	K0MWS0	0.32	-0.24	-1.18244
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	0.74	-0.24	-1.18118
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	ldh	BN194_26560	K0N7J5	0.70	-0.24	-1.18064
Response regulator ArlR	Signal transduction	arlR	BN194_18650	K0N5X3	0.43	-0.24	-1.18015
UPF0337 protein yhjA	General prediction only	yhjA	BN194_24800	K0N7S1	0.26	-0.24	-1.17863
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	tsf	BN194_17670	K0NB01	0.70	-0.23	-1.17505
HTH-type transcriptional repressor yvoA	Transcriptional regulation	yvoA_2	BN194_19880	K0N9L8	0.30	-0.23	-1.17329
Uncharacterized protein	Cofactor-related metabolism		BN194_18720	K0NB69	1.47	-0.23	-1.17207
>tr|K0N1M9|K0N1M9_LACCA Probable phosphoketolase OS=Lactobacillus casei W56 GN=xpkA PE=3 SV=1	Central glycolytic/intermediary pathways	xpkA		K0N1M9;K0N8X7	1.19	-0.22	-1.16254
DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	1.05	-0.21	-1.16013
Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	aspC	BN194_16770	K0NAU6	0.34	-0.20	-1.15128
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	murC	BN194_18950	K0N600	0.39	-0.20	-1.14877
>tr|K0N6A9|K0N6A9_LACCA Tyrosine--tRNA ligase OS=Lactobacillus casei W56 GN=tyrS PE=4 SV=1	tRNA aminoacyl synthesis	tyrS		K0N6A9	0.34	-0.20	-1.14741
Aspartate racemase (EC 5.1.1.13)	Amino acid-related metabolism		BN194_02170	K0N7H2	0.53	-0.20	-1.14476
Uncharacterized protein YqhY	Unknown/uncharacterized	yqhY	BN194_18230	K0N9A7	0.69	-0.19	-1.14346
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshB	BN194_08460	K0N356	0.65	-0.19	-1.1432
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	ndk	BN194_08160	K0N340	0.11	-0.19	-1.14313

Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	pepQ	BN194_08740	K0MTP0	1.15	-0.19	-1.14246
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	oppD	BN194_17920	K0NB35	0.84	-0.19	-1.13947
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	pyrDA, pyrD	BN194_19150	K0N623	0.70	-0.19	-1.13751
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	gmuB	BN194_23840	K0MXC7	0.50	-0.18	-1.13438
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_4	BN194_29900	K0N971	0.56	-0.18	-1.13179
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	nadE	BN194_19840	K0MWF6	1.56	-0.18	-1.12903
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	rnr	BN194_11100	K0N3S4	1.02	-0.17	-1.12817
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	purA	BN194_01160	K0N1J0	0.65	-0.17	-1.12308
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	rbfA	BN194_17540	K0MVV7	0.66	-0.16	-1.12102
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	tig	BN194_15330	K0N884	0.54	-0.16	-1.1182
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	lysS	BN194_26380	K0NAN7	0.33	-0.16	-1.11626
Bifunctional protein FolD	Cofactor-related metabolism	folD	BN194_18210	K0N5K0	1.08	-0.16	-1.11428
Acetyltransferase	General prediction only		BN194_08200	K0N2Z8	0.40	-0.16	-1.11346
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	groS,grES	BN194_23760	K0N700	0.14	-0.15	-1.11111
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	murA2,murA	BN194_26780	K0NAR9	0.38	-0.15	-1.1098
tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	dus1	BN194_26390	K0MXV9	0.53	-0.14	-1.10436
Transcriptional regulator, XRE family	Transcriptional regulation		BN194_30170	K0NDP4	0.28	-0.14	-1.10428
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	trpS	BN194_27360	K0N7S4	0.35	-0.14	-1.10422
Probable flavodoxin-1	Membrane bioenergetics	ykuN_2	BN194_12220	K0NA19	0.21	-0.13	-1.0967
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	zwf	BN194_08420	K0N966	0.22	-0.12	-1.08357
50S ribosomal protein L7/L12	Ribosomal proteins	rplL	BN194_24080	K0NA98	0.47	-0.12	-1.08319
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	0.61	-0.12	-1.083
Uncharacterized protein ylxR	General prediction only	ylxR	BN194_17570	K0NAZ6	0.32	-0.11	-1.08098
GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	relA	BN194_17230	K0N8Y0	0.13	-0.11	-1.07606
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	dnaN	BN194_00020	K0N6S3	0.25	-0.10	-1.07503

Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	rnc	BN194_17870	K0NB31	0.56	-0.10	-1.07333
Elongation factor P	Protein translation (elongation)	efp	BN194_18240	K0MW57	0.23	-0.10	-1.0722
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	prfA	BN194_13510	K0N4C6	0.16	-0.09	-1.06579
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	valS	BN194_14510	K0N4J6	0.21	-0.08	-1.0597
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	atpH	BN194_13590	K0MV16	0.21	-0.08	-1.05914
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	0.29	-0.08	-1.05839
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	murD	BN194_14720	K0NAG5	0.24	-0.08	-1.05629
MreB-like protein	Cytokinesis	mbl	BN194_13650	K0N4K5	0.21	-0.08	-1.05367
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	yfeX	BN194_07170	K0N8U9	0.42	-0.07	-1.05274
Translation initiation factor IF-1	Protein translation (initiation)	infA	BN194_26000	K0N847	0.11	-0.07	-1.04791
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	gatA	BN194_11960	K0N3Z6	0.34	-0.07	-1.04637
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	fpaP_3	BN194_21160	K0N682	0.20	-0.06	-1.04578
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	manD	BN194_02950	K0N1P4	0.26	-0.06	-1.04383
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	ybeY	BN194_17010	K0N594	0.10	-0.06	-1.04265
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	map	BN194_12230	K0N7E0	0.15	-0.06	-1.04022
Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	leuS	BN194_09210	K0N3A9	0.49	-0.06	-1.03963
>tr|K0NB98|K0NB98_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_19420 PE=4 SV=1	Unknown/uncharacterized	K0NB98		K0NB98	0.04	-0.05	-1.03569
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	def	BN194_15060	K0N4N6	0.13	-0.04	-1.0262
50S ribosomal protein L9	Ribosomal proteins	rplI	BN194_01130	K0N4K3	0.09	-0.04	-1.02577
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	nagA	BN194_19890	K0MWF9	0.16	-0.03	-1.02273
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	greA	BN194_18520	K0NB62	0.08	-0.03	-1.02063
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	pepDB	BN194_21110	K0N678	0.10	-0.03	-1.02011
Thioredoxin	Posttranslational modification	trxA_2	BN194_08570	K0N975	0.03	-0.02	-1.01153

Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	ppaC	BN194_16110	K0N4Z4	0.06	-0.02	-1.0108
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	hprK	BN194_10330	K0N6Y3	0.02	-0.02	-1.01056
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	serS	BN194_20080	K0N9N4	0.04	-0.01	-1.01003
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	gpsA	BN194_10350	K0N3I2	0.03	-0.01	-1.0098
Lipoprotein	ABC-type transporter systems	metQ_2	BN194_13740	K0MV23	0.02	-0.01	-1.00813
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	pheS	BN194_18570	K0NB64	0.02	-0.01	-1.0074
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	murI	BN194_08640	K0MTN4	0.02	-0.01	-1.00713
UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	0.02	-0.01	-1.00642

(1g) Protein FC >2 Tween 80 dosed Vs control P1

Protein names	**Functional Class**	**Gene**	**names**	**Protein IDs**	**-Log t-test p-value**	**t-test Difference**	**Foldc change**
UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	3.97391	3.3598	10.26598
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	msmK	BN194_11180	K0N747	3.41781	3.08548	8.488326
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	bglP	BN194_06940	K0MT60	5.18976	2.32271	5.002711
UPF0092 membrane protein yrbF	Protein export	yrbF	BN194_08390	K0MTL6	1.10648	2.29134	4.895106
ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	atpF	BN194_13580	K0N7S9	2.22616	2.1759	4.518676
>tr|K0N4Z7|K0N4Z7_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02080 PE=4 SV=1	Unknown/uncharacterized	K0N4Z7		K0N4Z7	1.43341	2.11955	4.345584
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	4.25928	1.88186	3.685499
GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	1.75104	1.84914	3.602854
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	ndk	BN194_08160	K0N340	1.50717	1.84833	3.600831
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	oppF	BN194_17910	K0N5I3	3.24901	1.84018	3.580547
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	rny	BN194_10100	K0N3E5	2.69269	1.78276	3.440838

>tr|K0N6D0|K0N6D0_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_20650 PE=4 SV=1	Unknown/uncharacterized	K0N6D0		K0N6D0	1.71841	1.7325	3.323032
Uncharacterized protein yghZ	General prediction only	yghZ	BN194_27510	K0N7U8	2.84893	1.72733	3.311145
Biotin carboxyl carrier protein	Tricarboxylic acid pathway	bcc	BN194_20370	K0NBF7	4.028	1.72014	3.294684
Uncharacterized protein ynbB	Cell defense/detoxification	ynbB	BN194_18380	K0N9B7	3.74857	1.71491	3.282762
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	Posttranslational modification	citC	BN194_20340	K0MWJ1	2.04796	1.68475	3.214847
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	3.76121	1.67431	3.191667
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC_2, deoC	BN194_02790	K0MSB5	4.04205	1.65343	3.145807
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	eno	BN194_11040	K0MU67	4.56605	1.64793	3.133837
Chaperone protein ClpB	Protein folding/turnover	clpB	BN194_15500	K0N4Z8	5.38862	1.64015	3.116982
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	rpe	BN194_18000	K0N5T1	2.63298	1.63114	3.097577
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	purB	BN194_12520	K0NA41	3.15184	1.62663	3.087908
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	metG	BN194_27130	K0NAU5	4.15407	1.60245	3.036586
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	hisS	BN194_17110	K0N5A0	3.5355	1.57559	2.980574
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	grpE	BN194_17470	K0NAZ2	3.94725	1.54813	2.924378
5-dehydro-2-deoxygluconokinase (EC 2.7.1.92) (2-deoxy-5-keto-D-gluconate kinase)	Carbohydrate-related metabolism	iolC	BN194_02250	K0N1H4	1.58238	1.53574	2.899371
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	yutF	BN194_08910	K0N383	3.31274	1.53071	2.88928
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	lysS	BN194_26380	K0NAN7	2.58309	1.52157	2.871033
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	pta	BN194_11340	K0MU95	3.65669	1.50253	2.833392
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	pgk	BN194_11020	K0N9R1	2.83525	1.47487	2.779586
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	oppD	BN194_17920	K0NB35	3.74324	1.46808	2.766535
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	gpmA2,gpmA	BN194_22740	K0MX58	3.85151	1.46095	2.752896
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	prfA	BN194_13510	K0N4C6	3.49837	1.4544	2.740426

Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	1.85044	1.44809	2.728466
Transcriptional regulatory protein YycF	Signal transduction	yycF_2	BN194_29510	K0N8E4	2.50035	1.41711	2.6705
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	glcK	BN194_18420	K0NB57	3.2409	1.40667	2.651245
PTS-dependent dihydroxyacetone kinase, dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	dhaK_2	BN194_04980	K0N5Q3	2.38527	1.39729	2.634063
NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	1.05161	1.37878	2.600484
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	tsf	BN194_17670	K0NB01	3.76507	1.37667	2.596683
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	3.25909	1.36925	2.583362
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	mtnN	BN194_14890	K0MV90	1.90959	1.343	2.536783
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	argS	BN194_19120	K0NB86	3.19225	1.3407	2.532742
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	cysK	BN194_05520	K0N8E6	3.55947	1.33786	2.527761
>tr|K0N7I1|K0N7I1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02220 PE=4 SV=1	Unknown/uncharacterized	K0N7I1		K0N7I1	0.773229	1.31705	2.491561
Pur operon repressor	Transcriptional regulation	purR_2	BN194_26960	K0N7M9	1.02875	1.31692	2.491337
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	2.54116	1.30065	2.463398
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	3.4868	1.29738	2.457821
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	htrA	BN194_29460	K0N8D9	2.33127	1.29301	2.450388
Glutamine-binding periplasmic protein	ABC-type transporter systems	glnH_2	BN194_29910	K0N8I1	1.49741	1.29278	2.449997
Uncharacterized protein	Unknown/uncharacterized		BN194_28350	K0N8V3	1.73364	1.26047	2.395738
UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	3.96442	1.24288	2.366705
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	guaB	BN194_02100	K0N1G3	4.03854	1.23939	2.360987
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	valS	BN194_14510	K0N4J6	3.78591	1.23574	2.355021
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	hslO	BN194_26400	K0N893	5.78066	1.21648	2.32379
UPF0342 protein yheA	Unknown/uncharacterized	yheA	BN194_19080	K0N9F7	1.7156	1.20404	2.303839
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdF	BN194_16610	K0N552	2.6889	1.1985	2.295009

Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	rpiA_2, ripA	BN194_28600	K0N8W9	0.673776	1.19178	2.284344
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	2.6223	1.18541	2.27428
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	typA	BN194_15150	K0N4W9	3.0176	1.17413	2.256568
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	3.02191	1.1673	2.24591
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	obg	BN194_15440	K0MVD3	2.81518	1.1459	2.212841
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	prfB	BN194_10180	K0N6W9	2.89243	1.1281	2.185707
Elongation factor G (EF-G)	Protein translation (elongation)	fusA	BN194_26270	K0NCN8	3.72624	1.12609	2.182664
Septum site-determining protein DivIVA	Cytokinesis	divIVA	BN194_14800	K0N4T8	1.52216	1.11856	2.171301
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	hprK	BN194_10330	K0N6Y3	2.87128	1.10969	2.157993
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	iscS1	BN194_14900	K0N4U8	1.93238	1.10334	2.148515
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	BN194_21350	BN194_21780	K0N6Q5	2.61151	1.10277	2.147667
Response regulator ArlR	Signal transduction	arlR	BN194_18650	K0N5X3	1.87561	1.10173	2.146119
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC	BN194_00080	K0N486	2.90848	1.07991	2.113904
Protein hit	tRNA aminoacyl synthesis	hit	BN194_19040	K0MWA8	2.35533	1.07298	2.103774
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	gpsB	BN194_16690	K0MVN5	4.69677	1.06963	2.098895
3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase (THcHDO hydrolase) (EC 3.7.1.22)	Carbohydrate-related metabolism	iolD	BN194_02260	K0N1T3	0.881007	1.04575	2.064439
Probable L-ascorbate-6-phosphate lactonase ulaG (EC 3.1.1.-)	Carbohydrate-related metabolism	ulaG	BN194_28590	K0MYF8	1.1839	1.03637	2.05106
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	pyrC	BN194_16470	K0NAS6	1.16406	1.03605	2.050606
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	2.5461	1.03528	2.049511
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	0.924617	1.0312	2.043723
Elongation factor P	Protein translation (elongation)	efp	BN194_18240	K0MW57	2.88092	1.01226	2.017068
50S ribosomal protein L7/L12	Ribosomal proteins	rplL	BN194_24080	K0NA98	4.32135	1.00965	2.013423
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	clpC	BN194_21680	K0N9Z7	1.2841	1.00218	2.003024

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Protein names	Functional Class	Gene	Gene locu	Protein IDs	-Log t-test p-value	t-test Difference_ _	Fold change
Uncharacterized protein yueI	Unknown/uncharacterized	yueI	BN194_13920	K0NAC7	1.14	0.98	1.98
>tr|K0N7I1|K0N7I1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02220 PE=4 SV=1	Unknown/uncharacterized	K0N7I1		K0N7I1	2.27	0.96	1.95
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC	BN194_00080	K0N486	1.90	0.96	1.94
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		BN194_18780	K0N9E0	1.24	0.95	1.93
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	yqjQ(K0N8A1)	BN194_15480	K0N8A1	2.15	0.94	1.92
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	glgC	BN194_21600	K0N6T3	4.00	0.94	1.92
Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	1.62	0.94	1.92
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	rny	BN194_10100	K0N3E5	3.47	0.92	1.89
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	ilvE	BN194_21620	K0NBM4	2.53	0.91	1.88
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	ung	BN194_11330	K0N758	0.59	0.89	1.85
Elongation factor P	Protein translation (elongation)	efp_2	BN194_22050	K0N712	1.69	0.87	1.83
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	glgD	BN194_21590	K0MWU4	2.29	0.85	1.80
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	manX_5	BN194_29720	K0NDL4	3.14	0.85	1.80
Glycerol-3-phosphate ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_11260	K0N3T6	2.66	0.84	1.80
UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	0.81	0.83	1.78
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	cysK	BN194_05520	K0N8E6	2.78	0.82	1.77
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	hmgCS1	BN194_19680	K0N9K3	3.53	0.80	1.74
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	glyr1	BN194_30100	K0N992	2.18	0.80	1.74
ABC-type uncharacterized transport system, ATPase component	ABC-type transporter systems		BN194_07730	K0N6C9	1.55	0.78	1.72
Glycosyl transferase family protein	Cell wall biogenesis		BN194_02420	K0N7L2	0.92	0.78	1.71
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	deoD	BN194_02810	K0N1Z0	1.62	0.77	1.71

Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	0.38	0.77	1.71
Uncharacterized protein	Unknown/uncharacterized		BN194_27530	K0NAX5	1.18	0.76	1.69
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	polA	BN194_18930	K0N9E7	2.07	0.76	1.69
ABC-type phosphate/phosphonate transport system,periplasmic component	ABC-type transporter systems		BN194_25680	K0NAI1	2.31	0.75	1.69
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	deoB	BN194_02800	K0N1N0	2.44	0.73	1.66
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	2.63	0.73	1.66
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC_2,deoC	BN194_02790	K0MSB5	2.61	0.73	1.66
Stage 0 sporulation protein J	Cytokinesis	spo0J	BN194_02050	K0N1F9	1.94	0.72	1.65
Cold shock protein 1	Transcription-associated proteins	csp	BN194_06990	K0MT67	0.66	0.72	1.65
Inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase (EC 1.1.1.18) (EC 1.1.1.369) (Myo-inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase)	Carbohydrate-related metabolism	iolG	BN194_02270	K0N7J1	0.98	0.72	1.65
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	mtlD_3mtlD	BN194_30400	K0N9C8	1.28	0.72	1.65
>tr|K0N4Z7|K0N4Z7_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02080 PE=4 SV=1	Unknown/uncharacterized	K0N4Z7		K0N4Z7	0.61	0.72	1.64
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	thyA	BN194_15800	K0N522	2.02	0.71	1.63
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	gnd	BN194_18660	K0N5N2	1.90	0.69	1.61
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		BN194_24180	K0NAA2	1.79	0.68	1.60
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	2.03	0.68	1.60
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	act	BN194_16090	K0MVI3	0.62	0.67	1.59
Uncharacterized protein YwcC	Carbohydrate-related metabolism	ywcC	BN194_09930	K0N6V0	2.52	0.66	1.58
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	1.90	0.66	1.58
ABC transporter, permease protein	ABC-type transporter systems		BN194_29810	K0N8H4	2.43	0.65	1.57
Sporulation initiation inhibitor protein soj	Cytokinesis	soj	BN194_02040	K0MS45	0.90	0.63	1.55
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	rex_2,rex	BN194_23820	K0NBZ5	0.81	0.62	1.53
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	0.68	0.61	1.53

Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	plsX	BN194_17940	K0MW37	0.24	0.60	1.51
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	mco	BN194_25410	K0N7A4	1.04	0.59	1.50
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	2.34	0.59	1.50
GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	0.41	0.58	1.50
Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	phoP	BN194_10220	K0N9J6	1.29	0.58	1.50
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	potA	BN194_11290	K0MU90	2.07	0.58	1.49
Rod shape-determining protein MreB	Cytokinesis	mreB	BN194_14550	K0N4R7	0.85	0.58	1.49
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07710	K0N2Z3	2.23	0.57	1.48
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	carB	BN194_16450	K0N587	1.17	0.57	1.48
Septum site-determining protein DivIVA	Cytokinesis	divIVA	BN194_14800	K0N4T8	0.90	0.56	1.48
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	maa	BN194_30010	K0N8I9	0.35	0.56	1.47
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		BN194_21400	K0N6R1	1.42	0.56	1.47
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	pyc	BN194_15170	K0NAI2	2.12	0.56	1.47
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	pgcA	BN194_10370	K0N9K8	2.37	0.53	1.44
DNA-binding protein HU	DNA replication-related	hup	BN194_15740	K0MVF4	1.30	0.53	1.44
>tr|K0N7I6|K0N7I6_LACCA Glucose-6-phosphate isomerase OS=Lactobacillus casei W56 GN=pgi PE=3 SV=1	Central glycolytic/intermediary pathways	pgi		K0N7I6;K0N4A6	1.72	0.52	1.44
Transcriptional regulator, xre family	Transcriptional regulation		BN194_23510	K0N6Y7	1.11	0.52	1.44
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	thiD_2	BN194_07650	K0N2U9	1.53	0.52	1.43
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	prsA	BN194_19060	K0N5Q8	1.17	0.51	1.42
Oligopeptide-binding protein oppA	ABC-type transporter systems	oppA	BN194_17880	K0N983	1.61	0.51	1.42
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	dacA	BN194_02140	K0MS53	2.13	0.49	1.41
Signal recognition particle protein (Fifty-four homolog)	Protein export	ffh	BN194_17820	K0NB27	1.33	0.49	1.41
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	proC	BN194_19900	K0N677	0.87	0.49	1.40
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	fruK_2	BN194_27700	K0N8P7	0.85	0.47	1.39

Autoinducer-2 (AI-2) kinase	General prediction only		BN194_27880	K0NB06	0.81	0.47	1.39
D-ribose-binding protein	ABC-type transporter systems	rbsB	BN194_03290	K0MSF6	1.41	0.47	1.38
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	lplJ	BN194_16640	K0MVN0	1.42	0.47	1.38
Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (Guanine insertion enzyme) (tRNA-guanine transglycosylase)	tRNA/Ribosome assembly/processing	tgt	BN194_08380	K0N6J4	0.35	0.45	1.37
Uncharacterized protein ykuJ	Unknown/uncharacterized	ykuJ	BN194_09100	K0N348	0.94	0.45	1.36
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	yuxL	BN194_19910	K0N5X4	2.86	0.44	1.36
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	asd	BN194_01060	K0N1I5	1.14	0.44	1.35
Non-specific ribonucleoside hydrolase rihC (EC 3.2.-.-)	Nucleic acid/nucleotide metabolism	rihC	BN194_03870	K0N803	0.39	0.43	1.35
Glucitol operon repressor	Transcriptional regulation	srlR	BN194_28690	K0MYG3	1.55	0.43	1.35
Thioredoxin-like protein ytpP	Posttranslational modification	ytpP	BN194_18980	K0N9F1	1.00	0.43	1.35
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatC	BN194_11950	K0N436	0.88	0.43	1.35
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	luxS	BN194_08330	K0N6J0	0.26	0.42	1.34
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	1.74	0.42	1.34
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	hslV	BN194_16000	K0N542	0.42	0.42	1.34
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	pepO_2	BN194_16630	K0N8Q0	1.43	0.41	1.33
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	11E,P100	BN194_02180	K0N513	1.13	0.41	1.33
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	pmi	BN194_02920	K0N7U2	0.89	0.40	1.32
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	yfmL	BN194_12120	K0NA13	0.64	0.40	1.32
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	ywpJ	BN194_11320	K0N9U2	0.99	0.39	1.31
30S ribosomal protein S14	Ribosomal proteins	rpsN	BN194_09950	K0N3D1	0.53	0.38	1.30
UPF0342 protein yheA	Unknown/uncharacterized	yheA	BN194_19080	K0N9F7	0.28	0.36	1.29
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	yclJ	BN194_11790	K0MUE5	1.64	0.35	1.27
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	msrA_2,msrA	BN194_15860	K0N4W6	0.76	0.33	1.26

Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_3	BN194_21440	K0MWS9	0.43	0.33	1.26
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	1.32	0.33	1.26
Uncharacterized protein ycaC	General prediction only	ycaC	BN194_29650	K0N948	1.72	0.32	1.25
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	ispA	BN194_18180	K0N9A2	0.96	0.30	1.24
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	pepV	BN194_08800	K0N324	1.81	0.30	1.23
Nucleic acid-binding protein	Unknown/uncharacterized		BN194_18680	K0N9D5	0.26	0.30	1.23
>tr|K0N699|K0N699_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA PE=3 SV=1;>tr|K0MWW4|K0MWW4_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA_2 PE=3 SV=1	Cell wall biogenesis	rmlA		K0N699;K0MWW4	0.64	0.30	1.23
Probable catabolite control protein A	Transcriptional regulation	ccpA	BN194_08750	K0N323	1.45	0.30	1.23
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	ycnE	BN194_13230	K0N7R3	0.34	0.29	1.22
Aldose 1-epimerase	Central glycolytic/intermediary pathways		BN194_16020	K0NAP4	0.82	0.28	1.22
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	ptsH	BN194_19430	K0N9I2	0.34	0.27	1.21
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE	BN194_02970	K0N7U7	0.86	0.27	1.21
Cold shock-like protein CspLA	Transcription-associated proteins	cspLA	BN194_12460	K0N438	0.27	0.27	1.20
>tr|K0N5T2|K0N5T2_LACCA Phosphoenolpyruvate-protein phosphotransferase OS=Lactobacillus casei W56 GN=ptsI PE=3 SV=1	Phosphotransferase systems	ptsI		K0N5T2	1.49	0.27	1.20
Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	nfo	BN194_17070	K0NAW5	0.25	0.26	1.20
Transcriptional regulator	Transcriptional regulation		BN194_08230	K0N6I4	0.61	0.25	1.19
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	coaD	BN194_15200	K0N4X3	2.20	0.24	1.18
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	pncB	BN194_19860	K0N5X0	0.96	0.24	1.18
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	1.89	0.24	1.18
Penicillin-binding protein 1A	Cell wall biogenesis	ponA	BN194_16720	K0NAU3	0.25	0.24	1.18
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	oppF	BN194_17910	K0N5I3	0.71	0.23	1.17
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	mhqD	BN194_18770	K0NB71	0.18	0.23	1.17

Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	gntK	BN194_02340	K0MS76	0.55	0.22	1.16
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	prs1,prs	BN194_26930	K0NAT2	0.61	0.21	1.16
Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		BN194_08520	K0N972	0.33	0.21	1.16
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	tpx	BN194_08090	K0MTJ5	0.83	0.21	1.16
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	purB	BN194_12520	K0NA41	0.45	0.20	1.15
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	ysgA	BN194_18610	K0N5M8	0.20	0.20	1.15
Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	0.79	0.20	1.15
Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		BN194_20000	K0N684	1.07	0.20	1.15
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	murE	BN194_02160	K0N1S5	0.65	0.20	1.15
Regulatory protein vanR	Signal transduction	vanR	BN194_02120	K0N7G4	0.69	0.20	1.14
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	cysS	BN194_24430	K0NAB2	0.42	0.19	1.14
Cell division protein FtsZ	Cytokinesis	ftsZ	BN194_14760	K0N4L6	0.83	0.19	1.14
Putative nrdI-like protein	Nucleic acid/nucleotide metabolism		BN194_08250	K0N300	0.60	0.19	1.14
>tr|K0N2V4|K0N2V4_LACCA GlpO protein OS=Lactobacillus casei W56 GN=glpO PE=4 SV=1	Carbohydrate-related metabolism	glpO		K0N2V4	0.58	0.18	1.14
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	0.81	0.18	1.13
Uncharacterized protein YxeH	General prediction only	yxeH	BN194_04750	K0N1Y7	0.68	0.18	1.13
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	0.48	0.18	1.13
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	BN194_21350	BN194_21780	K0N6Q5	1.33	0.18	1.13
Cold shock protein CspA	Transcription-associated proteins	cspA	BN194_14820	K0NAH0	0.43	0.17	1.13
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	prs1_2	BN194_30370	K0NDQ5	0.46	0.17	1.12
Chaperone protein ClpB	Protein folding/turnover	clpB_2	BN194_26350	K0N887	0.39	0.17	1.12
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	tpiA	BN194_11030	K0N736	0.69	0.16	1.12
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	0.33	0.16	1.12
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	rnjA	BN194_15020	K0NAH6	0.56	0.16	1.12

Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	Steap4	BN194_01990	K0MS41	0.31	0.15	1.11
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	dut	BN194_24640	K0MXG3	0.47	0.15	1.11
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		BN194_08960	K0N387	0.40	0.15	1.11
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		BN194_13770	K0NAC0	0.27	0.15	1.11
Oligoendopeptidase, pepF/M3 family	Amino acid-related metabolism		BN194_11580	K0N779	0.28	0.15	1.11
Uncharacterized protein yutG	Lipid-related metabolism	yutG	BN194_08940	K0MTQ3	0.45	0.14	1.10
Transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	0.21	0.14	1.10
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	pepS	BN194_12180	K0N7D5	0.18	0.13	1.09
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	nox_2	BN194_02850	K0N1N9	0.29	0.12	1.09
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	htrA	BN194_29460	K0N8D9	0.25	0.12	1.09
>tr|K0N9X8|K0N9X8_LACCA SpsK protein OS=Lactobacillus casei W56 GN=spsK PE=4 SV=1;>tr|K0N6D6|K0N6D6_LACCA SpsK_2 protein OS=Lactobacillus casei W56 GN=spsK_2 PE=4 SV=1	Cell wall biogenesis	spsK_2		K0N9X8;K0N6D6	0.39	0.11	1.08
Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	rbsK	BN194_03300	K0N1R2	0.29	0.11	1.08
Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	0.54	0.10	1.07
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	0.25	0.10	1.07
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	patB_2	BN194_09790	K0MTW3	0.28	0.09	1.07
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	phoU	BN194_10290	K0MTZ9	0.16	0.09	1.07
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	agaS	BN194_02940	K0MSD9	0.34	0.09	1.06
Virulence factor mviM	General prediction only	mviM	BN194_13310	K0N4B2	0.12	0.08	1.06
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	nrnA	BN194_08450	K0N309	0.35	0.08	1.06
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	gpsB	BN194_16690	K0MVN5	0.19	0.08	1.06
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2_2,lacD	BN194_27060	K0N7P0	0.19	0.08	1.06
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		BN194_27170	K0NCZ6	0.43	0.07	1.05
Cellobiose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	celA_5	BN194_29600	K0N945	0.11	0.07	1.05
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	pheT	BN194_18560	K0N5M4	0.23	0.07	1.05

N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	nusB	BN194_18220	K0NB49	0.15	0.06	1.04
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	0.14	0.06	1.04
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatB	BN194_11970	K0NA01	0.20	0.06	1.04
UPF0659 protein YMR090W	General prediction only	ylbE	BN194_07030	K0N671	0.16	0.06	1.04
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	ftsH	BN194_26460	K0N7I8	0.21	0.06	1.04
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	yqeC	BN194_02330	K0N532	0.14	0.05	1.04
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	rpe	BN194_18000	K0N5T1	0.11	0.05	1.03
Single-stranded DNA-binding protein (SSB)	DNA replication-related	ssb	BN194_00110	K0N1C2	0.06	0.04	1.03
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	frr	BN194_17650	K0N5M3	0.08	0.04	1.03
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	gpmA2,gpmA	BN194_22740	K0MX58	0.12	0.04	1.03
DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	gyrB	BN194_00060	K0N1B8	0.06	0.04	1.03
PTS system IIB component, Gat family	Phosphotransferase systems		BN194_07430	K0N6A5	0.07	0.03	1.02
Oligoendopeptidase F	Amino acid-related metabolism	yjbG_2	BN194_08130	K0N6H7	0.16	0.03	1.02
Glutamine-binding periplasmic protein	ABC-type transporter systems	glnH_2	BN194_29910	K0N8I1	0.03	0.03	1.02
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	0.07	0.02	1.01
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	ykwC	BN194_02520	K0N7M3	0.02	0.01	1.01
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	glcK	BN194_18420	K0NB57	0.02	0.01	1.01
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	patA_2	BN194_22950	K0N7F8	0.00	0.00	1.00
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	glmM	BN194_11550	K0N3Y7	0.01	0.00	1.00
Cell division protein FtsA	Cytokinesis	ftsA	BN194_14750	K0N4T3	0.00	0.00	1.00
Uncharacterized protein	General prediction only		BN194_21200	K0N6M8	0.01	0.00	1.00
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	dltA	BN194_08590	K0MTN0	0.01	-0.01	1.00
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	5.41	-7.33	-160.783

Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	fabD	BN194_22570	K0NBT1	5.68	-6.68	-102.2
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	fabZ	BN194_22520	K0NBS8	6.66	-6.47	-88.4745
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	bkr4	BN194_22550	K0N799	4.16	-5.98	-63.1675
>tr|K0N788|K0N788_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_22500 PE=4 SV=1	Unknown/uncharacterized	K0N788		K0N788	4.21	-5.82	-56.4394
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	fabK	BN194_22580	K0NA38	3.67	-5.35	-40.8689
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)	Lipid-related metabolism	accC	BN194_22510	K0N6M5	4.08	-4.81	-27.9943
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	fabH	BN194_22600	K0N7B0	6.08	-4.52	-22.9207
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	fabF	BN194_22540	K0MX40	2.02	-4.30	-19.7652
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	accB	BN194_22530	K0NA35	2.92	-3.93	-15.2529
>tr|K0NAP8|K0NAP8_LACCA ParC protein OS=Lactobacillus casei W56 GN=parC PE=4 SV=1	Phosphotransferase systems	K0NAP8		K0NAP8	0.86	-3.23	-9.3543
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	fabG	BN194_22560	K0N6N3	2.29	-3.14	-8.81335
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	fabZ_2	BN194_22620	K0NBT3	1.18	-2.66	-6.32016
Acyl carrier protein (ACP)	Lipid-related metabolism	acpP_2, acpP	BN194_22590	K0MX45	1.99	-2.61	-6.08885
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	accA	BN194_22470	K0NBS6	2.35	-2.51	-5.69056
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	helD	BN194_21130	K0N9W3	1.20	-2.32	-4.99956
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	clpC	BN194_21680	K0N9Z7	2.37	-2.01	-4.03531
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	treA	BN194_06930	K0N662	3.18	-1.82	-3.54027
Tautomerase (EC 5.3.2.-)	General prediction only		BN194_16890	K0MVQ1	0.54	-1.82	-3.53622
PspC domain-containing protein	Unknown/uncharacterized	ythC	BN194_10300	K0N3H5	3.80	-1.41	-2.65516
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism	K0N6M0	BN194_22460	K0N6M0	1.80	-1.36	-2.57323
50S ribosomal protein L32	Ribosomal proteins	rpmF	BN194_15510	K0N4T0	0.70	-1.33	-2.51027
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE_3	BN194_04780	K0N5N9	2.84	-1.31	-2.4857
ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	clpX	BN194_15340	K0MVC6	4.05	-1.31	-2.47169
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	yabO	BN194_26520	K0NCR8	1.00	-1.29	-2.44693
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	uvrA	BN194_10450	K0N3J2	3.17	-1.25	-2.37805
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	pepN	BN194_05410	K0N2F5	4.13	-1.13	-2.18389

Uncharacterized protein	Unknown/uncharacterized		BN194_29450	K0N932	2.16	-1.10	-2.14938
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	guaB	BN194_02100	K0N1G3	2.97	-1.10	-2.14933
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	gmk	BN194_18110	K0N5J6	2.23	-1.07	-2.10006
30S ribosomal protein S14 type Z	Ribosomal proteins	rpsZ,rpsN	BN194_26090	K0MXS9	1.31	-1.06	-2.09052
30S ribosomal protein S18	Ribosomal proteins	rpsR	BN194_00120	K0N6T2	0.58	-1.05	-2.07719
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	1.84	-1.04	-2.05482
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	msmK	BN194_11180	K0N747	1.40	-1.03	-2.04051
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	npr	BN194_04740	K0MSP8	3.32	-1.02	-2.02467
50S ribosomal protein L17	Ribosomal proteins	rplQ	BN194_25950	K0N841	1.15	-1.00	-1.99362
30S ribosomal protein S11	Ribosomal proteins	rpsK	BN194_25970	K0NCJ0	1.75	-0.99	-1.98136
Translation initiation factor IF-3	Protein translation (initiation)	infC	BN194_18820	K0NB73	2.33	-0.96	-1.94637
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	typA	BN194_15150	K0N4W9	3.56	-0.96	-1.94001
50S ribosomal protein L21	Ribosomal proteins	rplU	BN194_18290	K0MW61	0.81	-0.95	-1.93582
Dumpy	Cell surface proteins/internalins	dp	BN194_05390	K0MSV0	1.58	-0.94	-1.91287
30S ribosomal protein S19	Ribosomal proteins	rpsS	BN194_26180	K0NAM1	1.87	-0.92	-1.8959
50S ribosomal protein L16	Ribosomal proteins	rplP	BN194_26150	K0N863	1.76	-0.92	-1.89099
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshA	BN194_26700	K0N8C7	4.42	-0.91	-1.8789
30S ribosomal protein S5	Ribosomal proteins	rpsE	BN194_26050	K0N853	2.21	-0.89	-1.85007
50S ribosomal protein L30	Ribosomal proteins	rpmD	BN194_26040	K0MXS6	3.25	-0.88	-1.84458
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	yhaA	BN194_30550	K0N9E4	0.68	-0.86	-1.82117
50S ribosomal protein L13	Ribosomal proteins	rplM	BN194_25850	K0N828	2.71	-0.86	-1.81713
30S ribosomal protein S3	Ribosomal proteins	rpsC	BN194_26160	K0N7G5	1.56	-0.85	-1.80093
30S ribosomal protein S13	Ribosomal proteins	rpsM	BN194_25980	K0NAK3	1.81	-0.85	-1.7989
50S ribosomal protein L10	Ribosomal proteins	rplJ	BN194_24090	K0MXD8	3.12	-0.84	-1.79562
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	gyrA	BN194_00070	K0N6S7	2.19	-0.84	-1.7949
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	obg	BN194_15440	K0MVD3	1.78	-0.84	-1.7895
Putative tRNA-binding protein ytpR	General prediction only	ytpR	BN194_18970	K0NB80	1.59	-0.83	-1.78268

30S ribosomal protein S8	Ribosomal proteins	rpsH	BN194_26080	K0NAL1	2.06	-0.82	-1.76167
Pur operon repressor	Transcriptional regulation	purR_2	BN194_26960	K0N7M9	0.57	-0.81	-1.75054
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	pfkA	BN194_15570	K0NAK6	3.16	-0.81	-1.74886
Elongation factor G (EF-G)	Protein translation (elongation)	fusA	BN194_26270	K0NCN8	3.34	-0.80	-1.74515
30S ribosomal protein S17	Ribosomal proteins	rpsQ	BN194_26130	K0NAL6	3.16	-0.80	-1.74172
50S ribosomal protein L4	Ribosomal proteins	rplD	BN194_26210	K0N7H0	2.34	-0.80	-1.73889
50S ribosomal protein L23	Ribosomal proteins	rplW	BN194_26200	K0N869	2.00	-0.79	-1.73457
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	iscS1	BN194_14900	K0N4U8	1.36	-0.76	-1.69748
PTS system IIB component, L-Asc family	Phosphotransferase systems		BN194_28560	K0N861	0.11	-0.76	-1.69254
50S ribosomal protein L6	Ribosomal proteins	rplF	BN194_26070	K0NCK5	3.02	-0.76	-1.69008
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	2.16	-0.75	-1.6864
50S ribosomal protein L5	Ribosomal proteins	rplE	BN194_26100	K0N859	2.85	-0.75	-1.6808
Inosose dehydratase (EC 4.2.1.44) (2-keto-myo-inositol dehydratase)	Carbohydrate-related metabolism	iolE	BN194_02290	K0MS68	1.26	-0.74	-1.67559
Uncharacterized protein ynbB	Cell defense/detoxification	ynbB	BN194_18380	K0N9B7	1.88	-0.74	-1.66802
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	yutF	BN194_08910	K0N383	2.03	-0.74	-1.66521
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdF	BN194_16610	K0N552	1.66	-0.73	-1.66264
50S ribosomal protein L11	Ribosomal proteins	rplK	BN194_24160	K0N724	1.96	-0.73	-1.65809
50S ribosomal protein L18	Ribosomal proteins	rplR	BN194_26060	K0N7F4	1.59	-0.72	-1.6525
30S ribosomal protein S10	Ribosomal proteins	rpsJ	BN194_26230	K0NAM5	2.31	-0.72	-1.64676
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	lacC	BN194_07470	K0N8Y4	3.03	-0.72	-1.64396
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	guaA	BN194_21070	K0NBJ2	2.99	-0.70	-1.62622
Transcriptional regulatory protein YycF	Signal transduction	yycF_2	BN194_29510	K0N8E4	1.80	-0.70	-1.62621
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	1.99	-0.70	-1.62582
50S ribosomal protein L35	Ribosomal proteins	rpmI	BN194_18810	K0N5P1	2.40	-0.70	-1.62318
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	aspS	BN194_17100	K0N5F3	2.02	-0.70	-1.62242
Transcriptional regulator, TetR family	Transcriptional regulation		BN194_12190	K0MUM1	2.88	-0.69	-1.60895

Transcriptional regulatory protein spaR	Signal transduction	spaR	BN194_05330	K0N5S9	0.26	-0.68	-1.60617
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07700	K0N2V5	1.27	-0.68	-1.59993
50S ribosomal protein L19	Ribosomal proteins	rplS	BN194_17770	K0NB12	2.04	-0.68	-1.59974
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	lacB	BN194_07490	K0MTB7	2.25	-0.68	-1.59742
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	prfB	BN194_10180	K0N6W9	1.94	-0.67	-1.58814
30S ribosomal protein S4	Ribosomal proteins	rpsD	BN194_14440	K0MV63	3.14	-0.66	-1.5811
Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	fba_2	BN194_05060	K0N2C9	2.28	-0.66	-1.57892
50S ribosomal protein L14	Ribosomal proteins	rplN	BN194_26120	K0NCL3	2.72	-0.66	-1.57725
50S ribosomal protein L3	Ribosomal proteins	rplC	BN194_26220	K0NCN1	2.36	-0.66	-1.57552
50S ribosomal protein L2	Ribosomal proteins	rplB	BN194_26190	K0MXU1	2.76	-0.65	-1.57433
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	alsS	BN194_20150	K0N695	3.19	-0.65	-1.56868
50S ribosomal protein L22	Ribosomal proteins	rplV	BN194_26170	K0NCM1	2.25	-0.65	-1.56805
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		BN194_01410	K0N1L0	0.75	-0.65	-1.56594
50S ribosomal protein L1	Ribosomal proteins	rplA	BN194_24150	K0N7M7	2.26	-0.64	-1.55637
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	yqeL,rsfS	BN194_18710	K0N5N6	2.40	-0.63	-1.54272
30S ribosomal protein S12	Ribosomal proteins	rpsL	BN194_26290	K0MXV0	1.76	-0.62	-1.54137
30S ribosomal protein S20	Ribosomal proteins	rpsT	BN194_15250	K0N4X9	1.05	-0.62	-1.53632
Transcription termination/antitermination protein NusG	Transcription-associated proteins	nusG	BN194_24260	K0N730	0.95	-0.62	-1.53469
>tr|K0N6D0|K0N6D0_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_20650 PE=4 SV=1	Unknown/uncharacterized	K0N6D0		K0N6D0	0.63	-0.61	-1.52932
30S ribosomal protein S7	Ribosomal proteins	rpsG	BN194_26280	K0NAM9	2.12	-0.60	-1.51808
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	1.86	-0.60	-1.51721
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	rpoC	BN194_26330	K0NAN3	2.99	-0.60	-1.51577
FeS cluster assembly protein sufB	Cofactor-related metabolism	sufB	BN194_13810	K0N4E5	1.40	-0.60	-1.51457
Uncharacterized protein SE_0534	tRNA/Ribosome assembly/processing		BN194_10150	K0N3F2	2.35	-0.59	-1.50512

S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	metK	BN194_09150	K0N352	2.85	-0.59	-1.50126
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	hisS	BN194_17110	K0N5A0	1.78	-0.59	-1.50106
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	clpE	BN194_19450	K0N644	1.64	-0.58	-1.49813
Chaperone protein DnaJ	Protein folding/turnover	dnaJ	BN194_17450	K0N5J4	2.28	-0.58	-1.49807
30S ribosomal protein S9	Ribosomal proteins	rpsI	BN194_25840	K0MXR0	1.08	-0.58	-1.49729
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC	BN194_24670	K0NC50	1.27	-0.57	-1.48895
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	groL,groEL	BN194_23750	K0N7K7	2.70	-0.57	-1.4874
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	glyS	BN194_16950	K0N5D3	1.86	-0.56	-1.47641
Translation initiation factor IF-2	Protein translation (initiation)	infB	BN194_17550	K0N5K7	1.52	-0.56	-1.47135
50S ribosomal protein L27	Ribosomal proteins	rpmA	BN194_18270	K0NB51	0.79	-0.55	-1.46546
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		BN194_11600	K0N3Z3	0.92	-0.55	-1.4631
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	yqeH	BN194_18740	K0MW90	1.58	-0.55	-1.46303
50S ribosomal protein L20	Ribosomal proteins	rplT	BN194_18800	K0N5Y4	1.86	-0.55	-1.46287
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	1.65	-0.55	-1.46254
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	atpA	BN194_13600	K0N4K1	1.98	-0.55	-1.46057
30S ribosomal protein S2	Ribosomal proteins	rpsB	BN194_17680	K0N936	2.73	-0.55	-1.45992
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	HBN1	BN194_16550	K0N597	0.98	-0.53	-1.4447
50S ribosomal protein L15	Ribosomal proteins	rplO	BN194_26030	K0NAK7	1.69	-0.53	-1.4423
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	mtnN	BN194_14890	K0MV90	0.94	-0.53	-1.44008
Uncharacterized protein	Lipid-related metabolism	YerQ	BN194_11980	K0N7B3	1.82	-0.52	-1.43805
30S ribosomal protein S21	Ribosomal proteins	rpsU	BN194_17050	K0N5E5	1.39	-0.52	-1.43722
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2,lacD	BN194_07480	K0N6A8	1.72	-0.52	-1.4337
50S ribosomal protein L29	Ribosomal proteins	rpmC	BN194_26140	K0MXT6	2.83	-0.51	-1.42622
Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	1.82	-0.51	-1.42432
NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	1.61	-0.51	-1.4239

50S ribosomal protein L31 type B	Ribosomal proteins	rpmE2	BN194_26770	K0NCV4	1.48	-0.51	-1.42273
RNA polymerase sigma factor SigA	RNA polymerase	rpoD,sigA	BN194_16920	K0NAV6	0.43	-0.51	-1.41967
30S ribosomal protein S15	Ribosomal proteins	rpsO	BN194_15260	K0N4Q6	0.99	-0.50	-1.41
Bifunctional protein GlmU	Cell wall biogenesis	glmU	BN194_26940	K0MY10	0.77	-0.49	-1.40849
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	cmk	BN194_15710	K0N4V1	1.22	-0.49	-1.40269
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC_2	BN194_24680	K0NAC2	1.64	-0.48	-1.39811
Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	upp	BN194_13550	K0N4J8	1.76	-0.48	-1.39414
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	hpt	BN194_26470	K0NCR2	0.82	-0.47	-1.38498
Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	pyk	BN194_15580	K0N8B6	2.90	-0.47	-1.38218
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	dnaK	BN194_17460	K0N5C7	1.28	-0.46	-1.37975
50S ribosomal protein L33	Ribosomal proteins	rpmG	BN194_20200	K0N697	0.90	-0.46	-1.37599
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	queA	BN194_08370	K0N965	1.26	-0.45	-1.36565
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	clpP_2, clpP	BN194_10510	K0N3M4	1.47	-0.45	-1.36276
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	apt	BN194_17380	K0N902	0.60	-0.45	-1.36219
30S ribosomal protein S16	Ribosomal proteins	rpsP	BN194_17810	K0N5H1	0.48	-0.44	-1.35953
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	rpoB	BN194_26340	K0MXV4	2.70	-0.44	-1.35894
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	grpE	BN194_17470	K0NAZ2	1.07	-0.44	-1.35491
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	murF	BN194_26720	K0NCU5	0.94	-0.44	-1.354
>tr|K0NBL8|K0NBL8_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_21520 PE=3 SV=1	Unknown/uncharacterized	K0NBL8		K0NBL8	1.33	-0.43	-1.34874
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	cap4C	BN194_12280	K0N7E3	1.78	-0.43	-1.34516
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	atpG	BN194_13610	K0N4D3	0.96	-0.43	-1.34455
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	asnS	BN194_16760	K0N569	0.71	-0.43	-1.34288
Ribosome-binding ATPase YchF	Protein translation (peptide release)	engD,ychF	BN194_02070	K0N7F7	1.99	-0.42	-1.34079

Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	adk	BN194_26010	K0N7F0	1.33	-0.42	-1.33984
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	ykpA	BN194_07220	K0N8V6	1.52	-0.42	-1.33761
DegV domain-containing protein CA_C1624	Unknown/uncharacterized		BN194_14170	K0NAD8	0.25	-0.42	-1.33424
Chaperone protein ClpB	Protein folding/turnover	clpB	BN194_15500	K0N4Z8	0.82	-0.41	-1.33268
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	argS	BN194_19120	K0NB86	1.23	-0.41	-1.33164
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	3.19	-0.41	-1.33139
50S ribosomal protein L24	Ribosomal proteins	rplX	BN194_26110	K0N7F9	0.93	-0.40	-1.32393
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	hslO	BN194_26400	K0N893	1.28	-0.40	-1.32199
Probable dipeptidase (EC 3.4.-.-)	Amino acid-related metabolism		BN194_13380	K0N7S0	1.64	-0.40	-1.31724
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	der	BN194_15730	K0N8E1	1.35	-0.39	-1.30734
Protein translocase subunit SecA	Protein export	secA	BN194_10170	K0N9J2	1.55	-0.38	-1.30477
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	pyrH	BN194_17660	K0N5E6	1.27	-0.38	-1.30212
Transcription termination/antitermination protein NusA	Transcription-associated proteins	nusA	BN194_17580	K0N927	1.67	-0.38	-1.30169
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	ileS	BN194_14810	K0N4L9	0.90	-0.38	-1.29836
30S ribosomal protein S6	Ribosomal proteins	rpsF	BN194_00100	K0N0Z1	1.34	-0.38	-1.29798
Predicted hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	0.52	-0.37	-1.28834
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	pyrG	BN194_26790	K0MXZ1	1.65	-0.36	-1.2852
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	1.36	-0.35	-1.27867
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	1.34	-0.35	-1.27721
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	nagB	BN194_30440	K0MYW0	1.17	-0.35	-1.27607
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	lacA	BN194_07500	K0N2T4	1.68	-0.35	-1.27393
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	ddl	BN194_01390	K0MRY4	0.31	-0.35	-1.27366
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	atpD	BN194_13620	K0NAB3	2.28	-0.35	-1.27086
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	rpoA	BN194_25960	K0N7E5	1.67	-0.34	-1.26896

Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	eno	BN194_11040	K0MU67	1.47	-0.34	-1.2689
Lactaldehyde dehydrogenase (EC 1.2.1.21) (EC 1.2.1.22)	Cell defense/detoxification	aldA	BN194_25470	K0NCB9	1.23	-0.34	-1.26553
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	xpt	BN194_12490	K0MUR6	1.74	-0.33	-1.26123
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	ohrR	BN194_10500	K0N3J7	0.40	-0.33	-1.26076
30S ribosomal protein S1 homolog	Ribosomal proteins	ypfD	BN194_15720	K0NAL9	0.87	-0.33	-1.25999
Protein RecA (Recombinase A)	DNA repair/recombination	recA_2,recA	BN194_27650	K0N8P0	0.47	-0.33	-1.25373
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	pcp	BN194_01980	K0N4Y4	1.79	-0.33	-1.25333
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	gltX	BN194_24470	K0NC38	1.01	-0.32	-1.2522
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	asnB	BN194_22990	K0MX90	0.89	-0.32	-1.2492
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	alaS	BN194_08480	K0N6K2	0.98	-0.32	-1.24728
>tr|K0N3R3|K0N3R3_LACCA Gap protein OS=Lactobacillus casei W56 GN=gap PE=3 SV=1	Central glycolytic/intermediary pathways	gap		K0N3R3;K0N4X1	0.80	-0.31	-1.24157
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	rpoZ	BN194_18100	K0N5T7	0.66	-0.31	-1.23893
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	thrS	BN194_18860	K0N5P5	2.51	-0.31	-1.23884
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	metG	BN194_27130	K0NAU5	1.86	-0.31	-1.23641
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	glnA_2	BN194_18340	K0MW64	0.99	-0.31	-1.23575
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	0.73	-0.30	-1.2272
Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	0.62	-0.29	-1.22647
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	aldB	BN194_20140	K0MWH5	0.43	-0.29	-1.22276
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		BN194_03130	K0N5D9	1.49	-0.29	-1.22157
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	glpK	BN194_07280	K0N694	0.62	-0.29	-1.21983
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	proS	BN194_17610	K0N5E2	1.30	-0.29	-1.21849
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	pgk	BN194_11020	K0N9R1	0.64	-0.28	-1.21663
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	pth	BN194_26550	K0N8B3	0.19	-0.28	-1.21575

Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdE2	BN194_16600	K0N5A1	1.14	-0.28	-1.21216
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	rpoE	BN194_26810	K0N7L4	0.80	-0.27	-1.20896
Nucleoid-associated protein BN194_23980	General prediction only		BN194_23980	K0NA95	1.00	-0.27	-1.2082
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	trxB	BN194_10360	K0N3L1	1.27	-0.27	-1.20585
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	yabR	BN194_26500	K0N8A7	0.76	-0.27	-1.20429
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	bglP	BN194_06940	K0MT60	1.06	-0.26	-1.20132
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	rluB	BN194_15650	K0N509	1.20	-0.26	-1.19889
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	mnmA	BN194_14930	K0N844	1.49	-0.26	-1.1967
Uncharacterized protein MJ0282	Cofactor-related metabolism		BN194_03700	K0N1T2	0.39	-0.25	-1.19038
Protein LemA	Unknown/uncharacterized	lemA	BN194_27350	K0N8J7	0.54	-0.25	-1.18985
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	tuf	BN194_15310	K0N4R1	1.68	-0.25	-1.18897
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	ftsY	BN194_17850	K0N5R8	0.67	-0.25	-1.18816
Protein ytsP	Signal transduction	ytsP	BN194_14450	K0N4Q9	0.22	-0.25	-1.18765
ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit) (F-ATPase epsilon subunit)	Membrane bioenergetics	atpC	BN194_13630	K0N7T2	0.14	-0.25	-1.18653
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	rmlB	BN194_21340	K0MWS0	0.32	-0.24	-1.18244
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	0.74	-0.24	-1.18118
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	ldh	BN194_26560	K0N7J5	0.70	-0.24	-1.18064
Response regulator ArlR	Signal transduction	arlR	BN194_18650	K0N5X3	0.43	-0.24	-1.18015
UPF0337 protein yhjA	General prediction only	yhjA	BN194_24800	K0N7S1	0.26	-0.24	-1.17863
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	tsf	BN194_17670	K0NB01	0.70	-0.23	-1.17505
HTH-type transcriptional repressor yvoA	Transcriptional regulation	yvoA_2	BN194_19880	K0N9L8	0.30	-0.23	-1.17329
Uncharacterized protein	Cofactor-related metabolism		BN194_18720	K0NB69	1.47	-0.23	-1.17207
>tr|K0N1M9|K0N1M9_LACCA Probable phosphoketolase OS=Lactobacillus casei W56 GN=xpkA PE=3 SV=1	Central glycolytic/intermediary pathways	xpkA		K0N1M9;K0N8X7	1.19	-0.22	-1.16254
DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	1.05	-0.21	-1.16013

Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	aspC	BN194_16770	K0NAU6	0.34	-0.20	-1.15128
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	murC	BN194_18950	K0N600	0.39	-0.20	-1.14877
>tr|K0N6A9|K0N6A9_LACCA Tyrosine--tRNA ligase OS=Lactobacillus casei W56 GN=tyrS PE=4 SV=1	tRNA aminoacyl synthesis	tyrS		K0N6A9	0.34	-0.20	-1.14741
Aspartate racemase (EC 5.1.1.13)	Amino acid-related metabolism		BN194_02170	K0N7H2	0.53	-0.20	-1.14476
Uncharacterized protein YqhY	Unknown/uncharacterized	yqhY	BN194_18230	K0N9A7	0.69	-0.19	-1.14346
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshB	BN194_08460	K0N356	0.65	-0.19	-1.1432
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	ndk	BN194_08160	K0N340	0.11	-0.19	-1.14313
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	pepQ	BN194_08740	K0MTP0	1.15	-0.19	-1.14246
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	oppD	BN194_17920	K0NB35	0.84	-0.19	-1.13947
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	pyrDA, pyrD	BN194_19150	K0N623	0.70	-0.19	-1.13751
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	gmuB	BN194_23840	K0MXC7	0.50	-0.18	-1.13438
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_4	BN194_29900	K0N971	0.56	-0.18	-1.13179
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	nadE	BN194_19840	K0MWF6	1.56	-0.18	-1.12903
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	rnr	BN194_11100	K0N3S4	1.02	-0.17	-1.12817
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	purA	BN194_01160	K0N1J0	0.65	-0.17	-1.12308
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	rbfA	BN194_17540	K0MVV7	0.66	-0.16	-1.12102
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	tig	BN194_15330	K0N884	0.54	-0.16	-1.1182
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	lysS	BN194_26380	K0NAN7	0.33	-0.16	-1.11626
Bifunctional protein FolD	Cofactor-related metabolism	folD	BN194_18210	K0N5K0	1.08	-0.16	-1.11428
Acetyltransferase	General prediction only		BN194_08200	K0N2Z8	0.40	-0.16	-1.11346
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	groS,grES	BN194_23760	K0N700	0.14	-0.15	-1.11111
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	murA2,murA	BN194_26780	K0NAR9	0.38	-0.15	-1.1098
tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	dus1	BN194_26390	K0MXV9	0.53	-0.14	-1.10436

Transcriptional regulator, XRE family	Transcriptional regulation		BN194_30170	K0NDP4	0.28	-0.14	-1.10428
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	trpS	BN194_27360	K0N7S4	0.35	-0.14	-1.10422
Probable flavodoxin-1	Membrane bioenergetics	ykuN_2	BN194_12220	K0NA19	0.21	-0.13	-1.0967
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	zwf	BN194_08420	K0N966	0.22	-0.12	-1.08357
50S ribosomal protein L7/L12	Ribosomal proteins	rplL	BN194_24080	K0NA98	0.47	-0.12	-1.08319
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	0.61	-0.12	-1.083
Uncharacterized protein ylxR	General prediction only	ylxR	BN194_17570	K0NAZ6	0.32	-0.11	-1.08098
GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	relA	BN194_17230	K0N8Y0	0.13	-0.11	-1.07606
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	dnaN	BN194_00020	K0N6S3	0.25	-0.10	-1.07503
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	rnc	BN194_17870	K0NB31	0.56	-0.10	-1.07333
Elongation factor P	Protein translation (elongation)	efp	BN194_18240	K0MW57	0.23	-0.10	-1.0722
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	prfA	BN194_13510	K0N4C6	0.16	-0.09	-1.06579
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	valS	BN194_14510	K0N4J6	0.21	-0.08	-1.0597
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	atpH	BN194_13590	K0MV16	0.21	-0.08	-1.05914
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	0.29	-0.08	-1.05839
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	murD	BN194_14720	K0NAG5	0.24	-0.08	-1.05629
MreB-like protein	Cytokinesis	mbl	BN194_13650	K0N4K5	0.21	-0.08	-1.05367
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	yfeX	BN194_07170	K0N8U9	0.42	-0.07	-1.05274
Translation initiation factor IF-1	Protein translation (initiation)	infA	BN194_26000	K0N847	0.11	-0.07	-1.04791
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	gatA	BN194_11960	K0N3Z6	0.34	-0.07	-1.04637
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	fpaP_3	BN194_21160	K0N682	0.20	-0.06	-1.04578
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	manD	BN194_02950	K0N1P4	0.26	-0.06	-1.04383
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	ybeY	BN194_17010	K0N594	0.10	-0.06	-1.04265
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	map	BN194_12230	K0N7E0	0.15	-0.06	-1.04022

Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	leuS	BN194_09210	K0N3A9	0.49	-0.06	-1.03963
>tr|K0NB98|K0NB98_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_19420 PE=4 SV=1	Unknown/uncharacterized	K0NB98		K0NB98	0.04	-0.05	-1.03569
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	def	BN194_15060	K0N4N6	0.13	-0.04	-1.0262
50S ribosomal protein L9	Ribosomal proteins	rplI	BN194_01130	K0N4K3	0.09	-0.04	-1.02577
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	nagA	BN194_19890	K0MWF9	0.16	-0.03	-1.02273
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	greA	BN194_18520	K0NB62	0.08	-0.03	-1.02063
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	pepDB	BN194_21110	K0N678	0.10	-0.03	-1.02011
Thioredoxin	Posttranslational modification	trxA_2	BN194_08570	K0N975	0.03	-0.02	-1.01153
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	ppaC	BN194_16110	K0N4Z4	0.06	-0.02	-1.0108
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	hprK	BN194_10330	K0N6Y3	0.02	-0.02	-1.01056
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	serS	BN194_20080	K0N9N4	0.04	-0.01	-1.01003
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	gpsA	BN194_10350	K0N3I2	0.03	-0.01	-1.0098
Lipoprotein	ABC-type transporter systems	metQ_2	BN194_13740	K0MV23	0.02	-0.01	-1.00813
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	pheS	BN194_18570	K0NB64	0.02	-0.01	-1.0074
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	murI	BN194_08640	K0MTN4	0.02	-0.01	-1.00713
UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	0.02	-0.01	-1.00642

(1i)Protein FC >2 Tween 80 Vs citrate P1

Protein names	**Functional Class**	**Gene**	**names**	**Protein IDs**	**-Log t-test p-value**	**t -test Difference**	**Fold change**
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	4.75021	6.33338	80.63756
Autoinducer-2 (AI-2) kinase (BLAST Class II aldolase/adducin N-terminal)	General prediction only		BN194_27880	K0NB06	5.06492	2.81596	7.041877

>tr|K0NAP8|K0NAP8_LACCA ParC protein OS=Lactobacillus casei W56 GN=parC PE=4 SV=1	Phosphotransferase systems	K0NAP8		K0NAP8	0.335257	2.7138	6.560474
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	yfeX	BN194_07170	K0N8U9	4.13742	2.32955	5.026485
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	msmK	BN194_11180	K0N747	1.516	1.94404	3.847817
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	treA	BN194_06930	K0N662	3.66801	1.77683	3.426724
2-oxoisovalerate dehydrogenase subunit beta (EC 1.2.4.4)	Lipid-related metabolism	bfmBAB	BN194_16390	K0MVK8	3.30849	1.68319	3.211372
>tr|K0N6D0|K0N6D0_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_20650 PE=4 SV=1	Unknown/uncharacterized	K0N6D0		K0N6D0	1.64986	1.54236	2.912706
Cold shock protein 1	Transcription-associated proteins	csp	BN194_06990	K0MT67	1.88361	1.53558	2.89905
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	fruK_2	BN194_27700	K0N8P7	3.14656	1.47369	2.777313
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE_3	BN194_04780	K0N5N9	2.7999	1.46198	2.754862
50S ribosomal protein L7/L12	Ribosomal proteins	rplL	BN194_24080	K0NA98	2.9679	1.29914	2.460821
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	HBN1	BN194_16550	K0N597	4.08709	1.29521	2.454127
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	1.30138	1.26355	2.400858
Uncharacterized protein ynbB	Cell defense/detoxification	ynbB	BN194_18380	K0N9B7	3.39549	1.25206	2.381813
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshA	BN194_26700	K0N8C7	4.15964	1.19587	2.290829
2-dehydropantoate 2-reductase (EC 1.1.1.169) (Ketopantoate reductase)	Cofactor-related metabolism		BN194_16370	K0NAS0	1.56497	1.16957	2.249446
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		BN194_01410	K0N1L0	4.51967	1.1518	2.221909
Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	3.14025	1.1501	2.219293
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	bglP	BN194_06940	K0MT60	2.17564	1.1237	2.179051
50S ribosomal protein L32	Ribosomal proteins	rpmF	BN194_15510	K0N4T0	0.695424	1.12052	2.174253
30S ribosomal protein S18	Ribosomal proteins	rpsR	BN194_00120	K0N6T2	0.761322	1.10807	2.155571
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	pepN	BN194_05410	K0N2F5	3.32709	1.07688	2.109469
Uncharacterized protein	Unknown/uncharacterized		BN194_27530	K0NAX5	0.592159	1.07654	2.108972
30S ribosomal protein S17	Ribosomal proteins	rpsQ	BN194_26130	K0NAL6	1.45608	1.06402	2.090749
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	3.02673	1.06196	2.087766
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	asnS	BN194_16760	K0N569	3.11601	1.05808	2.082159

50S ribosomal protein L16	Ribosomal proteins	rplP	BN194_26150	K0N863	3.73894	1.03925	2.055159
Elongation factor G (EF-G)	Protein translation (elongation)	fusA	BN194_26270	K0NCN8	4.91159	1.02534	2.035439
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	nagB	BN194_30440	K0MYW0	2.69223	1.01774	2.024745
UPF0342 protein yheA	Unknown/uncharacterized	yheA	BN194_19080	K0N9F7	1.26538	1.01298	2.018075
Glutamine-binding periplasmic protein	ABC-type transporter systems	glnH_2	BN194_29910	K0N8I1	2.12402	1.00795	2.011051
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	obg	BN194_15440	K0MVD3	3.7616	1.00326	2.004524
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	hisS	BN194_17110	K0N5A0	3.28	1.00	2.00

(1j) Protein FC < 2 Tween 80 Vs citrate P1

Protein names	**Functional Class**	**Gene**	**names**	**Protein IDs**	**-Log t-test p-value**	**t-test Difference**	**Fold change**
50S ribosomal protein L17	Ribosomal proteins	rplQ	BN194_25950	K0N841	0.91	0.99	1.98
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	clpC	BN194_21680	K0N9Z7	1.93	0.98	1.97
50S ribosomal protein L18	Ribosomal proteins	rplR	BN194_26060	K0N7F4	2.15	0.97	1.96
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	uvrA	BN194_10450	K0N3J2	2.67	0.97	1.96
50S ribosomal protein L6	Ribosomal proteins	rplF	BN194_26070	K0NCK5	3.13	0.96	1.95
Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	fba_2	BN194_05060	K0N2C9	3.51	0.96	1.94
30S ribosomal protein S21	Ribosomal proteins	rpsU	BN194_17050	K0N5E5	2.39	0.94	1.92
50S ribosomal protein L21	Ribosomal proteins	rplU	BN194_18290	K0MW61	0.53	0.94	1.92
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		BN194_11600	K0N3Z3	2.07	0.93	1.90
30S ribosomal protein S8	Ribosomal proteins	rpsH	BN194_26080	K0NAL1	2.28	0.92	1.90
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	typA	BN194_15150	K0N4W9	2.88	0.91	1.88
Transcription termination/antitermination protein NusG	Transcription-associated proteins	nusG	BN194_24260	K0N730	1.53	0.90	1.86
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	2.40	0.89	1.85

tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	mnmA	BN194_14930	K0N844	2.21	0.86	1.81
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	glnA_2	BN194_18340	K0MW64	2.69	0.85	1.80
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	tpiA	BN194_11030	K0N736	2.63	0.84	1.79
Probable dipeptidase (EC 3.4.-.-)	Amino acid-related metabolism		BN194_23190	K0MXA1	1.86	0.83	1.78
50S ribosomal protein L11	Ribosomal proteins	rplK	BN194_24160	K0N724	2.55	0.83	1.77
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	yqeL,rsfS	BN194_18710	K0N5N6	3.80	0.83	1.77
ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	clpX	BN194_15340	K0MVC6	2.24	0.82	1.77
50S ribosomal protein L4	Ribosomal proteins	rplD	BN194_26210	K0N7H0	3.12	0.82	1.76
Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	upp	BN194_13550	K0N4J8	2.93	0.81	1.76
50S ribosomal protein L13	Ribosomal proteins	rplM	BN194_25850	K0N828	2.83	0.80	1.74
50S ribosomal protein L5	Ribosomal proteins	rplE	BN194_26100	K0N859	3.42	0.80	1.74
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	1.25	0.80	1.74
Uncharacterized protein MJ0282	Cofactor-related metabolism		BN194_03700	K0N1T2	0.97	0.80	1.74
30S ribosomal protein S9	Ribosomal proteins	rpsI	BN194_25840	K0MXR0	2.45	0.80	1.74
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	serS	BN194_20080	K0N9N4	3.30	0.78	1.72
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	dltA	BN194_08590	K0MTN0	2.78	0.78	1.72
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	yutF	BN194_08910	K0N383	3.50	0.78	1.72
Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	pyk	BN194_15580	K0N8B6	3.10	0.77	1.71
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	aspS	BN194_17100	K0N5F3	1.83	0.77	1.71
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	lacC	BN194_07470	K0N8Y4	2.37	0.77	1.70
50S ribosomal protein L19	Ribosomal proteins	rplS	BN194_17770	K0NB12	3.52	0.77	1.70
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	1.25	0.76	1.69
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	guaA	BN194_21070	K0NBJ2	4.38	0.76	1.69

CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	pyrG	BN194_26790	K0MXZ1	3.17	0.75	1.68
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	pfkA	BN194_15570	K0NAK6	1.90	0.75	1.68
50S ribosomal protein L23	Ribosomal proteins	rplW	BN194_26200	K0N869	2.11	0.74	1.68
50S ribosomal protein L20	Ribosomal proteins	rplT	BN194_18800	K0N5Y4	3.32	0.74	1.67
S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	metK	BN194_09150	K0N352	2.24	0.74	1.67
Pur operon repressor	Transcriptional regulation	purR_2	BN194_26960	K0N7M9	0.75	0.74	1.67
50S ribosomal protein L22	Ribosomal proteins	rplV	BN194_26170	K0NCM1	2.54	0.74	1.67
30S ribosomal protein S15	Ribosomal proteins	rpsO	BN194_15260	K0N4Q6	2.97	0.74	1.67
50S ribosomal protein L10	Ribosomal proteins	rplJ	BN194_24090	K0MXD8	4.15	0.73	1.66
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	mtnN	BN194_14890	K0MV90	3.05	0.73	1.66
30S ribosomal protein S3	Ribosomal proteins	rpsC	BN194_26160	K0N7G5	1.63	0.73	1.66
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	pgk	BN194_11020	K0N9R1	1.62	0.73	1.66
30S ribosomal protein S4	Ribosomal proteins	rpsD	BN194_14440	K0MV63	2.75	0.73	1.66
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	proS	BN194_17610	K0N5E2	3.48	0.73	1.66
Translation initiation factor IF-1	Protein translation (initiation)	infA	BN194_26000	K0N847	1.36	0.73	1.66
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	ileS	BN194_14810	K0N4L9	1.59	0.73	1.65
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_4	BN194_29900	K0N971	2.70	0.72	1.65
50S ribosomal protein L1	Ribosomal proteins	rplA	BN194_24150	K0N7M7	3.55	0.71	1.64
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	purA	BN194_01160	K0N1J0	3.30	0.71	1.63
>tr|K0N6A9|K0N6A9_LACCA Tyrosine--tRNA ligase OS=Lactobacillus casei W56 GN=tyrS PE=4 SV=1	tRNA aminoacyl synthesis	tyrS		K0N6A9	1.80	0.70	1.63
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	argS	BN194_19120	K0NB86	2.14	0.70	1.62
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	dnaK	BN194_17460	K0N5C7	2.47	0.69	1.62

>tr|K0N3R3|K0N3R3_LACCA Gap protein OS=Lactobacillus casei W56 GN=gap PE=3 SV=1	Central glycolytic/intermediary pathways	gap		K0N3R3;K0N4X1	1.63	0.69	1.61
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	1.94	0.69	1.61
Probable dipeptidase (EC 3.4.-.-)	Amino acid-related metabolism		BN194_13380	K0N7S0	2.85	0.69	1.61
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	glyS	BN194_16950	K0N5D3	2.45	0.68	1.61
50S ribosomal protein L14	Ribosomal proteins	rplN	BN194_26120	K0NCL3	2.58	0.68	1.61
30S ribosomal protein S10	Ribosomal proteins	rpsJ	BN194_26230	K0NAM5	2.63	0.68	1.60
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	gltX	BN194_24470	K0NC38	2.47	0.67	1.60
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	groL,groEL	BN194_23750	K0N7K7	3.38	0.67	1.60
30S ribosomal protein S6	Ribosomal proteins	rpsF	BN194_00100	K0N0Z1	2.74	0.66	1.58
Translation initiation factor IF-3	Protein translation (initiation)	infC	BN194_18820	K0NB73	2.30	0.66	1.58
30S ribosomal protein S13	Ribosomal proteins	rpsM	BN194_25980	K0NAK3	2.80	0.66	1.58
Cold shock-like protein CspLA	Transcription-associated proteins	cspLA	BN194_12460	K0N438	0.40	0.66	1.57
30S ribosomal protein S16	Ribosomal proteins	rpsP	BN194_17810	K0N5H1	0.90	0.65	1.57
30S ribosomal protein S11	Ribosomal proteins	rpsK	BN194_25970	K0NCJ0	1.95	0.65	1.57
30S ribosomal protein S12	Ribosomal proteins	rpsL	BN194_26290	K0MXV0	2.46	0.65	1.57
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	rpoB	BN194_26340	K0MXV4	2.92	0.65	1.56
30S ribosomal protein S5	Ribosomal proteins	rpsE	BN194_26050	K0N853	2.37	0.64	1.56
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	eno	BN194_11040	K0MU67	3.77	0.63	1.55
50S ribosomal protein L15	Ribosomal proteins	rplO	BN194_26030	K0NAK7	1.80	0.63	1.55
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	oppD	BN194_17920	K0NB35	3.19	0.63	1.55
50S ribosomal protein L30	Ribosomal proteins	rpmD	BN194_26040	K0MXS6	3.15	0.63	1.55
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	ptsH	BN194_19430	K0N9I2	0.57	0.63	1.55
30S ribosomal protein S14 type Z	Ribosomal proteins	rpsZ,rpsN	BN194_26090	K0MXS9	0.98	0.62	1.54
30S ribosomal protein S2	Ribosomal proteins	rpsB	BN194_17680	K0N936	2.43	0.62	1.54

50S ribosomal protein L3	Ribosomal proteins	rplC	BN194_26220	K0NCN1	2.30	0.62	1.53
Transcription termination/antitermination protein NusA	Transcription-associated proteins	nusA	BN194_17580	K0N927	2.58	0.62	1.53
Putative tRNA-binding protein ytpR	General prediction only	ytpR	BN194_18970	K0NB80	2.15	0.60	1.52
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	2.23	0.59	1.51
30S ribosomal protein S19	Ribosomal proteins	rpsS	BN194_26180	K0NAM1	3.00	0.59	1.50
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	1.63	0.59	1.50
>tr|K0N9X8|K0N9X8_LACCA SpsK protein OS=Lactobacillus casei W56 GN=spsK PE=4 SV=1;>tr|K0N6D6|K0N6D6_LACCA SpsK_2 protein OS=Lactobacillus casei W56 GN=spsK_2 PE=4 SV=1	Cell wall biogenesis	spsK_2		K0N9X8;K0N6D6	2.06	0.57	1.49
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	fruA_4	BN194_27690	K0MY77	1.21	0.57	1.48
50S ribosomal protein L2	Ribosomal proteins	rplB	BN194_26190	K0MXU1	2.06	0.57	1.48
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	lysS	BN194_26380	K0NAN7	1.27	0.56	1.47
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	rmlB	BN194_21340	K0MWS0	1.57	0.56	1.47
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	mco	BN194_25410	K0N7A4	3.56	0.55	1.47
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	lacA	BN194_07500	K0N2T4	1.84	0.55	1.47
Translation initiation factor IF-2	Protein translation (initiation)	infB	BN194_17550	K0N5K7	2.04	0.55	1.46
50S ribosomal protein L33	Ribosomal proteins	rpmG	BN194_20200	K0N697	1.23	0.54	1.46
Dumpy	Cell surface proteins/internalins	dp	BN194_05390	K0MSV0	3.31	0.54	1.46
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	helD	BN194_21130	K0N9W3	1.05	0.54	1.46
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC	BN194_24670	K0NC50	1.08	0.54	1.45
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	ykpA	BN194_07220	K0N8V6	1.72	0.53	1.45
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	pepO_2	BN194_16630	K0N8Q0	2.13	0.53	1.45
50S ribosomal protein L29	Ribosomal proteins	rpmC	BN194_26140	K0MXT6	2.84	0.53	1.45
>tr|K0NBL8|K0NBL8_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_21520 PE=3 SV=1	Unknown/uncharacterized	K0NBL8		K0NBL8	1.63	0.53	1.45
Uncharacterized protein SE_0534	tRNA/Ribosome assembly/processing		BN194_10150	K0N3F2	1.80	0.53	1.44

Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	rpiA_2, ripA	BN194_28600	K0N8W9	0.16	0.53	1.44
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	prfB	BN194_10180	K0N6W9	1.65	0.52	1.43
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	thrS	BN194_18860	K0N5P5	6.25	0.52	1.43
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	BN194_21350	BN194_21780	K0N6Q5	1.96	0.51	1.42
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	rpoC	BN194_26330	K0NAN3	3.43	0.51	1.42
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	tig	BN194_15330	K0N884	2.68	0.51	1.42
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	cmk	BN194_15710	K0N4V1	1.81	0.50	1.41
Transcriptional regulatory protein YycF	Signal transduction	yycF_2	BN194_29510	K0N8E4	1.48	0.50	1.41
Elongation factor P	Protein translation (elongation)	efp	BN194_18240	K0MW57	1.84	0.50	1.41
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	luxS	BN194_08330	K0N6J0	0.42	0.50	1.41
30S ribosomal protein S7	Ribosomal proteins	rpsG	BN194_26280	K0NAM9	1.81	0.49	1.41
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	rpoE	BN194_26810	K0N7L4	1.42	0.49	1.41
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	greA	BN194_18520	K0NB62	2.26	0.48	1.40
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	yabR	BN194_26500	K0N8A7	1.66	0.48	1.40
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2,lacD	BN194_07480	K0N6A8	1.71	0.48	1.40
Chaperone protein ClpB	Protein folding/turnover	clpB	BN194_15500	K0N4Z8	1.88	0.48	1.39
30S ribosomal protein S20	Ribosomal proteins	rpsT	BN194_15250	K0N4X9	0.93	0.48	1.39
PTS system IIB component, Gat family	Phosphotransferase systems		BN194_07430	K0N6A5	1.27	0.47	1.39
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	lacB	BN194_07490	K0MTB7	1.16	0.47	1.39
Lipoprotein	ABC-type transporter systems	metQ_2	BN194_13740	K0MV23	2.57	0.47	1.38
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	tuf	BN194_15310	K0N4R1	2.19	0.46	1.38
FeS cluster assembly protein sufB	Cofactor-related metabolism	sufB	BN194_13810	K0N4E5	0.77	0.46	1.38

Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	ndk	BN194_08160	K0N340	0.23	0.45	1.37
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	gmk	BN194_18110	K0N5J6	0.96	0.45	1.36
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshB	BN194_08460	K0N356	1.76	0.44	1.36
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	murF	BN194_26720	K0NCU5	1.01	0.44	1.36
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		BN194_08960	K0N387	1.19	0.42	1.34
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	pyrH	BN194_17660	K0N5E6	0.93	0.40	1.32
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	rnr	BN194_11100	K0N3S4	1.22	0.40	1.32
Ribosome-binding ATPase YchF	Protein translation (peptide release)	engD,ychF	BN194_02070	K0N7F7	2.72	0.40	1.32
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	ldh	BN194_26560	K0N7J5	2.37	0.40	1.31
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	hpt	BN194_26470	K0NCR2	0.57	0.39	1.31
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	iscS1	BN194_14900	K0N4U8	0.70	0.39	1.31
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	yqjQ(K0N8A1)	BN194_15480	K0N8A1	0.22	0.39	1.31
50S ribosomal protein L35	Ribosomal proteins	rpmI	BN194_18810	K0N5P1	0.77	0.38	1.30
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	asnB	BN194_22990	K0MX90	1.51	0.37	1.30
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	yqeH	BN194_18740	K0MW90	1.28	0.36	1.28
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07700	K0N2V5	0.86	0.36	1.28
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	rpoA	BN194_25960	K0N7E5	0.97	0.36	1.28
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	tsf	BN194_17670	K0NB01	1.72	0.35	1.27
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	gyrA	BN194_00070	K0N6S7	0.50	0.35	1.27
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	murC	BN194_18950	K0N600	1.37	0.34	1.27
Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	adk	BN194_26010	K0N7F0	2.01	0.34	1.26
Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	leuS	BN194_09210	K0N3A9	1.22	0.33	1.26
50S ribosomal protein L24	Ribosomal proteins	rplX	BN194_26110	K0N7F9	1.28	0.32	1.25

UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	0.75	0.32	1.25
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	1.52	0.32	1.25
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	groS,grES	BN194_23760	K0N700	0.47	0.32	1.24
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	def	BN194_15060	K0N4N6	0.98	0.32	1.24
>tr|K0N5T2|K0N5T2_LACCA Phosphoenolpyruvate-protein phosphotransferase OS=Lactobacillus casei W56 GN=ptsI PE=3 SV=1	Phosphotransferase systems	ptsI		K0N5T2	1.47	0.31	1.24
>tr|K0NB98|K0NB98_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_19420 PE=4 SV=1	Unknown/uncharacterized	K0NB98		K0NB98	0.76	0.31	1.24
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	ddl	BN194_01390	K0MRY4	0.48	0.30	1.23
50S ribosomal protein L27	Ribosomal proteins	rpmA	BN194_18270	K0NB51	0.30	0.30	1.23
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	grpE	BN194_17470	K0NAZ2	1.16	0.30	1.23
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	hslO	BN194_26400	K0N893	1.15	0.29	1.23
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	ppaC	BN194_16110	K0N4Z4	1.36	0.29	1.22
Response regulator ArlR	Signal transduction	arlR	BN194_18650	K0N5X3	0.88	0.29	1.22
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	gmuB	BN194_23840	K0MXC7	0.80	0.28	1.22
Uncharacterized protein ylxR	General prediction only	ylxR	BN194_17570	K0NAZ6	0.83	0.28	1.21
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	alaS	BN194_08480	K0N6K2	0.70	0.28	1.21
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	valS	BN194_14510	K0N4J6	0.63	0.27	1.21
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	pepDB	BN194_21110	K0N678	0.87	0.27	1.21
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	pepQ	BN194_08740	K0MTP0	1.07	0.25	1.19
Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	1.01	0.25	1.19
ABC-type uncharacterized transport system, ATPase component	ABC-type transporter systems		BN194_07730	K0N6C9	0.42	0.25	1.19
Probable flavodoxin-1	Membrane bioenergetics	ykuN_2	BN194_12220	K0NA19	0.50	0.24	1.18
Nucleoid-associated protein BN194_23980	General prediction only		BN194_23980	K0NA95	0.61	0.24	1.18
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism	K0N6M0	BN194_22460	K0N6M0	0.67	0.22	1.17
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	pheS	BN194_18570	K0NB64	0.61	0.22	1.16

Uncharacterized protein	Cofactor-related metabolism		BN194_18720	K0NB69	1.17	0.21	1.16
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	2.84	0.21	1.16
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	ybeY	BN194_17010	K0N594	1.19	0.21	1.16
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	pheT	BN194_18560	K0N5M4	1.01	0.21	1.16
30S ribosomal protein S1 homolog	Ribosomal proteins	ypfD	BN194_15720	K0NAL9	0.41	0.21	1.16
Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	plsX	BN194_17940	K0MW37	0.37	0.20	1.15
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	pncB	BN194_19860	K0N5X0	0.56	0.20	1.15
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	gpmA2,gpmA	BN194_22740	K0MX58	0.89	0.19	1.14
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	murD	BN194_14720	K0NAG5	0.44	0.18	1.14
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	pmi	BN194_02920	K0N7U2	0.47	0.18	1.14
UPF0659 protein YMR090W	General prediction only	ylbE	BN194_07030	K0N671	0.45	0.18	1.13
NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	0.54	0.17	1.13
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	trpS	BN194_27360	K0N7S4	0.44	0.16	1.12
50S ribosomal protein L31 type B	Ribosomal proteins	rpmE2	BN194_26770	K0NCV4	0.23	0.16	1.12
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	0.38	0.16	1.12
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	queA	BN194_08370	K0N965	0.25	0.16	1.12
Transcriptional regulator, TetR family	Transcriptional regulation		BN194_12190	K0MUM1	1.05	0.15	1.11
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	nadE	BN194_19840	K0MWF6	0.62	0.14	1.10
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	patA_2	BN194_22950	K0N7F8	0.25	0.12	1.09
Aspartate racemase (EC 5.1.1.13)	Amino acid-related metabolism		BN194_02170	K0N7H2	0.19	0.12	1.09
RNA polymerase sigma factor SigA	RNA polymerase	rpoD,sigA	BN194_16920	K0NAV6	0.17	0.12	1.09
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	yjlD	BN194_24330	K0NAA7	0.18	0.11	1.08

ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	atpG	BN194_13610	K0N4D3	0.12	0.11	1.08
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	dnaN	BN194_00020	K0N6S3	0.29	0.11	1.08
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	map	BN194_12230	K0N7E0	0.49	0.11	1.08
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	clpE	BN194_19450	K0N644	0.35	0.11	1.08
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	pyrDA, pyrD	BN194_19150	K0N623	0.37	0.11	1.08
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	atpA	BN194_13600	K0N4K1	0.51	0.11	1.08
Uncharacterized protein ykuJ	Unknown/uncharacterized	ykuJ	BN194_09100	K0N348	0.22	0.10	1.07
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatC	BN194_11950	K0N436	0.51	0.10	1.07
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	rbfA	BN194_17540	K0MVV7	0.31	0.10	1.07
Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	0.19	0.09	1.06
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	clpP_2, clpP	BN194_10510	K0N3M4	0.28	0.09	1.06
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	deoB	BN194_02800	K0N1N0	0.48	0.09	1.06
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	0.61	0.08	1.06
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	atpD	BN194_13620	K0NAB3	0.32	0.07	1.05
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	ftsY	BN194_17850	K0N5R8	0.15	0.07	1.05
MreB-like protein	Cytokinesis	mbl	BN194_13650	K0N4K5	0.41	0.07	1.05
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC_2	BN194_24680	K0NAC2	0.19	0.07	1.05
DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	0.17	0.07	1.05
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2_2,lacD	BN194_27060	K0N7P0	0.15	0.06	1.04
Oligopeptide-binding protein oppA	ABC-type transporter systems	oppA	BN194_17880	K0N983	0.36	0.06	1.04
Acetyltransferase	General prediction only		BN194_08200	K0N2Z8	0.07	0.05	1.03
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	prfA	BN194_13510	K0N4C6	0.09	0.04	1.03
Transcriptional regulator	Transcriptional regulation		BN194_08230	K0N6I4	0.05	0.04	1.02
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	xpt	BN194_12490	K0MUR6	0.05	0.03	1.02

GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	der	BN194_15730	K0N8E1	0.05	0.02	1.01
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	nrnA	BN194_08450	K0N309	0.01	0.00	1.00
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	mtlD_3mtlD	BN194_30400	K0N9C8	0.00	0.00	1.00
Bifunctional protein GlmU	Cell wall biogenesis	glmU	BN194_26940	K0MY10	0.00	0.00	1.00
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	gatA	BN194_11960	K0N3Z6	0.01	0.00	1.00
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	ftsH	BN194_26460	K0N7I8	0.00	0.00	1.00
Penicillin-binding protein 1A	Cell wall biogenesis	ponA	BN194_16720	K0NAU3	0.01	0.00	1.00
>tr|K0N4Z7|K0N4Z7_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02080 PE=4 SV=1	Unknown/uncharacterized	K0N4Z7		K0N4Z7	0.01	-0.01	1.00
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	purB	BN194_12520	K0NA41	0.01	-0.01	1.00
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	fabZ	BN194_22520	K0NBS8	6.16	-6.42	-85.491
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)	Lipid-related metabolism	accC	BN194_22510	K0N6M5	5.83	-6.10	-68.7087
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	bkr4	BN194_22550	K0N799	6.11	-5.90	-59.5215
>tr|K0N788|K0N788_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_22500 PE=4 SV=1	Unknown/uncharacterized	K0N788		K0N788	4.74	-5.89	-59.4403
Uncharacterized oxidoreductase YrbE (EC 1.-.-.-)	Carbohydrate-related metabolism	yrbE	BN194_02280	K0N524	3.64	-5.82	-56.602
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	fabG	BN194_22560	K0N6N3	2.88	-5.67	-50.8738
>tr|K0N8W1|K0N8W1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07270 PE=4 SV=1	Unknown/uncharacterized	K0N8W1		K0N8W1	4.00	-5.65	-50.2614
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	fabD	BN194_22570	K0NBT1	6.20	-5.64	-49.8866
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	fabK	BN194_22580	K0NA38	4.58	-5.21	-37.1284
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	fabZ_2	BN194_22620	K0NBT3	2.71	-4.91	-29.969
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	glpK	BN194_07280	K0N694	3.34	-4.64	-24.8794
>tr|K0N2V4|K0N2V4_LACCA GlpO protein OS=Lactobacillus casei W56 GN=glpO PE=4 SV=1	Carbohydrate-related metabolism	glpO		K0N2V4	3.02	-4.61	-24.4871

Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	pdhD	BN194_15110	K0N4P1	5.47	-4.56	-23.6071
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	fabF	BN194_22540	K0MX40	5.03	-4.42	-21.4269
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	accB	BN194_22530	K0NA35	3.80	-4.37	-20.7131
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	pdhC	BN194_15100	K0N4W5	4.74	-4.22	-18.6716
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	alsS	BN194_20150	K0N695	2.60	-4.01	-16.0687
>tr|K0N7I1|K0N7I1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02220 PE=4 SV=1	Unknown/uncharacterized	K0N7I1		K0N7I1	3.75	-3.95	-15.4076
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	pdhA	BN194_15080	K0N860	4.59	-3.78	-13.7655
PTS system IIB component, L-Asc family	Phosphotransferase systems		BN194_28560	K0N861	0.95	-3.78	-13.728
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	yacO	BN194_24420	K0NC34	0.88	-3.75	-13.4756
3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase (THcHDO hydrolase) (EC 3.7.1.22)	Carbohydrate-related metabolism	iolD	BN194_02260	K0N1T3	2.57	-3.74	-13.3935
Acyl carrier protein (ACP)	Lipid-related metabolism	acpP_2, acpP	BN194_22590	K0MX45	2.71	-3.69	-12.9369
Lactaldehyde dehydrogenase (EC 1.2.1.21) (EC 1.2.1.22)	Cell defense/detoxification	aldA	BN194_25470	K0NCB9	3.84	-3.68	-12.8049
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	fabH	BN194_22600	K0N7B0	5.09	-3.53	-11.5463
Uncharacterized protein ACIAD3023	Cell defense/detoxification		BN194_07010	K0N2T5	5.19	-3.45	-10.9288
5-dehydro-2-deoxygluconokinase (EC 2.7.1.92) (2-deoxy-5-keto-D-gluconate kinase)	Carbohydrate-related metabolism	iolC	BN194_02250	K0N1H4	2.79	-3.44	-10.8798
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	pdhB	BN194_15090	K0MVA7	5.66	-3.38	-10.4198
Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	pox5	BN194_19670	K0NBB6	4.97	-3.38	-10.3925
Inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase (EC 1.1.1.18) (EC 1.1.1.369) (Myo-inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase)	Carbohydrate-related metabolism	iolG	BN194_02270	K0N7J1	3.17	-3.26	-9.60982
Pyruvate, phosphate dikinase (EC 2.7.9.1)	Central glycolytic/intermediary pathways	ppdK	BN194_24730	K0NAC6	4.04	-3.23	-9.39928

>tr|K0N518|K0N518_LACCA IolA protein OS=Lactobacillus casei W56 GN=iolA PE=3 SV=1	Carbohydrate-related metabolism	iolA		K0N518	3.84	-3.22	-9.34154
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	fbp	BN194_21660	K0N6C3	5.02	-3.17	-9.00003
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	ldh1,Idh	BN194_06970	K0N8S5	3.94	-2.93	-7.63416
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	pycB	BN194_20290	K0MWI8	4.09	-2.68	-6.39689
Transcriptional regulatory protein spaR	Signal transduction	spaR	BN194_05330	K0N5S9	2.16	-2.60	-6.06968
PspC domain-containing protein	Unknown/uncharacterized	ythC	BN194_10300	K0N3H5	6.11	-2.55	-5.85525
Aldose 1-epimerase (EC 5.1.3.3)	Central glycolytic/intermediary pathways		BN194_07390	K0MTA8	4.40	-2.53	-5.76148
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	dkgB	BN194_08260	K0N347	4.02	-2.50	-5.67012
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	ssdA	BN194_24140	K0MXE0	4.71	-2.49	-5.60281
Uncharacterized protein ycaC	General prediction only	ycaC	BN194_29650	K0N948	6.84	-2.48	-5.57044
Uncharacterized protein	Unknown/uncharacterized		BN194_01760	K0N1N3	3.66	-2.46	-5.49809
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	rex_2,rex	BN194_23820	K0NBZ5	1.11	-2.45	-5.44877
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		BN194_24180	K0NAA2	4.81	-2.37	-5.18376
Glutathione peroxidase	Cell defense/detoxification	gpo	BN194_09780	K0N6T6	4.60	-2.37	-5.17425
Cadmium efflux system accessory protein	Other transporter proteins	cadC	BN194_21540	K0MWU0	2.17	-2.32	-4.97926
>tr|K0N7B1|K0N7B1_LACCA Acetate kinase OS=Lactobacillus casei W56 GN=ackA PE=3 SV=1	Central glycolytic/intermediary pathways	ackA		K0N7B1;K0N6W4	6.10	-2.30	-4.93148
Biotin carboxyl carrier protein	Tricarboxylic acid pathway	bcc	BN194_20370	K0NBF7	2.08	-2.28	-4.85183
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	citE	BN194_20320	K0NBF4	4.91	-2.19	-4.54739
Maltose ABC transporter, periplasmic maltose-binding protein	ABC-type transporter systems		BN194_11200	K0N3U4	3.33	-2.18	-4.54588
Inosose dehydratase (EC 4.2.1.44) (2-keto-myo-inositol dehydratase)	Carbohydrate-related metabolism	iolE	BN194_02290	K0MS68	1.97	-2.14	-4.40472
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	ilvE	BN194_21620	K0NBM4	4.43	-2.13	-4.38732
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	citF	BN194_20310	K0N607	2.76	-2.13	-4.38091
DegV domain-containing protein CA_C1624	Unknown/uncharacterized		BN194_14170	K0NAD8	2.02	-2.05	-4.14456
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	pflB	BN194_16080	K0N8I5	3.31	-2.04	-4.12542

Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	mhqA_3	BN194_18760	K0N5N7	3.90	-1.95	-3.87122
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	nox_2	BN194_02850	K0N1N9	3.29	-1.95	-3.85882
Uncharacterized protein	Unknown/uncharacterized		BN194_24010	K0N715	4.16	-1.95	-3.85241
Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	fhs	BN194_16520	K0NAT0	3.93	-1.85	-3.59963
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	htrA	BN194_29460	K0N8D9	3.84	-1.83	-3.54425
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	citD	BN194_20330	K0N9Q5	4.99	-1.80	-3.48824
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	galK	BN194_07340	K0MTA3	3.09	-1.79	-3.46912
Uncharacterized protein yghZ	General prediction only	yghZ	BN194_27510	K0N7U8	3.82	-1.76	-3.39008
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	garB	BN194_27400	K0N8K3	5.95	-1.75	-3.3533
Uncharacterized protein	Central glycolytic/intermediary pathways		BN194_04970	K0N8A3	4.68	-1.74	-3.34267
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	dhaK_2	BN194_04980	K0N5Q3	3.63	-1.74	-3.33413
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	tpx	BN194_08090	K0MTJ5	3.12	-1.73	-3.32285
Chaperone protein ClpB	Protein folding/turnover	clpB_2	BN194_26350	K0N887	3.30	-1.71	-3.27683
Uncharacterized protein	Unknown/uncharacterized		BN194_20380	K0N9Q9	1.91	-1.68	-3.20217
Histidinol-phosphatase	General prediction only		BN194_14010	K0N4F8	1.84	-1.68	-3.20188
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		BN194_18780	K0N9E0	1.39	-1.67	-3.18058
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	phoU	BN194_10290	K0MTZ9	4.04	-1.67	-3.17609
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	hslU	BN194_16010	K0N4Y1	4.90	-1.62	-3.08327
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	galE	BN194_07350	K0N2R3	3.97	-1.56	-2.94627
>tr|K0N8X1|K0N8X1_LACCA Galactose-1-phosphate uridylyltransferase OS=Lactobacillus casei W56 GN=galT PE=3 SV=1	Carbohydrate-related metabolism	K0N8X1		K0N8X1	5.03	-1.55	-2.91925
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	pta	BN194_11340	K0MU95	3.85	-1.54	-2.90438
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	lplJ	BN194_16640	K0MVN0	3.36	-1.50	-2.82269
>tr|K0N2W3|K0N2W3_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07360 PE=4 SV=1	Unknown/uncharacterized	K0N2W3		K0N2W3	4.29	-1.49	-2.80796

Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	glyA	BN194_13540	K0MV12	3.29	-1.47	-2.77702
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	iolS	BN194_29680	K0NB94	3.36	-1.47	-2.77031
Transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	4.20	-1.47	-2.76832
Uncharacterized protein	Unknown/uncharacterized		BN194_11770	K0N9Y6	3.12	-1.46	-2.75836
Phosphatase YidA (EC 3.1.3.-)	General prediction only	yidA	BN194_28520	K0NDD5	4.16	-1.45	-2.73178
Uncharacterized protein YxeH	General prediction only	yxeH	BN194_04750	K0N1Y7	1.65	-1.42	-2.66957
Uncharacterized protein	Unknown/uncharacterized		BN194_29450	K0N932	2.80	-1.41	-2.66253
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	dhaM	BN194_04960	K0N2C2	3.14	-1.41	-2.65546
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	ydgI_2	BN194_16210	K0N508	2.52	-1.41	-2.65051
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	ysgA	BN194_18610	K0N5M8	0.98	-1.38	-2.60481
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	yabO	BN194_26520	K0NCR8	1.49	-1.35	-2.54481
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	Posttranslational modification	citC	BN194_20340	K0MWJ1	3.52	-1.35	-2.5419
Glucitol operon repressor	Transcriptional regulation	srlR	BN194_28690	K0MYG3	0.62	-1.34	-2.52774
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	agl	BN194_27950	K0N8T1	3.30	-1.34	-2.52534
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	hmgCS1	BN194_19680	K0N9K3	4.46	-1.33	-2.52081
Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	0.42	-1.33	-2.51758
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	Cell wall biogenesis	glmS	BN194_11560	K0N3V9	1.93	-1.28	-2.43517
GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	0.51	-1.27	-2.41938
Tautomerase (EC 5.3.2.-)	General prediction only		BN194_16890	K0MVQ1	0.23	-1.27	-2.41098
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	yhfP	BN194_07740	K0MTE1	1.94	-1.26	-2.39461
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	citX	BN194_20300	K0N6A3	1.55	-1.25	-2.3856
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	cysK	BN194_05520	K0N8E6	3.53	-1.25	-2.3726
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	glyr1	BN194_30100	K0N992	2.43	-1.24	-2.36651

HTH-type transcriptional repressor yvoA	Transcriptional regulation	yvoA_2	BN194_19880	K0N9L8	1.82	-1.24	-2.36482
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdE2	BN194_16600	K0N5A1	3.87	-1.24	-2.35927
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	rny	BN194_10100	K0N3E5	0.82	-1.23	-2.33827
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	pcp	BN194_01980	K0N4Y4	2.43	-1.22	-2.33314
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	accA	BN194_22470	K0NBS6	2.78	-1.22	-2.32569
Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	Steap4	BN194_01990	K0MS41	1.69	-1.21	-2.3176
Nucleic acid-binding protein	Unknown/uncharacterized		BN194_18680	K0N9D5	1.07	-1.21	-2.30803
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	ispA	BN194_18180	K0N9A2	1.18	-1.20	-2.29947
Cell division protein FtsA	Cytokinesis	ftsA	BN194_14750	K0N4T3	2.93	-1.19	-2.28105
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	3.89	-1.18	-2.27337
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	hslV	BN194_16000	K0N542	2.05	-1.11	-2.15937
Cell division ATP-binding protein FtsE	Cytokinesis	ftsE	BN194_10190	K0MTZ2	3.68	-1.10	-2.13837
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC	BN194_00080	K0N486	2.54	-1.09	-2.12198
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	2.70	-1.08	-2.10951
Elongation factor P	Protein translation (elongation)	efp_2	BN194_22050	K0N712	1.28	-1.08	-2.10805
Uncharacterized protein	Unknown/uncharacterized		BN194_01870	K0N7D4	1.72	-1.08	-2.10703
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	thiD_2	BN194_07650	K0N2U9	1.89	-1.07	-2.09815
Aldose 1-epimerase	Central glycolytic/intermediary pathways		BN194_16020	K0NAP4	4.63	-1.07	-2.09279
Sporulation initiation inhibitor protein soj	Cytokinesis	soj	BN194_02040	K0MS45	1.39	-1.06	-2.08759
Uncharacterized protein	General prediction only		BN194_17420	K0NAY8	2.45	-1.04	-2.06272
UPF0337 protein yhjA	General prediction only	yhjA	BN194_24800	K0N7S1	2.14	-1.04	-2.06054
Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	ptp3	BN194_23520	K0NBX6	2.41	-1.02	-2.03431
ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	atpF	BN194_13580	K0N7S9	1.23	-1.02	-2.03048
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	carB	BN194_16450	K0N587	0.82	-0.93	-1.90573
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	npr	BN194_04740	K0MSP8	2.97	-0.92	-1.89794

Virulence factor mviM	General prediction only	mviM	BN194_13310	K0N4B2	2.90	-0.92	-1.89558
UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	2.27	-0.92	-1.88818
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	glgD	BN194_21590	K0MWU4	2.17	-0.91	-1.88417
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	sph	BN194_04930	K0N5Q0	1.83	-0.91	-1.88365
ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit) (F-ATPase epsilon subunit)	Membrane bioenergetics	atpC	BN194_13630	K0N7T2	1.46	-0.91	-1.88307
Probable L-ascorbate-6-phosphate lactonase ulaG (EC 3.1.1.-)	Carbohydrate-related metabolism	ulaG	BN194_28590	K0MYF8	0.47	-0.91	-1.88081
Septum site-determining protein DivIVA	Cytokinesis	divIVA	BN194_14800	K0N4T8	1.12	-0.91	-1.87624
Uncharacterized protein ypuA	Unknown/uncharacterized	ypuA	BN194_27250	K0N8I3	2.88	-0.91	-1.87385
Uncharacterized protein	Unknown/uncharacterized		BN194_28350	K0N8V3	3.99	-0.91	-1.87376
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	11E,P100	BN194_02180	K0N513	1.78	-0.90	-1.86086
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	yclJ	BN194_11790	K0MUE5	2.46	-0.88	-1.84596
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	gnd	BN194_18660	K0N5N2	3.50	-0.87	-1.82514
Uncharacterized protein	Unknown/uncharacterized		BN194_08190	K0MTK3	2.30	-0.84	-1.78957
UPF0337 protein lp_1708	General prediction only		BN194_05810	K0N2J8	1.90	-0.83	-1.77504
30S ribosomal protein S14	Ribosomal proteins	rpsN	BN194_09950	K0N3D1	0.95	-0.82	-1.7713
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	ung	BN194_11330	K0N758	0.71	-0.82	-1.7662
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	manX_5	BN194_29720	K0NDL4	3.20	-0.81	-1.74754
Signal recognition particle protein (Fifty-four homolog)	Protein export	ffh	BN194_17820	K0NB27	1.59	-0.80	-1.74331
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	pth	BN194_26550	K0N8B3	0.89	-0.80	-1.74137
Predicted hydrolase of the HAD superfamily	General prediction only	mtlD	BN194_30450	K0N9D4	2.70	-0.80	-1.73727
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	mhqD	BN194_18770	K0NB71	2.17	-0.79	-1.72421
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	proC	BN194_19900	K0N677	3.17	-0.77	-1.70132
Mannose permease IID component	Phosphotransferase systems	manZ	BN194_02990	K0MSE1	0.35	-0.77	-1.70129
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	polA	BN194_18930	K0N9E7	1.03	-0.76	-1.688
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	yhaA	BN194_30550	K0N9E4	0.98	-0.76	-1.68798

GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	relA	BN194_17230	K0N8Y0	1.47	-0.75	-1.68412
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	pgcA	BN194_10370	K0N9K8	3.34	-0.75	-1.68203
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	thyA	BN194_15800	K0N522	2.12	-0.73	-1.66045
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		BN194_13770	K0NAC0	1.60	-0.73	-1.65551
Oligoendopeptidase, pepF/M3 family	Amino acid-related metabolism		BN194_11580	K0N779	1.81	-0.72	-1.64588
Protein lacX, plasmid	Carbohydrate-related metabolism	lacX	BN194_27070	K0NCY0	3.32	-0.72	-1.64395
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	pyc	BN194_15170	K0NAI2	2.34	-0.70	-1.62683
Uncharacterized protein YwcC	Carbohydrate-related metabolism	ywcC	BN194_09930	K0N6V0	1.83	-0.70	-1.62503
Penicillin acylase (EC 3.5.1.11)	Cell defense/detoxification		BN194_04910	K0N2B8	1.49	-0.70	-1.62069
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	1.41	-0.69	-1.61813
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	rnc	BN194_17870	K0NB31	3.27	-0.69	-1.61053
Protein QmcA	Unknown/uncharacterized	qmcA	BN194_12070	K0NA10	0.71	-0.68	-1.60391
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	maa	BN194_30010	K0N8I9	0.34	-0.68	-1.59966
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	murA2,murA	BN194_26780	K0NAR9	0.46	-0.67	-1.59291
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	frr	BN194_17650	K0N5M3	2.70	-0.67	-1.58762
Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	rp2	BN194_17060	K0N598	2.63	-0.66	-1.58535
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	1.58	-0.64	-1.55322
Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		BN194_08520	K0N972	0.62	-0.63	-1.55188
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	aldB	BN194_20140	K0MWH5	1.29	-0.62	-1.53857
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	asd	BN194_01060	K0N1I5	2.77	-0.62	-1.53758
UPF0478 protein SAOUHSC_01855	Signal transduction		BN194_08710	K0N365	1.10	-0.62	-1.5353
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	hprK	BN194_10330	K0N6Y3	1.80	-0.62	-1.53189

Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	phoP	BN194_10220	K0N9J6	1.34	-0.61	-1.5293
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	msrA_2,msrA	BN194_15860	K0N4W6	1.44	-0.61	-1.52638
Transcriptional regulator, xre family	Transcriptional regulation		BN194_23510	K0N6Y7	0.97	-0.61	-1.52603
Chaperone protein DnaJ	Protein folding/turnover	dnaJ	BN194_17450	K0N5J4	2.28	-0.61	-1.52541
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	1.05	-0.60	-1.51792
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	ohrR	BN194_10500	K0N3J7	1.54	-0.60	-1.51572
Thioredoxin	Posttranslational modification	trxA_2	BN194_08570	K0N975	3.02	-0.60	-1.5141
Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	ADH2	BN194_08400	K0N307	3.16	-0.60	-1.51365
DNA-binding protein HU	DNA replication-related	hup	BN194_15740	K0MVF4	1.47	-0.59	-1.50603
Cellobiose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	celA_5	BN194_29600	K0N945	0.39	-0.57	-1.4866
Protein RecA (Recombinase A)	DNA repair/recombination	recA_2,recA	BN194_27650	K0N8P0	1.29	-0.57	-1.48398
ABC-type phosphate/phosphonate transport system,periplasmic component	ABC-type transporter systems		BN194_25680	K0NAI1	1.62	-0.56	-1.47859
Transcriptional regulator lytR	Transcriptional regulation	lytR_3	BN194_21700	K0N6U3	0.71	-0.56	-1.47416
Regulatory protein vanR	Signal transduction	vanR	BN194_02120	K0N7G4	1.21	-0.56	-1.46964
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	glgC	BN194_21600	K0N6T3	1.93	-0.55	-1.46557
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		BN194_27170	K0NCZ6	2.53	-0.55	-1.46347
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	1.17	-0.53	-1.4474
Rod shape-determining protein MreB	Cytokinesis	mreB	BN194_14550	K0N4R7	0.71	-0.53	-1.44424
Glycerol-3-phosphate ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_11260	K0N3T6	1.48	-0.51	-1.42897
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	rluB	BN194_15650	K0N509	0.74	-0.51	-1.42774
Uncharacterized protein	General prediction only		BN194_21200	K0N6M8	0.96	-0.51	-1.42269
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	patB_2	BN194_09790	K0MTW3	1.38	-0.51	-1.42167
>tr|K0N7I6|K0N7I6_LACCA Glucose-6-phosphate isomerase OS=Lactobacillus casei W56 GN=pgi PE=3 SV=1	Central glycolytic/intermediary pathways	pgi		K0N7I6;K0N4A6	0.97	-0.51	-1.42062

Bifunctional protein FolD	Cofactor-related metabolism	folD	BN194_18210	K0N5K0	2.33	-0.50	-1.41884
Cold shock protein CspA	Transcription-associated proteins	cspA	BN194_14820	K0NAH0	0.26	-0.50	-1.4173
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	apbE_3	BN194_21550	K0N6S8	1.36	-0.50	-1.4114
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	oppF	BN194_17910	K0N5I3	0.25	-0.50	-1.4098
Stage 0 sporulation protein J	Cytokinesis	spo0J	BN194_02050	K0N1F9	1.54	-0.49	-1.40364
FMN-binding domain protein	General prediction only		BN194_24320	K0NC29	1.00	-0.47	-1.38431
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	1.02	-0.47	-1.38341
Uncharacterized protein yueI	Unknown/uncharacterized	yueI	BN194_13920	K0NAC7	0.51	-0.46	-1.37777
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	pepS	BN194_12180	K0N7D5	0.59	-0.43	-1.3508
>tr|K0N1M9|K0N1M9_LACCA Probable phosphoketolase OS=Lactobacillus casei W56 GN=xpkA PE=3 SV=1	Central glycolytic/intermediary pathways	xpkA		K0N1M9;K0N8X7	2.78	-0.43	-1.34525
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE	BN194_02970	K0N7U7	1.87	-0.43	-1.34499
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	deoD	BN194_02810	K0N1Z0	1.90	-0.42	-1.34121
Uncharacterized protein	Lipid-related metabolism	YerQ	BN194_11980	K0N7B3	1.44	-0.42	-1.33379
50S ribosomal protein L9	Ribosomal proteins	rplI	BN194_01130	K0N4K3	1.09	-0.41	-1.33145
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	agaS	BN194_02940	K0MSD9	1.15	-0.41	-1.33051
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	1.61	-0.41	-1.32989
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	2.12	-0.41	-1.32664
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	murE	BN194_02160	K0N1S5	2.90	-0.41	-1.32572
Protein LemA	Unknown/uncharacterized	lemA	BN194_27350	K0N8J7	1.63	-0.40	-1.32178
Oligoendopeptidase F	Amino acid-related metabolism	yjbG_2	BN194_08130	K0N6H7	1.97	-0.40	-1.32113
>tr|K0N699|K0N699_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA PE=3 SV=1;>tr|K0MWW4|K0MWW4_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA_2 PE=3 SV=1	Cell wall biogenesis	rmlA		K0N699;K0MWW4	1.57	-0.40	-1.32096
Thioredoxin-like protein ytpP	Posttranslational modification	ytpP	BN194_18980	K0N9F1	1.68	-0.40	-1.31606
Cell division protein FtsX	Cytokinesis	ftsX	BN194_10200	K0N3G0	0.94	-0.39	-1.31367

Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	coaD	BN194_15200	K0N4X3	2.31	-0.39	-1.31079
Uncharacterized protein	Unknown/uncharacterized		BN194_16650	K0N5A4	1.75	-0.39	-1.30941
Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	aspC	BN194_16770	K0NAU6	0.80	-0.38	-1.30579
Non-specific ribonucleoside hydrolase rihC (EC 3.2.-.-)	Nucleic acid/nucleotide metabolism	rihC	BN194_03870	K0N803	1.56	-0.38	-1.3038
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	murI	BN194_08640	K0MTN4	1.26	-0.38	-1.30161
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	act	BN194_16090	K0MVI3	0.31	-0.38	-1.30003
Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (Guanine insertion enzyme) (tRNA-guanine transglycosylase)	tRNA/Ribosome assembly/processing	tgt	BN194_08380	K0N6J4	0.29	-0.36	-1.28527
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	1.52	-0.36	-1.27907
Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	1.19	-0.33	-1.26
D-ribose-binding protein	ABC-type transporter systems	rbsB	BN194_03290	K0MSF6	0.82	-0.33	-1.2534
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	mtlF	BN194_30410	K0N8N0	0.61	-0.32	-1.25112
Transcriptional regulator, XRE family	Transcriptional regulation		BN194_30170	K0NDP4	0.41	-0.32	-1.25017
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	ykwC	BN194_02520	K0N7M3	0.58	-0.32	-1.24786
Uncharacterized protein YqhY	Unknown/uncharacterized	yqhY	BN194_18230	K0N9A7	0.53	-0.32	-1.24442
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	gpsA	BN194_10350	K0N3I2	1.55	-0.31	-1.24125
Mannose permease IID component	Phosphotransferase systems	manZ_9	BN194_29700	K0N954	0.83	-0.31	-1.23991
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	gpsB	BN194_16690	K0MVN5	0.79	-0.31	-1.23907
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	yuxL	BN194_19910	K0N5X4	1.66	-0.31	-1.23585
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	nusB	BN194_18220	K0NB49	0.28	-0.30	-1.23101
Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		BN194_20000	K0N684	1.75	-0.30	-1.22875
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	ycnE	BN194_13230	K0N7R3	0.77	-0.29	-1.22362
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	rpoZ	BN194_18100	K0N5T7	0.99	-0.29	-1.22165
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	1.42	-0.29	-1.21992

Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	gntK	BN194_02340	K0MS76	0.64	-0.29	-1.21964
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	zwf	BN194_08420	K0N966	0.38	-0.28	-1.21698
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		BN194_21400	K0N6R1	0.97	-0.28	-1.21103
Putative nrdI-like protein	Nucleic acid/nucleotide metabolism		BN194_08250	K0N300	1.10	-0.27	-1.20949
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	atpH	BN194_13590	K0MV16	1.15	-0.27	-1.20443
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	0.95	-0.26	-1.19816
Cell division protein FtsZ	Cytokinesis	ftsZ	BN194_14760	K0N4L6	0.82	-0.24	-1.18416
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	0.92	-0.24	-1.18393
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	ywpJ	BN194_11320	K0N9U2	0.81	-0.24	-1.17893
Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	0.75	-0.24	-1.17821
Protein hit	tRNA aminoacyl synthesis	hit	BN194_19040	K0MWA8	0.84	-0.23	-1.1715
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	trxB	BN194_10360	K0N3L1	0.72	-0.22	-1.16604
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	yqeC	BN194_02330	K0N532	0.86	-0.22	-1.16386
Glycosyl transferase family protein	Cell wall biogenesis		BN194_02420	K0N7L2	0.23	-0.22	-1.16144
Uncharacterized protein yutG	Lipid-related metabolism	yutG	BN194_08940	K0MTQ3	0.85	-0.22	-1.16089
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	potA	BN194_11290	K0MU90	1.61	-0.21	-1.1578
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		BN194_03130	K0N5D9	0.41	-0.21	-1.15575
DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	gyrB	BN194_00060	K0N1B8	0.98	-0.21	-1.15324
>tr|K0N2Q1|K0N2Q1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_06460 PE=4 SV=1;>tr|K0MXJ1|K0MXJ1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_24990 PE=4 SV=1	Unknown/uncharacterized	K0N2Q1		K0N2Q1;K0MXJ1	0.43	-0.20	-1.15085
ABC transporter, permease protein	ABC-type transporter systems		BN194_29810	K0N8H4	0.32	-0.20	-1.14701
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	rpe	BN194_18000	K0N5T1	0.85	-0.17	-1.12785

Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	bceA_2	BN194_21230	K0N9X1	1.49	-0.17	-1.12766
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	pyrC	BN194_16470	K0NAS6	0.08	-0.17	-1.12521
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	yfmL	BN194_12120	K0NA13	0.31	-0.16	-1.11452
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	prs1,prs	BN194_26930	K0NAT2	0.36	-0.15	-1.11167
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	dut	BN194_24640	K0MXG3	0.80	-0.15	-1.1111
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	0.58	-0.14	-1.10572
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatB	BN194_11970	K0NA01	0.38	-0.14	-1.10542
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_3	BN194_21440	K0MWS9	0.36	-0.14	-1.10531
Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	nfo	BN194_17070	K0NAW5	0.25	-0.14	-1.10408
>tr|K0N1K5|K0N1K5_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_01360 PE=4 SV=1	Unknown/uncharacterized	K0N1K5		K0N1K5	0.06	-0.14	-1.10384
UPF0092 membrane protein yrbF	Protein export	yrbF	BN194_08390	K0MTL6	0.12	-0.14	-1.1005
Protein translocase subunit SecA	Protein export	secA	BN194_10170	K0N9J2	0.23	-0.13	-1.09088
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	metG	BN194_27130	K0NAU5	0.32	-0.12	-1.08983
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	dacA	BN194_02140	K0MS53	0.30	-0.12	-1.08569
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	fpaP_3	BN194_21160	K0N682	0.37	-0.12	-1.08463
Protein ytsP	Signal transduction	ytsP	BN194_14450	K0N4Q9	0.07	-0.12	-1.08358
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	glmM	BN194_11550	K0N3Y7	0.71	-0.11	-1.08064
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdF	BN194_16610	K0N552	0.23	-0.11	-1.07696
Probable catabolite control protein A	Transcriptional regulation	ccpA	BN194_08750	K0N323	0.42	-0.10	-1.07018
Single-stranded DNA-binding protein (SSB)	DNA replication-related	ssb	BN194_00110	K0N1C2	0.16	-0.09	-1.06648
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	glcK	BN194_18420	K0NB57	0.36	-0.09	-1.0624
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	prs1_2	BN194_30370	K0NDQ5	0.48	-0.08	-1.06

Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	guaB	BN194_02100	K0N1G3	0.38	-0.08	-1.05976
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	rnjA	BN194_15020	K0NAH6	0.19	-0.08	-1.05535
Predicted hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	0.18	-0.07	-1.05141
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	cysS	BN194_24430	K0NAB2	0.14	-0.07	-1.05003
tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	dus1	BN194_26390	K0MXV9	0.32	-0.06	-1.0441
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	manD	BN194_02950	K0N1P4	0.17	-0.06	-1.04365
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	0.33	-0.06	-1.04322
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	apt	BN194_17380	K0N902	0.08	-0.06	-1.03961
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	nagA	BN194_19890	K0MWF9	0.07	-0.05	-1.0374
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC_2,deoC	BN194_02790	K0MSB5	0.13	-0.05	-1.03557
Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	rbsK	BN194_03300	K0N1R2	0.10	-0.05	-1.03543
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	cap4C	BN194_12280	K0N7E3	0.19	-0.04	-1.02997
Putative secreted protein	cell wall biogenesis		BN194_02820	K0N7S8	0.10	-0.04	-1.02776
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	pepV	BN194_08800	K0N324	0.08	-0.04	-1.02583
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	prsA	BN194_19060	K0N5Q8	0.12	-0.03	-1.02263
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07710	K0N2Z3	0.28	-0.02	-1.01481

Annexure 02 : Fold change (FC >2 and FC <2) differences across different growth conditions (Experiment P2)

(2a) Protein FC >2 Tween 80 Vs control P2

Protein name	Functional Class	Gene/protein symbol	Gene Locus	Protein IDs	-Log t-test p-value	t t-test Difference	Fold change
50S ribosomal protein L18	Ribosomal proteins	RplR	BN194_26060	K0N7F4	1.39	3.44	10.84
50S ribosomal protein L17	Ribosomal proteins	RpsQ	BN194_25950	K0N841	1.14	3.32	9.96
two-component system histidine kinase	Signal transduction	CiaH	BN194_07810	K0N319	1.40	3.30	9.82
30S ribosomal protein S11	Ribosomal proteins	RpsK	BN194_25970	K0NCJ0	2.61	2.47	5.53
pyridoxine 5'-phosphate oxidase-like family protein	Cofactor-related metabolism		BN194_03700	K0N1T2	1.57	2.42	5.35
phosphopentomutase	Nucleic acid/nucleotide metabolism	DeoB	BN194_02800	K0N1N0	1.10	2.39	5.23
50S ribosomal protein L29	Ribosomal proteins	RpmC	BN194_26140	K0MXT6	0.67	2.24	4.72
response regulator ArlR	Signal transduction	ArlR	BN194_18650	K0N5X3	1.02	2.19	4.55
30S ribosomal protein S3	Ribosomal proteins	RpsC	BN194_26160	K0N7G5	1.14	2.11	4.32
class I heat-shock protein (chaperonin) large subunit	Protein folding/turnover	GroEL	BN194_23750	K0N7K7	2.12	2.08	4.23
oxaloacetate decarboxylase, alpha subunit	Tricarboxylic acid pathway	OadA	BN194_20290	K0MWI8	2.08	2.08	4.22
D-alanyl-D-alanine carboxypeptidase dacA	Cell wall biogenesis	DacA	BN194_02140	K0MS53	0.94	2.01	4.03
50S ribosomal protein L16	Ribosomal proteins	RplP	BN194_26150	K0N863	1.85	2.00	3.99
translation initiation factor IF-1	Protein translation (initiation)	InfA	BN194_26000	K0N847	1.02	1.98	3.95
fatty acid hydratase/isomerase (oleate hydratase, linoleate isomerase)	Lipid-related metabolism	Sph	BN194_04930	K0N5Q0	0.77	1.91	3.75
30S ribosomal protein S9	Ribosomal proteins	RpsI	BN194_25840	K0MXR0	0.51	1.88	3.67
50S ribosomal protein L9	Ribosomal proteins	RplI	BN194_01130	K0N4K3	1.04	1.86	3.64
tagatose 1,6-diphosphate aldolase 2	Carbohydrate-related metabolism	LacD2	BN194_07480	K0N6A8	3.13	1.86	3.63
maltogenic amylase	Carbohydrate-related metabolism	BbmA	BN194_11150	K0N3T4	2.08	1.85	3.61
ATP synthase subunit gamma	Membrane bioenergetics	AtpG	BN194_13610	K0N4D3	0.95	1.85	3.61
50S ribosomal protein L20	Ribosomal proteins	RplT	BN194_18800	K0N5Y4	0.61	1.79	3.45
uridylate kinase	Nucleic acid/nucleotide metabolism	PyrH	BN194_17660	K0N5E6	1.60	1.73	3.31

butyrate kinase	Lipid-related metabolism	Buk	BN194_16410	K0N529	1.25	1.70	3.25
DNA helicase IV	DNA repair/recombination	PcrA	BN194_21130	K0N9W3	3.09	1.70	3.24
ADP-glucose pyrophosphorylase	Carbohydrate-related metabolism	GlgC	BN194_21600	K0N6T3	1.92	1.67	3.18
30S ribosomal protein S19	Ribosomal proteins	RpsS	BN194_26180	K0NAM1	0.62	1.66	3.16
ribosome stabilisation protein, Iojap_YbeB family	tRNA/Ribosome assembly/processing	YqeL	BN194_18710	K0N5N6	3.09	1.62	3.07
Xaa-Pro aminopeptidase, APP_like family	Amino acid-related metabolism	PepQ	BN194_08740	K0MTP0	0.81	1.60	3.04
DNA polymerase III subunit beta	DNA replication-related	DnaN	BN194_00020	K0N6S3	1.64	1.60	3.03
50S ribosomal protein L11	Ribosomal proteins	RplK	BN194_24160	K0N724	4.51	1.58	2.99
2-dehydropantoate 2-reductase	Cofactor-related metabolism	PanE	BN194_16370	K0NAS0	3.72	1.58	2.98
chaperone protein ClpB	Protein folding/turnover	ClpB	BN194_15500	K0N4Z8	0.86	1.57	2.97
PTS(Glucose/Mannose family) IIA	Phosphotransferase systems	LevD/ManX	BN194_03000	K0N1P6	2.26	1.56	2.96
hypothetical protein BN194_08190	Unknown/uncharacterized		BN194_08190	K0MTK3	3.05	1.56	2.95
30S ribosomal protein S18	Ribosomal proteins	RspR	BN194_00120	K0N6T2	0.59	1.52	2.87
GTP-binding protein TypA/BipA	Protein translation (elongation)	TypA/BipA	BN194_15150	K0N4W9	1.65	1.50	2.83
phosphonate ABC transporter substrate-binding protein	ABC-type transporter systems	PhnD	BN194_25680	K0NAI1	2.50	1.50	2.82
aminopeptidase N	Amino acid-related metabolism	PepN	BN194_05410	K0N2F5	1.11	1.49	2.81
deoxyuridine 5'-triphosphate nucleotidohydrolase	Nucleic acid/nucleotide metabolism	Dut	BN194_24640	K0MXG3	0.98	1.47	2.77
phosphotransferase activator of gluconeogenesis	Transcriptional regulation	YqfL	BN194_17060	K0N598	0.49	1.47	2.76
aspartate racemase	Amino acid-related metabolism		BN194_02170	K0N7H2	2.27	1.46	2.76
phosphate butyryltransferase	Lipid-related metabolism	Ptb	BN194_16420	K0NAS3	0.90	1.43	2.70
mannose-6-phosphate isomerase	Carbohydrate-related metabolism	Pmi/ManA	BN194_02920	K0N7U2	1.17	1.41	2.66
serine hydroxymethyltransferase	Amino acid-related metabolism	GlyA	BN194_13540	K0MV12	0.79	1.39	2.62
phosphocarrier protein HPr	Phosphotransferase systems	PtsH	BN194_19430	K0N9I2	0.89	1.38	2.61
penicillin acylase family protein	Cell defense/detoxification		BN194_04910	K0N2B8	0.77	1.37	2.59
peptidoglycan-binding lysin	General prediction only	BacA	BN194_00330	K0N4B3	3.53	1.37	2.58

30S ribosomal protein S5	Ribosomal proteins	RpsE	BN194_26050	K0N853	0.34	1.36	2.57
30S ribosomal protein S13	Ribosomal proteins	RpsM	BN194_25980	K0NAK3	1.77	1.35	2.55
dihydrolipoyl dehydrogenase	Lipid-related metabolism	BFmBC	BN194_16400	K0N582	1.20	1.34	2.54
hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	MvaS	BN194_19680	K0N9K3	2.06	1.32	2.50
2-oxoisovalerate dehydrogenase subunit beta	Lipid-related metabolism	BfmBA	BN194_16390	K0MVK8	3.01	1.31	2.48
50S ribosomal protein L24	Ribosomal proteins	RpsX	BN194_26110	K0N7F9	0.62	1.26	2.39
DNA-binding protein HU	DNA replication-related	Hup/Hbs	BN194_15740	K0MVF4	1.45	1.25	2.38
dTDP-glucose 4,6-dehydratase	Cell wall biogenesis	RmlB	BN194_21340	K0MWS0	0.68	1.24	2.36
DUF1447 superfamily protein	Unknown/uncharacterized		BN194_15030	K0N856	1.79	1.24	2.35
glutamine synthetase	Amino acid-related metabolism	GlnA	BN194_18340	K0MW64	2.23	1.23	2.35
glucose-6-phosphate 1-dehydrogenase	Central glycolytic/intermediary pathways	Zwf	BN194_08420	K0N966	1.69	1.21	2.31
rod shape-determining protein MreB	Cytokinesis	MreB	BN194_14550	K0N4R7	1.57	1.19	2.27
peptide chain release factor 1	Protein translation (peptide release)	PrfA	BN194_13510	K0N4C6	0.89	1.18	2.27
hypothetical protein BN194_24780	Unknown/uncharacterized		BN194_24780	K0NAC8	1.11	1.18	2.27
galactose-6-phosphate isomerase subunit LacA	Carbohydrate-related metabolism	LacA	BN194_07500	K0N2T4	1.27	1.18	2.26
elongation factor G	Protein translation (elongation)	Fus	BN194_26270	K0NCN8	1.66	1.17	2.25
50S ribosomal protein L22	Ribosomal proteins	RplV	BN194_26170	K0NCM1	1.69	1.16	2.24
translation initiation factor IF-2	Protein translation (initiation)	InfB	BN194_17550	K0N5K7	2.23	1.15	2.22
elongation factor Ts	Protein translation (elongation)	Tsf	BN194_17670	K0NB01	1.23	1.15	2.21
xanthine phosphoribosyltransferase	Nucleic acid/nucleotide metabolism	Xpt	BN194_12490	K0MUR6	1.90	1.13	2.19
30S ribosomal protein S20	Ribosomal proteins	RpsT	BN194_15250	K0N4X9	1.14	1.08	2.12
Cys-based peroxiredoxin, OsmC superfamily	Cell defense/detoxification		BN194_07010	K0N2T5	1.55	1.08	2.11
uracil phosphoribosyltransferase	Nucleic acid/nucleotide metabolism	Upp	BN194_13550	K0N4J8	3.17	1.08	2.11
myo-inositol catabolism protein IolS	Carbohydrate-related metabolism	IolS	BN194_29680	K0NB94	0.53	1.05	2.07
Dyp-type iron-dependent peroxidase	Cell defense/detoxification	YfeX	BN194_07170	K0N8U9	1.30	1.04	2.06

pyruvate, phosphate dikinase	Central glycolytic/intermediary pathways	PpdK	BN194_24730	K0NAC6	3.30	1.04	2.05
ribonuclease J1	RNA degradation	RnjA	BN194_15020	K0NAH6	0.40	1.02	2.03
ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	ClpC	BN194_21680	K0N9Z7	0.44	1.02	2.03
trigger factor Tig	Protein folding/turnover	Tig	BN194_15330	K0N884	1.92	1.02	2.02
50S ribosomal protein L7/L12	Ribosomal proteins	RplL	BN194_24080	K0NA98	2.80	1.01	2.02
aspartate--tRNA ligase	tRNA aminoacyl synthesis	AspS	BN194_17100	K0N5F3	0.49	1.01	2.01
ssDNA-binding protein	DNA replication-related	Ssb	BN194_00110	K0N1C2	0.62	1.00	2.00
XRE family transcriptional regulator	Transcriptional regulation		BN194_23510	K0N6Y7	1.46	1.00	2.00

(2b) Protein FC <2 Tween 80 Vs control P2

Protein name	**Functional Class**	**Gene/protein symbol**	**Gene Locus**	**Protein IDs**	**-Log t-test p-value**	**t t-test Difference**	**Fold change**
ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	YkpA	BN194_07220	K0N8V6	0.74	0.98	1.97
L-lactate dehydrogenase	Carbohydrate-related metabolism		BN194_06970	K0N8S5	0.78	0.97	1.97
D-alanine-poly(phosphoribitol) ligase	Cell wall biogenesis	DltA	BN194_08590	K0MTN0	0.89	0.97	1.96
glycerol-3-phosphate dehydrogenase	Lipid-related metabolism	GpsA	BN194_10350	K0N3I2	0.82	0.96	1.95
phosphoglucosamine mutase	Cell wall biogenesis	GlmM	BN194_11550	K0N3Y7	1.74	0.96	1.95
50S ribosomal protein L21	Ribosomal proteins	RplU	BN194_18290	K0MW61	0.44	0.96	1.95
>tr|K0N9X8|K0N9X8_LACCA SpsK protein OS=Lactobacillus casei W56 GN=spsK PE=4 SV=1;>tr|K0N6D6|K0N6D6_LACCA SpsK_2 protein OS=Lactobacillus casei W56 GN=spsK_2 PE=4 SV=1	Cell wall biogenesis	spsK		K0N9X8;K0N6D6	1.35	0.96	1.94
deoxyribose-phosphate aldolase	Nucleic acid/nucleotide metabolism	DeoC	BN194_00080	K0N486	0.75	0.95	1.93
threonine--tRNA ligase	tRNA aminoacyl synthesis	ThrS	BN194_18860	K0N5P5	1.60	0.93	1.91

deoxyribose-phosphate aldolase	Nucleic acid/nucleotide metabolism	DeoC	BN194_02790	K0MSB5	0.44	0.93	1.90
oligo-1,6-glucosidase	Carbohydrate-related metabolism		BN194_27950	K0N8T1	0.71	0.92	1.89
spermidine/putrescine import ATP-binding protein PotA	ABC-type transporter systems	PotA	BN194_11290	K0MU90	1.42	0.92	1.89
ribosome-recycling factor	Protein translation (peptide release)	Frr	BN194_17650	K0N5M3	2.60	0.89	1.86
ribonucleoside-diphosphate reductase subunit alpha 2	Nucleic acid/nucleotide metabolism	NrdE2	BN194_16600	K0N5A1	0.70	0.89	1.85
UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2	Cell wall biogenesis	MurA2	BN194_26780	K0NAR9	0.83	0.85	1.80
DNA-directed RNA polymerase subunit delta	RNA polymerase	RpoE	BN194_26810	K0N7L4	2.93	0.84	1.79
lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	Lipid-related metabolism	BfmBB	BN194_16380	K0N8M3	0.81	0.84	1.79
fructose-bisphosphate aldolase	Central glycolytic/intermediary pathways	Fba2	BN194_05060	K0N2C9	3.09	0.84	1.78
glucosamine-1-phosphate N-acetyltransferase / UDP-N-acetylglucosamine pyrophosphorylase	Cell wall biogenesis	GlmU	BN194_26940	K0MY10	1.17	0.84	1.78
tRNA-binding protein, tRNA_domain_binding superfamily	General prediction only	YtpR	BN194_18970	K0NB80	1.39	0.83	1.78
dipeptidase, peptidase C69 family	Amino acid-related metabolism	PepD	BN194_23190	K0MXA1	0.81	0.83	1.78
ribonuclease R	tRNA/Ribosome assembly/processing	Rnr	BN194_11100	K0N3S4	1.45	0.81	1.75
Protein translocase subunit SecA	Protein export	SecA	BN194_10170	K0N9J2	2.52	0.81	1.75
DEAD/DEAH box helicase	tRNA/Ribosome assembly/processing	CshA	BN194_26700	K0N8C7	1.20	0.80	1.74
Pur operon repressor	Transcriptional regulation	PurR2	BN194_26960	K0N7M9	1.04	0.79	1.73
Galactose-6-phosphate isomerase subunit lacB	Carbohydrate-related metabolism	LacB	BN194_07490	K0MTB7	0.78	0.78	1.72
pyruvate kinase	Central glycolytic/intermediary pathways	Pyk	BN194_15580	K0N8B6	1.69	0.77	1.71
ribose-phosphate pyrophosphokinase 1	Nucleic acid/nucleotide metabolism	Prs2	BN194_30370	K0NDQ5	0.71	0.76	1.69
lactaldehyde dehydrogenase/glycolaldehyde dehydrogenase	Cell defense/detoxification		BN194_25470	K0NCB9	0.76	0.76	1.69
multifunctional methylglyoxal reductase, putative	Cell defense/detoxification		BN194_02180	K0N513	0.36	0.75	1.68
aspartate aminotransferase	Amino acid-related metabolism	AspC	BN194_16770	K0NAU6	2.91	0.74	1.67
hypothetical protein BN194_24010	Unknown/uncharacterized		BN194_24010	K0N715	0.50	0.74	1.67

50S ribosomal protein L10	Ribosomal proteins	RplJ	BN194_24090	K0MXD8	3.75	0.73	1.66
GMP synthase	Nucleic acid/nucleotide metabolism	GuaA	BN194_21070	K0NBJ2	2.22	0.72	1.64
adenylosuccinate synthetase	Nucleic acid/nucleotide metabolism	PurA	BN194_01160	K0N1J0	0.28	0.70	1.63
elongation factor Tu	Protein translation (elongation)	Tuf	BN194_15310	K0N4R1	1.90	0.69	1.61
transcription elongation protein NusA	Transcription-associated proteins	NusA	BN194_17580	K0N927	2.18	0.67	1.59
lipid peroxide thiol-specific peroxidase	Cell defense/detoxification	Tpx	BN194_08090	K0MTJ5	0.25	0.67	1.59
Cold shock-like protein CspLA	Transcription-associated proteins	CspLA	BN194_12460	K0N438	0.24	0.66	1.58
alanine--tRNA ligase	tRNA aminoacyl synthesis	AlaS	BN194_08480	K0N6K2	1.16	0.64	1.55
dihydroxyacetone kinase, N-terminal domain	Central glycolytic/intermediary pathways	DhaK	BN194_04980	K0N5Q3	0.33	0.63	1.55
L-lactate dehydrogenase	Carbohydrate-related metabolism	Ldh	BN194_26560	K0N7J5	1.89	0.61	1.53
phenylalanine--tRNA ligase subunit beta	tRNA aminoacyl synthesis	PheS	BN194_18560	K0N5M4	2.01	0.59	1.51
cysteine desulfurase IscS 1	Cofactor-related metabolism	IscS	BN194_14900	K0N4U8	0.94	0.59	1.50
DNA polymerase I	DNA repair/recombination	PolA	BN194_18930	K0N9E7	0.29	0.57	1.49
phosphate acetyltransferase	Carbohydrate-related metabolism	Pta	BN194_11340	K0MU95	2.81	0.57	1.48
50S ribosomal protein L19	Ribosomal proteins	RplS	BN194_17770	K0NB12	0.49	0.57	1.48
CTP synthase	Nucleic acid/nucleotide metabolism	PyrG	BN194_26790	K0MXZ1	2.54	0.56	1.48
NADH-dependent butanol dehydrogenase A	Carbohydrate-related metabolism	BdhA	BN194_22640	K0MX50	0.39	0.55	1.46
glycine cleavage system H protein	Amino acid-related metabolism	GcvH	BN194_13700	K0N4K8	0.36	0.55	1.46
DUF964 superfamily protein	Unknown/uncharacterized		BN194_19080	K0N9F7	1.25	0.55	1.46
catabolite control protein A	Transcriptional regulation	CcpA	BN194_08750	K0N323	1.02	0.54	1.46
purine nucleoside phosphorylase	Nucleic acid/nucleotide metabolism	DeoD	BN194_02810	K0N1Z0	0.42	0.54	1.46
aspartyl/glutamyl-tRNA amidotransferase subunit B	tRNA aminoacyl synthesis	GatB	BN194_11970	K0NA01	1.19	0.54	1.46
aldo_keto_reductase superfamily protein	General prediction only		BN194_27510	K0N7U8	0.90	0.54	1.45
Cold shock protein 1	Transcription-associated proteins	Csp	BN194_06990	K0MT67	0.14	0.53	1.44

50S ribosomal protein L15	Ribosomal proteins	RplO	BN194_26030	K0NAK7	1.16	0.51	1.42
hydrolase, HAD superfamily	General prediction only	YidA	BN194_28520	K0NDD5	1.34	0.50	1.41
fatty acid methyltransferase (cyclopropane fatty acid acyl synthase)	Lipid-related metabolism	fa methyl tranf	BN194_22460	K0N6M0	0.26	0.50	1.41
glucokinase	Central glycolytic/intermediary pathways	GlcK	BN194_18420	K0NB57	1.98	0.49	1.41
PTS(Glucose/Mannose family) IIB	Phosphotransferase systems	LevE/ManX	BN194_02970	K0N7U7	0.90	0.49	1.40
50S ribosomal protein L4	Ribosomal proteins	RplD	BN194_26210	K0N7H0	0.99	0.47	1.39
50S ribosomal protein L31	Ribosomal proteins	RpmE	BN194_26770	K0NCV4	0.80	0.47	1.39
glucosamine-6-phosphate deaminase	Carbohydrate-related metabolism	NagB	BN194_30440	K0MYW0	1.64	0.47	1.39
hypothetical protein BN194_01760	Unknown/uncharacterized		BN194_01760	K0N1N3	0.60	0.47	1.38
30S ribosomal protein S6	Ribosomal proteins	RspF	BN194_00100	K0N0Z1	0.57	0.47	1.38
50S ribosomal protein L1	Ribosomal proteins	RplA	BN194_24150	K0N7M7	1.90	0.47	1.38
formate acetyltransferase	Carbohydrate-related metabolism	PflB	BN194_16080	K0N8I5	1.82	0.47	1.38
universal stress protein, UspA superfamily	Signal transduction		BN194_13870	K0NAC5	0.69	0.46	1.38
30S ribosomal protein S1	Ribosomal proteins	RpsA	BN194_15720	K0NAL9	0.95	0.44	1.36
nucleoside diphosphate kinase	Nucleic acid/nucleotide metabolism	Ndk	BN194_08160	K0N340	0.33	0.43	1.35
peptidase S9 superfamily protein	Amino acid-related metabolism	YuxL	BN194_19910	K0N5X4	0.57	0.43	1.35
glutamate--tRNA ligase	tRNA aminoacyl synthesis	GltX	BN194_24470	K0NC38	0.38	0.43	1.34
DUF711 (RNR_PFL-like) superfamily protein	Unknown/uncharacterized		BN194_09830	K0N6U0	0.34	0.42	1.34
leucine--tRNA ligase	tRNA aminoacyl synthesis	LeuS	BN194_09210	K0N3A9	0.57	0.42	1.34
50S ribosomal protein L6	Ribosomal proteins	RplF	BN194_26070	K0NCK5	0.56	0.41	1.33
N-acetylglucosamine-6-phosphate deacetylase	Carbohydrate-related metabolism	NagA	BN194_19890	K0MWF9	0.91	0.41	1.33
30S ribosomal protein S4	Ribosomal proteins	RpsD	BN194_14440	K0MV63	1.04	0.41	1.33
ATP-dependent chaperone/Clp protease	Protein folding/turnover	ClpB	BN194_19460	K0N5T8	0.32	0.40	1.32
50S ribosomal protein L23	Ribosomal proteins	RplW	BN194_26200	K0N869	1.05	0.40	1.32
dipeptidase, peptidase C69 family	Amino acid-related metabolism	PepD	BN194_13380	K0N7S0	1.57	0.40	1.32

nitroreductase family protein	General prediction only		BN194_16550	K0N597	0.50	0.37	1.29
hydroquinone dioxygenase-like GLO_EDI_BRP_like superfamily protein	General prediction only	MqhA	BN194_18760	K0N5N7	0.69	0.36	1.29
glycogen/starch synthase	Carbohydrate-related metabolism	GlgA	BN194_21580	K0N9Z2	0.36	0.36	1.28
histidine--tRNA ligase	tRNA aminoacyl synthesis	HisS	BN194_17110	K0N5A0	0.47	0.35	1.28
DNA-directed RNA polymerase subunit beta	RNA polymerase	RpoB	BN194_26340	K0MXV4	1.47	0.35	1.28
hypothetical protein BN194_17400	Unknown/uncharacterized		BN194_17400	K0N5I7	0.36	0.35	1.28
RNA polymerase sigma factor A	RNA polymerase	RpoD/SigA	BN194_16920	K0NAV6	0.52	0.35	1.27
NH(3)-dependent NAD(+) synthetase	Cofactor-related metabolism	NadE	BN194_19840	K0MWF6	1.04	0.35	1.27
50S ribosomal protein L3	Ribosomal proteins	RplC	BN194_26220	K0NCN1	1.04	0.34	1.26
DNA-binding regulatory protein, YebC/PmpR family	Transcriptional regulation		BN194_11600	K0N3Z3	0.19	0.34	1.26
redox (NADH)-sensing transcriptional repressor	Transcriptional regulation	Rex	BN194_23820	K0NBZ5	0.69	0.34	1.26
6-phosphofructokinase	Central glycolytic/intermediary pathways	Pfk	BN194_15570	K0NAK6	0.78	0.34	1.26
promiscuous ribonucleotide (NMP) phosphatase	Nucleic acid/nucleotide metabolism	YutF	BN194_08910	K0N383	0.77	0.33	1.26
DNA gyrase subunit A	DNA replication-related	GyrB	BN194_00070	K0N6S7	0.04	0.33	1.26
50S ribosomal protein L2	Ribosomal proteins	RplB	BN194_26190	K0MXU1	1.90	0.33	1.25
adenylosuccinate lyase	Nucleic acid/nucleotide metabolism	PurB	BN194_12520	K0NA41	0.30	0.33	1.25
NADH peroxidase	Cell defense/detoxification	Npr	BN194_04740	K0MSP8	0.47	0.33	1.25
lysine--tRNA ligase	tRNA aminoacyl synthesis	LysS	BN194_26380	K0NAN7	0.16	0.32	1.25
PTS (Fructose/Mannitol family) subunit IIA	Phosphotransferase systems	MtlA	BN194_30410	K0N8N0	0.48	0.32	1.25
ATP-dependent zinc metalloprotease FtsH	Protein folding/turnover	FtsH	BN194_26460	K0N7I8	1.07	0.31	1.24
arginine--tRNA ligase	tRNA aminoacyl synthesis	ArgS	BN194_19120	K0NB86	0.71	0.30	1.23
formate--tetrahydrofolate ligase	Cofactor-related metabolism	Fhs	BN194_16520	K0NAT0	0.16	0.29	1.23
adenylate kinase	Nucleic acid/nucleotide metabolism	Adk	BN194_26010	K0N7F0	0.35	0.29	1.23
	Uncharacterized protein		BN194_07360	K0N2W3	0.51	0.29	1.22
LysR family transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	0.19	0.29	1.22

bifunctional oligoribonuclease and PAP phosphatase nrnA	RNA degradation	NrnA	BN194_08450	K0N309	0.85	0.28	1.22
D-lactate dehydrogenase, putative	Carbohydrate-related metabolism		BN194_01410	K0N1L0	1.03	0.28	1.22
galactose 1-epimerase, aldos_epim superfamily	Central glycolytic/intermediary pathways	GalM	BN194_07390	K0MTA8	0.67	0.28	1.21
50S ribosomal protein L14	Ribosomal proteins	RplN	BN194_26120	K0NCL3	0.66	0.27	1.20
lipoate-protein ligase LplJ	Cofactor-related metabolism	LplJ	BN194_16640	K0MVN0	0.20	0.26	1.20
ribosome-associated sigma 54 modulation protein	tRNA/Ribosome assembly/processing	Hpf	BN194_10150	K0N3F2	0.41	0.26	1.20
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-2,6-diaminopimelate ligase	Cell wall biogenesis	MurE	BN194_02160	K0N1S5	0.94	0.26	1.20
PTS(Glucose/Mannose family) IID	Phosphotransferase systems	LevG/ManZ	BN194_02990	K0MSE1	0.14	0.25	1.19
quinone-oxidoreductase	Membrane bioenergetics	YogA	BN194_18780	K0N9E0	0.31	0.25	1.19
DNA-directed RNA polymerase subunit alpha	RNA polymerase	RpoA	BN194_25960	K0N7E5	0.57	0.25	1.19
ribose-5-phosphate isomerase A	Central glycolytic/intermediary pathways	RpiA2	BN194_28600	K0N8W9	0.94	0.24	1.18
UDP-glucose 4-epimerase	Cell wall biogenesis	GalE	BN194_07350	K0N2R3	0.47	0.23	1.18
ABC transporter, ATP-binding component	ABC-type transporter systems		BN194_07730	K0N6C9	0.08	0.23	1.17
asparagine--tRNA ligase	tRNA aminoacyl synthesis	AsnS	BN194_16760	K0N569	0.80	0.23	1.17
6-phosphogluconolactonase	Carbohydrate-related metabolism	YwcC	BN194_09930	K0N6V0	0.65	0.23	1.17
copper homeostasis protein	Cell defense/detoxification	CutC	BN194_09910	K0N3H0	0.85	0.23	1.17
	Central glycolytic/intermediary pathways			K0N3R3	0.64	0.22	1.17
pyruvate carboxylase	Tricarboxylic acid pathway	Pyc	BN194_15170	K0NAI2	0.30	0.22	1.17
serine--tRNA ligase	tRNA aminoacyl synthesis	SerS	BN194_20080	K0N9N4	0.27	0.21	1.16
30S ribosomal protein S2	Ribosomal proteins	RpsB	BN194_17680	K0N936	0.90	0.21	1.16
tRNA-dihydrouridine synthase 1	tRNA/Ribosome assembly/processing	Dus1	BN194_26390	K0MXV9	0.24	0.20	1.15
citrate lyase alpha subunit	Tricarboxylic acid pathway	CitF	BN194_20310	K0N607	0.81	0.20	1.15
phosphoglucomutase	Central glycolytic/intermediary pathways	PgcA	BN194_10370	K0N9K8	0.55	0.19	1.14

aldose 1-epimerase	Central glycolytic/intermediary pathways	Ald 1 epim	BN194_16020	K0NAP4	0.15	0.18	1.13
30S ribosomal protein S12	Ribosomal proteins	RplL	BN194_26290	K0MXV0	1.16	0.18	1.13
DegV superfamily protein	Unknown/uncharacterized		BN194_16330	K0N8L5	0.18	0.18	1.13
triosephosphate isomerase	Central glycolytic/intermediary pathways	Tpi	BN194_11030	K0N736	0.16	0.15	1.11
PTS (Mannose/Fructose/Sorbose family) IIC	Phosphotransferase systems	ManY	BN194_29710	K0N8G4	0.06	0.15	1.11
UDP-glucose 4-epimerase	Cell wall biogenesis	GalE2	BN194_21400	K0N6R1	0.24	0.15	1.11
glycine--tRNA ligase subunit beta	tRNA aminoacyl synthesis	GlyS	BN194_16950	K0N5D3	0.24	0.15	1.11
Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Phosphotransferase system, enzyme I)	Phosphotransferase systems	ptsI		K0N5T2	0.69	0.14	1.10
beta-Ala-Xaa dipeptidase	Amino acid-related metabolism	PepV	BN194_08800	K0N324	0.51	0.13	1.10
glutathione amide reductase	Cofactor-related metabolism	GarB	BN194_27400	K0N8K3	0.38	0.13	1.09
RNA-binding protein, ASCH superfamily	General prediction only		BN194_17420	K0NAY8	0.23	0.13	1.09
acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase	Carbohydrate-related metabolism	AdhE	BN194_08400	K0N307	0.29	0.13	1.09
DNA-directed RNA polymerase subunit beta'	RNA polymerase	RpoC	BN194_26330	K0NAN3	0.57	0.13	1.09
maltose phosphorylase	Carbohydrate-related metabolism	YvdK	BN194_11160	K0N3S7	0.11	0.12	1.09
oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	OppD	BN194_17920	K0NB35	0.31	0.12	1.09
DUF1341 superfamily protein	Unknown/uncharacterized		BN194_28350	K0N8V3	0.07	0.08	1.06
50S ribosomal protein L13	Ribosomal proteins	RplM	BN194_25850	K0N828	0.39	0.08	1.06
NAD(P)H-disulfide dehydrogenase, pyr_redox superfamily	Membrane bioenergetics	YumB	BN194_24330	K0NAA7	0.04	0.08	1.06
galactokinase	Carbohydrate-related metabolism	GalK	BN194_07340	K0MTA3	0.09	0.07	1.05
6-phospho-beta-galactosidase	Carbohydrate-related metabolism	LacG	BN194_07320	K0N8W7	0.04	0.06	1.04
glucosamine--fructose-6-phosphate aminotransferase	Cell wall biogenesis	GlmS	BN194_11560	K0N3V9	0.14	0.06	1.04
	Central glycolytic/intermediary pathways			K0N7I6;K0N4A6	0.10	0.05	1.03
dihydroorotate dehydrogenase A	Nucleic acid/nucleotide metabolism	PyrDA	BN194_19150	K0N623	0.02	0.05	1.03
polar amino acid ABC-type importer, ATP-binding protein	ABC-type transporter systems	GlnQ4	BN194_29900	K0N971	0.12	0.04	1.03

coenzyme A disulfide reductase	Cell defense/detoxification		BN194_02850	K0N1N9	0.06	0.03	1.02
UPF0154 superfamily protein	Unknown/uncharacterized	YneF	BN194_17740	K0MVY5	0.04	0.02	1.02
3-oxoacyl-ACP synthase III	Lipid-related metabolism	FabH	BN194_22600	K0N7B0	0.03	0.02	1.02
maltose/maltodextrin ABC-type transporter, ATP-binding protein	ABC-type transporter systems	MsmK	BN194_11180	K0N747	0.01	0.01	1.01
50S ribosomal protein L5	Ribosomal proteins	RplE	BN194_26100	K0N859	0.01	0.01	1.01
3-oxoacyl-ACP synthase I/II	Lipid-related metabolism	FabF	BN194_22540	K0MX40	3.17	-4.46	-22.07
enoyl-[acyl-carrier protein] reductase II	Lipid-related metabolism	FabK	BN194_22580	K0NA38	3.63	-4.30	-19.72
(3R)-hydroxymyristoyl-ACP dehydratase	Lipid-related metabolism	FabZ	BN194_22520	K0NBS8	2.84	-3.47	-11.08
3-oxoacyl-ACP reductase	Lipid-related metabolism	FabG	BN194_22560	K0N6N3	2.14	-3.36	-10.23
transcriptional repression of sugar metabolism, DeoR family	Transcriptional regulation	SrlR	BN194_28690	K0MYG3	0.68	-3.05	-8.26
NADPH-dependent FMN reductase with a PAS domain	General prediction only		BN194_06540	K0MT25	2.80	-2.93	-7.63
acyl carrier protein	Lipid-related metabolism	AcpP2	BN194_22590	K0MX45	0.97	-2.59	-6.02
(3R)-hydroxymyristoyl-ACP dehydratase	Lipid-related metabolism	FabZ	BN194_22620	K0NBT3	2.84	-2.43	-5.37
DL-methionine uptake ABC transporter, substrate binding protein	ABC-type transporter systems	MetN	BN194_13740	K0MV23	2.62	-2.31	-4.97
acetyl-CoA carboxylase biotin carboxyl carrier protein	Lipid-related metabolism	AccB	BN194_22530	K0NA35	1.05	-2.16	-4.46
hypothetical protein BN194_29450	Unknown/uncharacterized		BN194_29450	K0N932	1.11	-2.06	-4.16
50S ribosomal protein L30	Ribosomal proteins	RpmD	BN194_26040	K0MXS6	0.50	-2.03	-4.08
malonyl CoA-acyl carrier protein transacylase	Lipid-related metabolism	FabD	BN194_22570	K0NBT1	0.90	-1.97	-3.93
[citrate (pro-3S)-lyase] ligase	Posttranslational modification	CitC	BN194_20340	K0MWJ1	1.52	-1.87	-3.64
cysteine synthase	Amino acid-related metabolism	CysK	BN194_05520	K0N8E6	1.96	-1.82	-3.52
NADH-flavin reductase, BVR-B_like_SDR_a family	General prediction only		BN194_07680	K0N6C4	1.35	-1.76	-3.38
hydrolase, HAD_like superfamily	General prediction only		BN194_11320	K0N9U2	1.62	-1.74	-3.34
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)	Lipid-related metabolism	accC		K0N6M5	2.15	-1.73	-3.31
class I heat-shock protein (chaperonin) small subunit	Protein folding/turnover	GroES	BN194_23760	K0N700	1.59	-1.50	-2.82
3-hydroxyisobutyrate dehydrogenase family protein	General prediction only		BN194_02520	K0N7M3	0.73	-1.46	-2.75
YbjQ_1 superfamily protein	Unknown/uncharacterized		BN194_07140	K0MT82	0.71	-1.42	-2.67
NIF3 superfamily protein	Unknown/uncharacterized		BN194_16900	K0N5C6	0.73	-1.42	-2.67

ribonuclease III	tRNA/Ribosome assembly/processing	Rnc	BN194_17870	K0NB31	1.51	-1.35	-2.56
2,5-diketo-D-gluconic acid reductase B	Cell defense/detoxification	DkgB	BN194_08260	K0N347	3.28	-1.34	-2.53
thiamine biosyn. ATP pyrophosphatase/tRNA sulfurtransferase	Cofactor-related metabolism	ThiI	BN194_14480	K0N7Z7	0.27	-1.33	-2.51
N-acetylglucosamine-6-phosphate deacetylase	Carbohydrate-related metabolism	ManD	BN194_02950	K0N1P4	1.40	-1.30	-2.47
signal recognition particle receptor	Protein export	FtsY	BN194_17850	K0N5R8	0.39	-1.28	-2.43
cell-shape determining protein Mbl	Cytokinesis	Mbl	BN194_13650	K0N4K5	1.80	-1.19	-2.28
phosphate transport system regulatory protein phoU	Transcriptional regulation	PhoU	BN194_10290	K0MTZ9	0.94	-1.19	-2.27
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	1.04	-1.16	-2.23
hypothetical protein BN194_11770	Unknown/uncharacterized		BN194_11770	K0N9Y6	1.35	-1.16	-2.23
apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	Tricarboxylic acid pathway	CitX	BN194_20300	K0N6A3	0.80	-1.13	-2.18
replicative DNA helicase	DNA replication-related	DnaC	BN194_01140	K0MRW2	2.82	-1.12	-2.18
S-adenosylmethionine--tRNA ribosyltransferase-isomerase	tRNA/Ribosome assembly/processing	QueA	BN194_08370	K0N965	0.50	-1.10	-2.14
glucose-1-phosphate adenylyltransferase	Carbohydrate-related metabolism	GlgD	BN194_21590	K0MWU4	1.30	-1.06	-2.08
phosphatidylethanolamine-binding protein, putative	General prediction only		BN194_27230	K0NAV1	0.65	-1.04	-2.05
citrate lyase beta subunit	Tricarboxylic acid pathway	CitE	BN194_20320	K0NBF4	1.62	-1.03	-2.05
acetate kinase	Carbohydrate-related metabolism	AckA	BN194_01620	K0N7B1	0.56	-1.03	-2.04
purine nucleoside phosphoramidase, putative	tRNA aminoacyl synthesis	HinT2	BN194_19040	K0MWA8	1.54	-1.02	-2.03
citrate lyase acyl carrier protein	Tricarboxylic acid pathway	CitD	BN194_20330	K0N9Q5	1.37	-1.01	-2.01
oligopeptide ABC-type transporter, substrate-binding protein	ABC-type transporter systems	OppA2	BN194_20640	K0MWL6	0.65	-1.00	-2.00
acetyltransferase GNAT family protein	General prediction only		BN194_03130	K0N5D9	0.82	-1.00	-2.00
ribonucleoside-diphosphate reductase subunit beta	Nucleic acid/nucleotide metabolism	NrdF	BN194_16610	K0N552	2.57	-0.99	-1.99
	Uncharacterized protein		BN194_22500	K0N788	0.62	-0.97	-1.96
signal recognition particle protein	Protein export	Ffh	BN194_17820	K0NB27	1.72	-0.96	-1.94
DUF1831 superfamily protein	Unknown/uncharacterized		BN194_14910	K0N4M6	1.96	-0.95	-1.94
cysteinyl aminopeptidase, peptidase C1 family	Amino acid-related metabolism	PepC	BN194_24670	K0NC50	0.64	-0.95	-1.93
>tr|K0N699|K0N699_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA	Cell wall biogenesis	rmlA		K0N699;K0MWW4	1.75	-0.93	-1.90

PE=3 SV=1;>tr|K0MWW4|K0MWW4_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA_2 PE=3 SV=1							
3-hydroxyisobutyrate dehydrogenase family protein	General prediction only		BN194_30100	K0N992	1.21	-0.92	-1.89
ATP-dependent Clp protease proteolytic subunit	Protein folding/turnover	ClpP2	BN194_10510	K0N3M4	2.67	-0.90	-1.86
PTS (Mannose/Fructose/Sorbose family) IID	Phosphotransferase systems	ManZ	BN194_29700	K0N954	3.49	-0.90	-1.86
PspC domain-containing protein	Unknown/uncharacterized		BN194_10300	K0N3H5	1.39	-0.87	-1.83
thioredoxin reductase	Posttranslational modification	TrxB	BN194_10360	K0N3L1	1.60	-0.83	-1.78
polar amino acid ABC-type exporter, ATP-binding protein	ABC-type transporter systems	GlnQ3	BN194_21440	K0MWS9	1.14	-0.83	-1.78
DUF1292 superfamily protein	Unknown/uncharacterized		BN194_08530	K0N6K6	5.03	-0.79	-1.73
sex pheromone lipoprotein (similar to cAD1 in E. faecalis)	General prediction only		BN194_24320	K0NC29	1.29	-0.79	-1.73
dTDP-4-dehydrorhamnose 3,5-epimerase	Cell wall biogenesis		BN194_21780	K0N6Q5	0.82	-0.75	-1.68
23S rRNA methyltransferase, SpoU_sub_bind/SpoU_methylase superfamily	tRNA/Ribosome assembly/processing	YsgA	BN194_18610	K0N5M8	0.51	-0.72	-1.65
N-acetylated sugar-phosphate isomerase	Carbohydrate-related metabolism	AgaS	BN194_02940	K0MSD9	1.94	-0.72	-1.64
3-oxoacyl-[acyl-carrier-protein] reductase 4	Lipid-related metabolism	Bkr4	BN194_22550	K0N799	0.44	-0.71	-1.64
tryptophan--tRNA ligase	tRNA aminoacyl synthesis	TrpS	BN194_27360	K0N7S4	0.37	-0.69	-1.61
ABC-type transporter, ATP-binding component	ABC-type transporter systems		BN194_06850	K0N2J7	1.13	-0.68	-1.61
tagatose 1,6-diphosphate aldolase 2	Carbohydrate-related metabolism	LacD2	BN194_27060	K0N7P0	3.67	-0.68	-1.60
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	ClpE	BN194_19450	K0N644	1.18	-0.67	-1.59
succinate-semialdehyde dehydrogenase [NADP(+)]	Amino acid-related metabolism	GabD	BN194_24140	K0MXE0	2.31	-0.66	-1.58
preprotein translocase insertion/stabilisation protein	Protein export	YajC	BN194_08390	K0MTL6	1.40	-0.65	-1.56
CBS pair domain superfamily protein	Unknown/uncharacterized		BN194_26610	K0N7J7	1.74	-0.64	-1.56
maltose/maltodextrin ABC-type transporter, substrate binding protein	ABC-type transporter systems	MdxE/MalE	BN194_11200	K0N3U4	1.77	-0.64	-1.56
Pyruvate dehydrogenase E1 component subunit alpha	Central glycolytic/intermediary pathways	PdhA	BN194_15080	K0N860	1.61	-0.63	-1.55
DUF3800 superfamily protein	Unknown/uncharacterized		BN194_07060	K0N2T7	0.46	-0.61	-1.53
translation initiation factor IF-3	Protein translation (initiation)	InfC	BN194_18820	K0NB73	1.49	-0.61	-1.53

aluminum resistance protein, AAT_I superfamily	Cell defense/detoxification	YnbB	BN194_18380	K0N9B7	0.88	-0.59	-1.50
HD superfamily phosphohydrolase	General prediction only	YwfO	BN194_26840	K0MXZ5	0.54	-0.58	-1.49
Dak2 domain fusion protein	Unknown/uncharacterized		BN194_17960	K0N5I6	1.18	-0.58	-1.49
adenine phosphoribosyltransferase	Nucleic acid/nucleotide metabolism	Apt	BN194_17380	K0N902	0.41	-0.56	-1.47
cysteinyl-tRNA synthetase	tRNA aminoacyl synthesis	CysS	BN194_24430	K0NAB2	0.37	-0.56	-1.47
peptide chain release factor 3	Protein translation (peptide release)	PrfC	BN194_19480	K0N9I7	0.83	-0.55	-1.46
aspartyl/glutamyl-tRNA amidotransferase subunit C	tRNA aminoacyl synthesis	GatC	BN194_11950	K0N436	0.18	-0.54	-1.46
Valine--tRNA ligase	tRNA aminoacyl synthesis	ValS	BN194_14510	K0N4J6	1.02	-0.54	-1.46
foldase protein prsA	Protein folding/turnover	PrsA	BN194_19060	K0N5Q8	3.29	-0.54	-1.45
asparagine synthetase [glutamine-hydrolyzing] 1	Amino acid-related metabolism	AsnB	BN194_22990	K0MX90	0.98	-0.50	-1.42
D-alanine--D-alanine ligase	Cell wall biogenesis	Ddl	BN194_01390	K0MRY4	1.72	-0.50	-1.41
HTH_XRE family transcriptional regulator	Transcriptional regulation		BN194_21960	K0N6F6	0.34	-0.49	-1.41
galactose mutarotase	Carbohydrate-related metabolism	LacX	BN194_27070	K0NCY0	1.26	-0.49	-1.40
divergent methyl-accepting chemotaxis-like domain, DUF948 superfamily	Signal transduction	YtxG	BN194_08710	K0N365	1.26	-0.48	-1.39
hypothetical protein BN194_25890	Unknown/uncharacterized		BN194_25890	K0MXR4	0.19	-0.46	-1.38
short chain dehydrogenase/reductase family protein	General prediction only	YqjQ	BN194_15480	K0N8A1	0.34	-0.46	-1.37
branched-chain amino acid aminotransferase	Lipid-related metabolism	IlvE	BN194_21620	K0NBM4	0.44	-0.45	-1.37
6-phosphogluconate dehydrogenase	Central glycolytic/intermediary pathways	Gnd	BN194_18660	K0N5N2	1.19	-0.45	-1.37
glycerol-3-phosphate ABC transporter substrate-binding protein	ABC-type transporter systems	UgpB	BN194_11260	K0N3T6	2.06	-0.45	-1.37
manganese-dependent inorganic pyrophosphatase	Membrane bioenergetics	PpaC	BN194_16110	K0N4Z4	1.48	-0.45	-1.36
Clp endopeptidase ATP-binding subunit	Protein folding/turnover	ClpB2	BN194_26350	K0N887	0.54	-0.44	-1.36
enolase	Central glycolytic/intermediary pathways	Eno	BN194_11040	K0MU67	1.68	-0.44	-1.35
dipeptidase B	Amino acid-related metabolism	PepDB	BN194_21110	K0N678	0.19	-0.44	-1.35
DegV superfamily protein	Unknown/uncharacterized		BN194_14170	K0NAD8	0.58	-0.42	-1.34
ABM/COG1359 superfamily protein YcnE/LsrG	General prediction only	YcnE	BN194_13230	K0N7R3	0.61	-0.41	-1.33

xylulose-5-phosphate phosphoketolase	Central glycolytic/intermediary pathways	XpaK	BN194_01710	K0N1M9	2.19	-0.41	-1.33
oligoendopeptidase F	Amino acid-related metabolism	YjbG2	BN194_08130	K0N6H7	1.59	-0.40	-1.32
PTS (Mannose/Fructose/Sorbose family) IIAB	Phosphotransferase systems	ManX	BN194_29720	K0NDL4	0.76	-0.40	-1.32
hypothetical protein BN194_23460	Unknown/uncharacterized		BN194_23460	K0N6Y5	0.22	-0.39	-1.31
polyphosphate kinase	Membrane bioenergetics	Ppk	BN194_27270	K0ND10	0.35	-0.39	-1.31
DUF322 superfamily protein	Unknown/uncharacterized	YqhY	BN194_18230	K0N9A7	0.15	-0.38	-1.30
ATP synthase subunit beta	Membrane bioenergetics	AtpD	BN194_13620	K0NAB3	1.58	-0.37	-1.29
ribosomal RNA small subunit methyltransferase H	tRNA/Ribosome assembly/processing	RsmH	BN194_14680	K0N814	0.33	-0.37	-1.29
glycogen/starch phosphorylase	Carbohydrate-related metabolism	GlgP	BN194_21570	K0NBM1	0.22	-0.37	-1.29
ATP synthase subunit alpha	Membrane bioenergetics	AtpA	BN194_13600	K0N4K1	2.16	-0.36	-1.29
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	Central glycolytic/intermediary pathways	PdhC	BN194_15100	K0N4W5	2.14	-0.35	-1.27
30S ribosomal protein S10	Ribosomal proteins	RpsJ	BN194_26230	K0NAM5	0.78	-0.35	-1.27
Nad(P)H-dependent nitroreductase family protein	General prediction only		BN194_16210	K0N508	0.47	-0.35	-1.27
neutral endopeptidase	Amino acid-related metabolism	PepO2	BN194_16630	K0N8Q0	0.63	-0.34	-1.27
glutathione peroxidase	Cell defense/detoxification	Gpo	BN194_09780	K0N6T6	0.69	-0.33	-1.25
aminopeptidase C	Amino acid-related metabolism	PepC2	BN194_24680	K0NAC2	1.36	-0.31	-1.24
chromosome partitioning regulatory protein	Cytokinesis	ParB	BN194_02050	K0N1F9	0.86	-0.30	-1.23
GntR family transcriptional regulator	Transcriptional regulation	YvoA	BN194_19880	K0N9L8	0.16	-0.28	-1.21
alcohol dehydrogenase, MDR superfamily	General prediction only		BN194_07740	K0MTE1	0.25	-0.27	-1.21
1,4-alpha-glucan branching enzyme	Carbohydrate-related metabolism	GlgB	BN194_21610	K0N6B8	0.28	-0.27	-1.21
30S ribosomal protein S8	Ribosomal proteins	RpsH	BN194_26080	K0NAL1	1.13	-0.26	-1.20
inosine-5'-monophosphate dehydrogenase	Nucleic acid/nucleotide metabolism	GuaB	BN194_02100	K0N1G3	0.45	-0.26	-1.20
DEAD/DEAH box helicase	tRNA/Ribosome assembly/processing	CshB	BN194_08460	K0N356	0.13	-0.24	-1.18

Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (EC 2.7.7.12) (UDP-glucose--hexose-1-phosphate uridylyltransferase)	Carbohydrate-related metabolism	galT	BN194_07370	K0N8X1	0.88	-0.24	-1.18
30S ribosomal protein S7	Ribosomal proteins	RpsG	BN194_26280	K0NAM9	1.23	-0.24	-1.18
phosphoglycerate kinase	Central glycolytic/intermediary pathways	Pgk	BN194_11020	K0N9R1	1.15	-0.24	-1.18
mannitol-1-phosphate 5-dehydrogenase	Carbohydrate-related metabolism	MtlD3	BN194_30400	K0N9C8	0.99	-0.23	-1.17
chaperone protein DnaK	Protein folding/turnover	DnaK	BN194_17460	K0N5C7	0.44	-0.22	-1.17
alpha-acetolactate decarboxylase	Carbohydrate-related metabolism	AlsD	BN194_20140	K0MWH5	0.07	-0.22	-1.16
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	Central glycolytic/intermediary pathways	GpmA2	BN194_22740	K0MX58	0.25	-0.22	-1.16
pyruvate dehydrogenase E1 component subunit beta	Central glycolytic/intermediary pathways	PdhB	BN194_15090	K0MVA7	1.66	-0.20	-1.15
two-component system response regulator	Signal transduction		BN194_11790	K0MUE5	0.15	-0.19	-1.14
cell wall integrity sensing response regulator CesR	Signal transduction	CesR	BN194_02120	K0N7G4	0.16	-0.18	-1.14
methionine--tRNA ligase	tRNA aminoacyl synthesis	MetS	BN194_27130	K0NAU5	0.31	-0.18	-1.14
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	HslU	BN194_16010	K0N4Y1	0.40	-0.18	-1.13
oligoendopeptidase F	Amino acid-related metabolism	PepF	BN194_11580	K0N779	0.39	-0.17	-1.13
30S ribosomal protein S14 type Z	Ribosomal proteins	RpsZ	BN194_26090	K0MXS9	0.11	-0.17	-1.12
acetyltransferase (GNAT) family protein	General prediction only		BN194_08200	K0N2Z8	0.16	-0.16	-1.12
bifunctional phosphatase/peptidyl-prolyl cis-trans isomerase	Protein folding/turnover	PpiB	BN194_08960	K0N387	0.20	-0.16	-1.11
cell division protein FtsA	Cytokinesis	FtsA	BN194_14750	K0N4T3	0.12	-0.15	-1.11
DUF965 superfamily protein	Unknown/uncharacterized		BN194_08510	K0N358	0.10	-0.15	-1.11
UDP-N-acetylmuramoylalanine--D-glutamate ligase	Cell wall biogenesis	MurD	BN194_14720	K0NAG5	0.05	-0.15	-1.11
hypothetical protein BN194_07660	Unknown/uncharacterized		BN194_07660	K0N2Y6	0.08	-0.13	-1.10
ribose-phosphate pyrophosphokinase 1	Nucleic acid/nucleotide metabolism	Prs1	BN194_26930	K0NAT2	0.37	-0.12	-1.09
Proline iminopeptidase	Amino acid-related metabolism	FpaP3	BN194_21160	K0N682	0.10	-0.11	-1.08
DUF161/DUF2179 superfamily protein	Unknown/uncharacterized		BN194_15780	K0N8E8	0.18	-0.11	-1.08

trehalose-6-phosphate hydrolase	Carbohydrate-related metabolism	TreA	BN194_06930	K0N662	0.14	-0.11	-1.08
30S ribosomal protein S16	Ribosomal proteins	RpsP	BN194_17810	K0N5H1	0.10	-0.10	-1.07
oligopeptide-binding protein OppA	ABC-type transporter systems	OppA	BN194_17880	K0N983	0.08	-0.10	-1.07
ribose ABC-type transport system, substrate=binding protein	ABC-type transporter systems	RsbB	BN194_03290	K0MSF6	0.11	-0.10	-1.07
pyruvate formate-lyase activating enzyme	Carbohydrate-related metabolism	PflA	BN194_16090	K0MVI3	0.20	-0.09	-1.06
PTS (fructose family) subunit IIABC	Phosphotransferase systems	FruA	BN194_27690	K0MY77	0.05	-0.09	-1.06
dTDP-glucose 4,6-dehydratase	Cell wall biogenesis	RmlB2	BN194_21770	K0NBN4	0.19	-0.07	-1.05
cell division ATP-binding protein FtsE	Cytokinesis	FtsE	BN194_10190	K0MTZ2	0.07	-0.07	-1.05
isoleucine--tRNA ligase	tRNA aminoacyl synthesis	IleS	BN194_14810	K0N4L9	0.22	-0.07	-1.05
fructose-1,6-bisphosphatase class 3	Central glycolytic/intermediary pathways	Fpb	BN194_21660	K0N6C3	0.04	-0.06	-1.05
dihydrolipoyl dehydrogenase	Central glycolytic/intermediary pathways	PdhD	BN194_15110	K0N4P1	0.11	-0.06	-1.04
glutamyl-tRNA(Gln) amidotransferase subunit A	tRNA aminoacyl synthesis	GatA	BN194_11960	K0N3Z6	0.22	-0.06	-1.04
nucleic-acid-binding protein, YlxR family protein	General prediction only	YlxR	BN194_17570	K0NAZ6	0.43	-0.06	-1.04
oligoendopeptidase F	Amino acid-related metabolism	YjbG	BN194_02530	K0N560	0.03	-0.05	-1.04
Proline--tRNA ligase	tRNA aminoacyl synthesis	ProS	BN194_17610	K0N5E2	0.09	-0.05	-1.03
L-2-hydroxyisocaproate dehydrogenase	Carbohydrate-related metabolism		BN194_27170	K0NCZ6	0.38	-0.05	-1.03
pyruvate oxidase	Carbohydrate-related metabolism	Pox5	BN194_19670	K0NBB6	0.05	-0.05	-1.03
30S ribosomal protein S15	Ribosomal proteins	RpsO	BN194_15260	K0N4Q6	0.03	-0.04	-1.03
amidase superfamily protein	General prediction only		BN194_24180	K0NAA2	0.17	-0.04	-1.03
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	Cofactor-related metabolism	ThiD2	BN194_07650	K0N2U9	0.06	-0.04	-1.03
YcaC related amidohydrolase family protein	General prediction only		BN194_29650	K0N948	0.08	-0.04	-1.03
PTS system HPr protein serine kinase	Phosphotransferase systems	HprK	BN194_10330	K0N6Y3	0.04	-0.04	-1.03
PTS system beta-glucoside-specific transporter subunit IIBCA	Phosphotransferase systems	BglP	BN194_06940	K0MT60	0.05	-0.03	-1.02
hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	0.05	-0.02	-1.02

aspartate-semialdehyde dehydrogenase	Amino acid-related metabolism	Asd	BN194_01060	K0N1I5	0.01	-0.01	-1.01
sugar/glycerol-3-phosphate uptake ABC-type importer, substrate-binding protein	ABC-type transporter systems		BN194_29810	K0N8H4	0.01	-0.01	-1.01

(2c) Protein FC >2 Citrate Vs control P2

Protein name	Functional Class	Gene/protein symbol	Gene Locus	Protein IDs	-Log t-test p-value	t t-test Difference	Fold change
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	5.05	6.09	68.26
oxaloacetate decarboxylase, alpha subunit	Tricarboxylic acid pathway	OadA	BN194_20290	K0MWI8	3.71	5.54	46.58
malonyl CoA-acyl carrier protein transacylase	Lipid-related metabolism	FabD	BN194_22570	K0NBT1	1.76	3.78	13.74
ADP-glucose pyrophosphorylase	Carbohydrate-related metabolism	GlgC	BN194_21600	K0N6T3	3.24	3.72	13.22
(3R)-hydroxymyristoyl-ACP dehydratase	Lipid-related metabolism	FabZ	BN194_22520	K0NBS8	4.22	3.59	12.06
3-oxoacyl-[acyl-carrier-protein] reductase 4	Lipid-related metabolism	Bkr4	BN194_22550	K0N799	4.25	3.59	12.04
hypothetical protein BN194_08190	Unknown/uncharacterized		BN194_08190	K0MTK3	4.52	3.12	8.69
glycogen/starch synthase	Carbohydrate-related metabolism	GlgA	BN194_21580	K0N9Z2	2.72	3.03	8.19
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)	Lipid-related metabolism	accC		K0N6M5	3.22	3.00	8.01
3-oxoacyl-ACP synthase III	Lipid-related metabolism	FabH	BN194_22600	K0N7B0	1.98	2.99	7.94
(3R)-hydroxymyristoyl-ACP dehydratase	Lipid-related metabolism	FabZ	BN194_22620	K0NBT3	3.26	2.88	7.34
phosphotransferase activator of gluconeogenesis	Transcriptional regulation	YqfL	BN194_17060	K0N598	1.02	2.85	7.19
50S ribosomal protein L18	Ribosomal proteins	RplR	BN194_26060	K0N7F4	1.13	2.80	6.95
acyl carrier protein	Lipid-related metabolism	AcpP2	BN194_22590	K0MX45	1.03	2.65	6.26
hypothetical protein BN194_24010	Unknown/uncharacterized		BN194_24010	K0N715	1.82	2.64	6.22

DNA polymerase III subunit beta	DNA replication-related	DnaN	BN194_00020	K0N6S3	2.40	2.63	6.21
penicillin acylase family protein	Cell defense/detoxification		BN194_04910	K0N2B8	1.51	2.59	6.04
hydrolase, HAD superfamily	General prediction only	YidA	BN194_28520	K0NDD5	3.86	2.54	5.82
citrate lyase alpha subunit	Tricarboxylic acid pathway	CitF	BN194_20310	K0N607	4.91	2.52	5.72
	Uncharacterized protein		BN194_22500	K0N788	2.32	2.48	5.59
LysR family transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	1.83	2.37	5.17
phosphopentomutase	Nucleic acid/nucleotide metabolism	DeoB	BN194_02800	K0N1N0	1.06	2.27	4.83
DUF322 superfamily protein	Unknown/uncharacterized	YqhY	BN194_18230	K0N9A7	3.05	2.25	4.77
50S ribosomal protein L9	Ribosomal proteins	RplI	BN194_01130	K0N4K3	1.25	2.22	4.67
acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase	Carbohydrate-related metabolism	AdhE	BN194_08400	K0N307	3.44	2.22	4.66
serine hydroxymethyltransferase	Amino acid-related metabolism	GlyA	BN194_13540	K0MV12	1.22	2.09	4.25
50S ribosomal protein L17	Ribosomal proteins	RpsQ	BN194_25950	K0N841	0.72	2.08	4.24
translation initiation factor IF-1	Protein translation (initiation)	InfA	BN194_26000	K0N847	1.07	2.08	4.24
myo-inositol catabolism protein IolS	Carbohydrate-related metabolism	IolS	BN194_29680	K0NB94	1.12	2.06	4.18
3-oxoacyl-ACP synthase I/II	Lipid-related metabolism	FabF	BN194_22540	K0MX40	3.13	2.04	4.12
ATP-dependent chaperone/Clp protease	Protein folding/turnover	ClpB	BN194_19460	K0N5T8	1.88	2.00	4.00
coenzyme A disulfide reductase	Cell defense/detoxification		BN194_02850	K0N1N9	4.24	2.00	4.00
class I heat-shock protein (chaperonin) large subunit	Protein folding/turnover	GroEL	BN194_23750	K0N7K7	2.60	1.94	3.84
DUF964 superfamily protein	Unknown/uncharacterized		BN194_19080	K0N9F7	1.42	1.92	3.79
Cys-based peroxiredoxin, OsmC superfamily	Cell defense/detoxification		BN194_07010	K0N2T5	1.60	1.89	3.71
GTP-binding protein TypA/BipA	Protein translation (elongation)	TypA/BipA	BN194_15150	K0N4W9	1.97	1.86	3.63
formate acetyltransferase	Carbohydrate-related metabolism	PflB	BN194_16080	K0N8I5	3.63	1.85	3.61
dihydroxyacetone kinase, N-terminal domain	Central glycolytic/intermediary pathways	DhaK	BN194_04980	K0N5Q3	1.19	1.84	3.58
glycerol-3-phosphate dehydrogenase	Lipid-related metabolism	GpsA	BN194_10350	K0N3I2	1.57	1.84	3.57
aldose 1-epimerase	Central glycolytic/intermediary pathways	Ald 1 epim	BN194_16020	K0NAP4	1.87	1.83	3.56
dihydrolipoyl dehydrogenase	Lipid-related metabolism	BFmBC	BN194_16400	K0N582	2.21	1.83	3.56

phosphate transport system regulatory protein phoU	Transcriptional regulation	PhoU	BN194_10290	K0MTZ9	1.78	1.83	3.55
glucosamine-1-phosphate N-acetyltransferase / UDP-N-acetylglucosamine pyrophosphorylase	Cell wall biogenesis	GlmU	BN194_26940	K0MY10	2.62	1.83	3.55
fatty acid methyltransferase (cyclopropane fatty acid acyl synthase)	Lipid-related metabolism	fa methyl tranf	BN194_22460	K0N6M0	1.10	1.80	3.49
response regulator ArlR	Signal transduction	ArlR	BN194_18650	K0N5X3	0.76	1.79	3.45
deoxyribose-phosphate aldolase	Nucleic acid/nucleotide metabolism	DeoC	BN194_00080	K0N486	1.47	1.75	3.37
dihydrolipoyl dehydrogenase	Central glycolytic/intermediary pathways	PdhD	BN194_15110	K0N4P1	2.59	1.74	3.34
ribonucleoside-diphosphate reductase subunit alpha 2	Nucleic acid/nucleotide metabolism	NrdE2	BN194_16600	K0N5A1	1.38	1.73	3.32
Dyp-type iron-dependent peroxidase	Cell defense/detoxification	YfeX	BN194_07170	K0N8U9	2.58	1.73	3.32
acetate kinase	Carbohydrate-related metabolism	AckA	BN194_01620	K0N7B1	1.27	1.73	3.31
ribose-phosphate pyrophosphokinase 1	Nucleic acid/nucleotide metabolism	Prs2	BN194_30370	K0NDQ5	1.66	1.73	3.31
rod shape-determining protein MreB	Cytokinesis	MreB	BN194_14550	K0N4R7	2.00	1.72	3.29
leucine--tRNA ligase	tRNA aminoacyl synthesis	LeuS	BN194_09210	K0N3A9	2.30	1.71	3.26
hypothetical protein BN194_07660	Unknown/uncharacterized		BN194_07660	K0N2Y6	3.45	1.70	3.24
uridylate kinase	Nucleic acid/nucleotide metabolism	PyrH	BN194_17660	K0N5E6	1.52	1.69	3.23
phosphate butyryltransferase	Lipid-related metabolism	Ptb	BN194_16420	K0NAS3	1.06	1.67	3.19
phosphate acetyltransferase	Carbohydrate-related metabolism	Pta	BN194_11340	K0MU95	3.77	1.66	3.16
tagatose 1,6-diphosphate aldolase 2	Carbohydrate-related metabolism	LacD2	BN194_07480	K0N6A8	2.79	1.65	3.14
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	Central glycolytic/intermediary pathways	PdhC	BN194_15100	K0N4W5	3.90	1.58	3.00
purine nucleoside phosphoramidase, putative	tRNA aminoacyl synthesis	HinT2	BN194_19040	K0MWA8	3.80	1.57	2.96
methionine--tRNA ligase	tRNA aminoacyl synthesis	MetS	BN194_27130	K0NAU5	2.36	1.56	2.95
ribosome-recycling factor	Protein translation (peptide release)	Frr	BN194_17650	K0N5M3	3.76	1.55	2.93
phosphonate ABC transporter substrate-binding protein	ABC-type transporter systems	PhnD	BN194_25680	K0NAI1	2.90	1.55	2.92
D-alanyl-D-alanine carboxypeptidase dacA	Cell wall biogenesis	DacA	BN194_02140	K0MS53	0.70	1.54	2.91
universal stress protein, UspA superfamily	Signal transduction		BN194_13870	K0NAC5	2.18	1.51	2.85
XRE family transcriptional regulator	Transcriptional regulation		BN194_23510	K0N6Y7	2.35	1.50	2.83
aspartate--tRNA ligase	tRNA aminoacyl synthesis	AspS	BN194_17100	K0N5F3	0.77	1.50	2.82

dTDP-glucose 4,6-dehydratase	Cell wall biogenesis	RmlB	BN194_21340	K0MWS0	0.84	1.49	2.82
DNA helicase IV	DNA repair/recombination	PcrA	BN194_21130	K0N9W3	2.65	1.47	2.77
citrate lyase acyl carrier protein	Tricarboxylic acid pathway	CitD	BN194_20330	K0N9Q5	2.60	1.47	2.77
alanine--tRNA ligase	tRNA aminoacyl synthesis	AlaS	BN194_08480	K0N6K2	2.36	1.47	2.77
UDP-N-acetylmuramoylalanine--D-glutamate ligase	Cell wall biogenesis	MurD	BN194_14720	K0NAG5	2.05	1.46	2.75
Proline iminopeptidase	Amino acid-related metabolism	FpaP3	BN194_21160	K0N682	2.28	1.43	2.70
Nad(P)H-dependent nitroreductase family protein	General prediction only		BN194_16210	K0N508	1.85	1.43	2.69
50S ribosomal protein L29	Ribosomal proteins	RpmC	BN194_26140	K0MXT6	0.40	1.43	2.69
oligo-1,6-glucosidase	Carbohydrate-related metabolism		BN194_27950	K0N8T1	1.13	1.43	2.69
pyruvate dehydrogenase E1 component subunit beta	Central glycolytic/intermediary pathways	PdhB	BN194_15090	K0MVA7	4.42	1.41	2.66
lipoate-protein ligase LplJ	Cofactor-related metabolism	LplJ	BN194_16640	K0MVN0	1.29	1.40	2.63
DNA-binding protein HU	DNA replication-related	Hup/Hbs	BN194_15740	K0MVF4	1.56	1.39	2.61
transcription elongation protein NusA	Transcription-associated proteins	NusA	BN194_17580	K0N927	3.98	1.37	2.58
tRNA-binding protein, tRNA_domain_binding superfamily	General prediction only	YtpR	BN194_18970	K0NB80	1.66	1.37	2.58
2-oxoisovalerate dehydrogenase subunit beta	Lipid-related metabolism	BfmBA	BN194_16390	K0MVK8	4.13	1.36	2.56
butyrate kinase	Lipid-related metabolism	Buk	BN194_16410	K0N529	1.00	1.35	2.55
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-2,6-diaminopimelate ligase	Cell wall biogenesis	MurE	BN194_02160	K0N1S5	2.63	1.34	2.53
peptide chain release factor 1	Protein translation (peptide release)	PrfA	BN194_13510	K0N4C6	0.97	1.30	2.46
dipeptidase, peptidase C69 family	Amino acid-related metabolism	PepD	BN194_23190	K0MXA1	1.31	1.29	2.45
peptidoglycan-binding lysin	General prediction only	BacA	BN194_00330	K0N4B3	3.68	1.29	2.44
PTS (Mannose/Fructose/Sorbose family) IIC	Phosphotransferase systems	ManY	BN194_29710	K0N8G4	1.59	1.29	2.44
aldo_keto_reductase superfamily protein	General prediction only		BN194_27510	K0N7U8	1.96	1.28	2.43
PTS(Glucose/Mannose family) IIB	Phosphotransferase systems	LevE/ManX	BN194_02970	K0N7U7	1.91	1.28	2.42
multifunctional methylglyoxal reductase, putative	Cell defense/detoxification		BN194_02180	K0N513	0.67	1.27	2.42
Pyruvate dehydrogenase E1 component subunit alpha	Central glycolytic/intermediary pathways	PdhA	BN194_15080	K0N860	3.40	1.27	2.41
L-lactate dehydrogenase	Carbohydrate-related metabolism		BN194_06970	K0N8S5	1.00	1.26	2.40
deoxyuridine 5'-triphosphate nucleotidohydrolase	Nucleic acid/nucleotide metabolism	Dut	BN194_24640	K0MXG3	0.85	1.24	2.37

mannose-6-phosphate isomerase	Carbohydrate-related metabolism	Pmi/ManA	BN194_02920	K0N7U2	1.02	1.23	2.34
hypothetical protein BN194_17400	Unknown/uncharacterized		BN194_17400	K0N5I7	1.23	1.21	2.32
purine nucleoside phosphorylase	Nucleic acid/nucleotide metabolism	DeoD	BN194_02810	K0N1Z0	1.10	1.20	2.30
30S ribosomal protein S9	Ribosomal proteins	RpsI	BN194_25840	K0MXR0	0.30	1.19	2.28
deoxyribose-phosphate aldolase	Nucleic acid/nucleotide metabolism	DeoC	BN194_02790	K0MSB5	0.60	1.18	2.26
glycogen/starch phosphorylase	Carbohydrate-related metabolism	GlgP	BN194_21570	K0NBM1	1.44	1.17	2.26
D-alanine-poly(phosphoribitol) ligase	Cell wall biogenesis	DltA	BN194_08590	K0MTN0	1.19	1.17	2.25
pyruvate oxidase	Carbohydrate-related metabolism	Pox5	BN194_19670	K0NBB6	1.80	1.16	2.23
PTS(Glucose/Mannose family) IIA	Phosphotransferase systems	LevD/ManX	BN194_03000	K0N1P6	2.46	1.15	2.22
ssDNA-binding protein	DNA replication-related	Ssb	BN194_00110	K0N1C2	0.75	1.15	2.21
Xaa-Pro aminopeptidase, APP_like family	Amino acid-related metabolism	PepQ	BN194_08740	K0MTP0	0.55	1.14	2.21
DegV superfamily protein	Unknown/uncharacterized		BN194_14170	K0NAD8	2.31	1.14	2.20
hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	MvaS	BN194_19680	K0N9K3	2.02	1.14	2.20
acetyl-CoA carboxylase biotin carboxyl carrier protein	Lipid-related metabolism	AccB	BN194_22530	K0NA35	0.57	1.14	2.20
formate--tetrahydrofolate ligase	Cofactor-related metabolism	Fhs	BN194_16520	K0NAT0	0.73	1.11	2.16
cysteine desulfurase IscS 1	Cofactor-related metabolism	IscS	BN194_14900	K0N4U8	1.71	1.10	2.14
enoyl-[acyl-carrier protein] reductase II	Lipid-related metabolism	FabK	BN194_22580	K0NA38	1.12	1.08	2.11
2-dehydropantoate 2-reductase	Cofactor-related metabolism	PanE	BN194_16370	K0NAS0	5.12	1.07	2.10
hypothetical protein BN194_23460	Unknown/uncharacterized		BN194_23460	K0N6Y5	0.73	1.07	2.10
50S ribosomal protein L7/L12	Ribosomal proteins	RplL	BN194_24080	K0NA98	2.59	1.06	2.09
30S ribosomal protein S5	Ribosomal proteins	RpsE	BN194_26050	K0N853	0.25	1.05	2.06
chaperone protein ClpB	Protein folding/turnover	ClpB	BN194_15500	K0N4Z8	0.53	1.04	2.06
maltogenic amylase	Carbohydrate-related metabolism	BbmA	BN194_11150	K0N3T4	1.35	1.04	2.05
ribose-5-phosphate isomerase A	Central glycolytic/intermediary pathways	RpiA2	BN194_28600	K0N8W9	3.51	1.03	2.04
lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	Lipid-related metabolism	BfmBB	BN194_16380	K0N8M3	1.12	1.03	2.04
ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	ClpC	BN194_21680	K0N9Z7	0.43	1.01	2.02

(2d) Protein FC <2 Citrate Vs control P2

Protein name	Functional Class	Gene/protein symbol	Gene Locus	Protein IDs	-Log t-test p-value	t t-test Difference	Fold change
glucose-6-phosphate 1-dehydrogenase	Central glycolytic/intermediary pathways	Zwf	BN194_08420	K0N966	1.41	0.99	1.98
1,4-alpha-glucan branching enzyme	Carbohydrate-related metabolism	GlgB	BN194_21610	K0N6B8	1.12	0.97	1.96
citrate lyase beta subunit	Tricarboxylic acid pathway	CitE	BN194_20320	K0NBF4	1.88	0.95	1.94
lactaldehyde dehydrogenase/glycolaldehyde dehydrogenase	Cell defense/detoxification		BN194_25470	K0NCB9	1.05	0.94	1.91
histidine--tRNA ligase	tRNA aminoacyl synthesis	HisS	BN194_17110	K0N5A0	1.40	0.93	1.90
pyruvate formate-lyase activating enzyme	Carbohydrate-related metabolism	PflA	BN194_16090	K0MVI3	1.06	0.93	1.90
threonine--tRNA ligase	tRNA aminoacyl synthesis	ThrS	BN194_18860	K0N5P5	1.62	0.92	1.89
adenylosuccinate synthetase	Nucleic acid/nucleotide metabolism	PurA	BN194_01160	K0N1J0	0.38	0.90	1.86
30S ribosomal protein S19	Ribosomal proteins	RpsS	BN194_26180	K0NAM1	0.30	0.89	1.86
arginine--tRNA ligase	tRNA aminoacyl synthesis	ArgS	BN194_19120	K0NB86	1.99	0.89	1.86
catabolite control protein A	Transcriptional regulation	CcpA	BN194_08750	K0N323	2.68	0.87	1.82
DUF965 superfamily protein	Unknown/uncharacterized		BN194_08510	K0N358	0.72	0.85	1.81
hypothetical protein BN194_01760	Unknown/uncharacterized		BN194_01760	K0N1N3	1.13	0.85	1.80
dihydroorotate dehydrogenase A	Nucleic acid/nucleotide metabolism	PyrDA	BN194_19150	K0N623	1.10	0.85	1.80
glucosamine--fructose-6-phosphate aminotransferase	Cell wall biogenesis	GlmS	BN194_11560	K0N3V9	2.60	0.85	1.80
spermidine/putrescine import ATP-binding protein PotA	ABC-type transporter systems	PotA	BN194_11290	K0MU90	2.20	0.84	1.79
Dak2 domain fusion protein	Unknown/uncharacterized		BN194_17960	K0N5I6	1.63	0.84	1.79
GntR family transcriptional regulator	Transcriptional regulation	YvoA	BN194_19880	K0N9L8	0.50	0.84	1.79
YcaC related amidohydrolase family protein	General prediction only		BN194_29650	K0N948	2.21	0.83	1.78
elongation factor Ts	Protein translation (elongation)	Tsf	BN194_17670	K0NB01	0.99	0.83	1.78
hypothetical protein BN194_24780	Unknown/uncharacterized		BN194_24780	K0NAC8	0.76	0.83	1.78
30S ribosomal protein S11	Ribosomal proteins	RpsK	BN194_25970	K0NCJ0	1.09	0.81	1.76
two-component system response regulator	Signal transduction		BN194_11790	K0MUE5	1.04	0.81	1.75
cell wall integrity sensing response regulator CesR	Signal transduction	CesR	BN194_02120	K0N7G4	0.89	0.80	1.75

Valine--tRNA ligase	tRNA aminoacyl synthesis	ValS	BN194_14510	K0N4J6	1.38	0.80	1.74
Protein translocase subunit SecA	Protein export	SecA	BN194_10170	K0N9J2	1.96	0.80	1.74
phenylalanine--tRNA ligase subunit beta	tRNA aminoacyl synthesis	PheS	BN194_18560	K0N5M4	2.52	0.79	1.73
foldase protein prsA	Protein folding/turnover	PrsA	BN194_19060	K0N5Q8	2.76	0.78	1.72
lipid peroxide thiol-specific peroxidase	Cell defense/detoxification	Tpx	BN194_08090	K0MTJ5	0.30	0.78	1.71
translation initiation factor IF-2	Protein translation (initiation)	InfB	BN194_17550	K0N5K7	1.84	0.77	1.71
50S ribosomal protein L24	Ribosomal proteins	RpsX	BN194_26110	K0N7F9	0.35	0.76	1.70
NAD(P)H-disulfide dehydrogenase, pyr_redox superfamily	Membrane bioenergetics	YumB	BN194_24330	K0NAA7	0.48	0.76	1.69
NADH-dependent butanol dehydrogenase A	Carbohydrate-related metabolism	BdhA	BN194_22640	K0MX50	0.58	0.75	1.68
alpha-acetolactate decarboxylase	Carbohydrate-related metabolism	AlsD	BN194_20140	K0MWH5	0.77	0.75	1.68
DegV superfamily protein	Unknown/uncharacterized		BN194_16330	K0N8L5	0.83	0.74	1.67
Galactose-6-phosphate isomerase subunit lacB	Carbohydrate-related metabolism	LacB	BN194_07490	K0MTB7	1.11	0.74	1.67
50S ribosomal protein L20	Ribosomal proteins	RplT	BN194_18800	K0N5Y4	0.22	0.74	1.67
aspartyl/glutamyl-tRNA amidotransferase subunit B	tRNA aminoacyl synthesis	GatB	BN194_11970	K0NA01	1.72	0.74	1.67
UDP-glucose 4-epimerase	Cell wall biogenesis	GalE	BN194_07350	K0N2R3	1.44	0.73	1.66
phosphoglucosamine mutase	Cell wall biogenesis	GlmM	BN194_11550	K0N3Y7	1.73	0.72	1.65
	Uncharacterized protein		BN194_07360	K0N2W3	1.93	0.72	1.65
ribonuclease J1	RNA degradation	RnjA	BN194_15020	K0NAH6	0.26	0.70	1.63
glutathione amide reductase	Cofactor-related metabolism	GarB	BN194_27400	K0N8K3	1.92	0.70	1.62
aspartate racemase	Amino acid-related metabolism		BN194_02170	K0N7H2	0.55	0.70	1.62
galactose 1-epimerase, aldos_epim superfamily	Central glycolytic/intermediary pathways	GalM	BN194_07390	K0MTA8	3.38	0.69	1.62
50S ribosomal protein L16	Ribosomal proteins	RplP	BN194_26150	K0N863	0.56	0.68	1.60
aspartyl/glutamyl-tRNA amidotransferase subunit C	tRNA aminoacyl synthesis	GatC	BN194_11950	K0N436	0.58	0.68	1.60
fatty acid hydratase/isomerase (oleate hydratase, linoleate isomerase)	Lipid-related metabolism	Sph	BN194_04930	K0N5Q0	0.23	0.68	1.60
PTS (Mannose/Fructose/Sorbose family) IIAB	Phosphotransferase systems	ManX	BN194_29720	K0NDL4	1.77	0.67	1.59
trigger factor Tig	Protein folding/turnover	Tig	BN194_15330	K0N884	1.44	0.67	1.59
glutamine synthetase	Amino acid-related metabolism	GlnA	BN194_18340	K0MW64	1.34	0.66	1.58
phosphocarrier protein HPr	Phosphotransferase systems	PtsH	BN194_19430	K0N9I2	0.68	0.66	1.58

ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	ClpE	BN194_19450	K0N644	0.86	0.65	1.57
RNA-binding protein, ASCH superfamily	General prediction only		BN194_17420	K0NAY8	1.32	0.64	1.55
DNA polymerase I	DNA repair/recombination	PolA	BN194_18930	K0N9E7	0.33	0.63	1.54
galactose-6-phosphate isomerase subunit LacA	Carbohydrate-related metabolism	LacA	BN194_07500	K0N2T4	0.85	0.62	1.54
DUF711 (RNR_PFL-like) superfamily protein	Unknown/uncharacterized		BN194_09830	K0N6U0	0.55	0.62	1.54
50S ribosomal protein L11	Ribosomal proteins	RplK	BN194_24160	K0N724	2.16	0.61	1.53
NADH peroxidase	Cell defense/detoxification	Npr	BN194_04740	K0MSP8	0.89	0.61	1.52
branched-chain amino acid aminotransferase	Lipid-related metabolism	IlvE	BN194_21620	K0NBM4	0.65	0.60	1.52
UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2	Cell wall biogenesis	MurA2	BN194_26780	K0NAR9	0.57	0.60	1.52
glycine cleavage system H protein	Amino acid-related metabolism	GcvH	BN194_13700	K0N4K8	0.40	0.60	1.51
DUF3800 superfamily protein	Unknown/uncharacterized		BN194_07060	K0N2T7	0.70	0.59	1.51
ribonuclease R	tRNA/Ribosome assembly/processing	Rnr	BN194_11100	K0N3S4	1.13	0.59	1.51
PTS (fructose family) subunit IIABC	Phosphotransferase systems	FruA	BN194_27690	K0MY77	0.41	0.57	1.49
cell division protein FtsA	Cytokinesis	FtsA	BN194_14750	K0N4T3	0.42	0.57	1.48
glucose-1-phosphate adenylyltransferase	Carbohydrate-related metabolism	GlgD	BN194_21590	K0MWU4	0.80	0.57	1.48
ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	YkpA	BN194_07220	K0N8V6	0.39	0.56	1.47
3-hydroxyisobutyrate dehydrogenase family protein	General prediction only		BN194_02520	K0N7M3	0.68	0.55	1.47
>tr|K0N9X8|K0N9X8_LACCA SpsK protein OS=Lactobacillus casei W56 GN=spsK PE=4 SV=1;>tr|K0N6D6|K0N6D6_LACCA SpsK_2 protein OS=Lactobacillus casei W56 GN=spsK_2 PE=4 SV=1	Cell wall biogenesis	spsK		K0N9X8;K0N6D6	0.71	0.55	1.46
tRNA-dihydrouridine synthase 1	tRNA/Ribosome assembly/processing	Dus1	BN194_26390	K0MXV9	0.72	0.53	1.45
redox (NADH)-sensing transcriptional repressor	Transcriptional regulation	Rex	BN194_23820	K0NBZ5	1.21	0.53	1.45
chromosome partitioning regulatory protein	Cytokinesis	ParB	BN194_02050	K0N1F9	1.04	0.53	1.44
50S ribosomal protein L10	Ribosomal proteins	RplJ	BN194_24090	K0MXD8	3.26	0.53	1.44
NADPH-dependent FMN reductase with a PAS domain	General prediction only		BN194_06540	K0MT25	0.58	0.52	1.43
phosphatidylethanolamine-binding protein, putative	General prediction only		BN194_27230	K0NAV1	0.88	0.52	1.43
aminopeptidase N	Amino acid-related metabolism	PepN	BN194_05410	K0N2F5	0.36	0.51	1.42
ribonuclease III	tRNA/Ribosome assembly/processing	Rnc	BN194_17870	K0NB31	0.53	0.51	1.42

Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	Cofactor-related metabolism	ThiD2	BN194_07650	K0N2U9	1.12	0.50	1.42
glycerol-3-phosphate ABC transporter substrate-binding protein	ABC-type transporter systems	UgpB	BN194_11260	K0N3T6	1.96	0.48	1.40
ribosome-associated sigma 54 modulation protein	tRNA/Ribosome assembly/processing	Hpf	BN194_10150	K0N3F2	0.76	0.47	1.38
ABC transporter, ATP-binding component	ABC-type transporter systems		BN194_07730	K0N6C9	2.06	0.46	1.38
uracil phosphoribosyltransferase	Nucleic acid/nucleotide metabolism	Upp	BN194_13550	K0N4J8	2.43	0.46	1.38
triosephosphate isomerase	Central glycolytic/intermediary pathways	Tpi	BN194_11030	K0N736	1.04	0.46	1.37
thiamine biosyn. ATP pyrophosphatase/tRNA sulfurtransferase	Cofactor-related metabolism	ThiI	BN194_14480	K0N7Z7	0.12	0.46	1.37
DUF1341 superfamily protein	Unknown/uncharacterized		BN194_28350	K0N8V3	0.41	0.43	1.35
aspartate-semialdehyde dehydrogenase	Amino acid-related metabolism	Asd	BN194_01060	K0N1I5	0.59	0.42	1.34
DEAD/DEAH box helicase	tRNA/Ribosome assembly/processing	CshA	BN194_26700	K0N8C7	0.90	0.41	1.33
sex pheromone lipoprotein (similar to cAD1 in E. faecalis)	General prediction only		BN194_24320	K0NC29	0.40	0.41	1.33
ATP-dependent zinc metalloprotease FtsH	Protein folding/turnover	FtsH	BN194_26460	K0N7I8	1.38	0.40	1.32
hypothetical protein BN194_25890	Unknown/uncharacterized		BN194_25890	K0MXR4	0.29	0.40	1.32
PTS (Fructose/Mannitol family) subunit IIA	Phosphotransferase systems	MtlA	BN194_30410	K0N8N0	0.65	0.40	1.32
Clp endopeptidase ATP-binding subunit	Protein folding/turnover	ClpB2	BN194_26350	K0N887	0.47	0.39	1.31
glutathione peroxidase	Cell defense/detoxification	Gpo	BN194_09780	K0N6T6	0.75	0.36	1.28
quinone-oxidoreductase	Membrane bioenergetics	YogA	BN194_18780	K0N9E0	0.46	0.34	1.27
short chain dehydrogenase/reductase family protein	General prediction only	YqjQ	BN194_15480	K0N8A1	0.25	0.34	1.27
50S ribosomal protein L22	Ribosomal proteins	RplV	BN194_26170	K0NCM1	0.56	0.34	1.27
xanthine phosphoribosyltransferase	Nucleic acid/nucleotide metabolism	Xpt	BN194_12490	K0MUR6	0.09	0.33	1.26
beta-Ala-Xaa dipeptidase	Amino acid-related metabolism	PepV	BN194_08800	K0N324	1.58	0.33	1.25
amidase superfamily protein	General prediction only		BN194_24180	K0NAA2	1.25	0.32	1.25
PTS(Glucose/Mannose family) IID	Phosphotransferase systems	LevG/ManZ	BN194_02990	K0MSE1	0.18	0.32	1.25
N-acetylglucosamine-6-phosphate deacetylase	Carbohydrate-related metabolism	NagA	BN194_19890	K0MWF9	0.89	0.32	1.25
lysine--tRNA ligase	tRNA aminoacyl synthesis	LysS	BN194_26380	K0NAN7	0.16	0.32	1.25
fructose-1,6-bisphosphatase class 3	Central glycolytic/intermediary pathways	Fpb	BN194_21660	K0N6C3	0.51	0.32	1.24
bifunctional oligoribonuclease and PAP phosphatase nrnA	RNA degradation	NrnA	BN194_08450	K0N309	0.95	0.32	1.24

6-phosphogluconolactonase	Carbohydrate-related metabolism	YwcC	BN194_09930	K0N6V0	1.06	0.31	1.24
phosphoglucomutase	Central glycolytic/intermediary pathways	PgcA	BN194_10370	K0N9K8	1.07	0.31	1.24
hydroquinone dioxygenase-like GLO_EDI_BRP_like superfamily protein	General prediction only	MqhA	BN194_18760	K0N5N7	0.66	0.30	1.23
peptide chain release factor 3	Protein translation (peptide release)	PrfC	BN194_19480	K0N9I7	0.37	0.30	1.23
YbjQ_1 superfamily protein	Unknown/uncharacterized		BN194_07140	K0MT82	0.25	0.28	1.22
aspartate aminotransferase	Amino acid-related metabolism	AspC	BN194_16770	K0NAU6	1.81	0.26	1.20
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	HslU	BN194_16010	K0N4Y1	0.31	0.26	1.20
PspC domain-containing protein	Unknown/uncharacterized		BN194_10300	K0N3H5	0.62	0.26	1.20
N-acetylglucosamine-6-phosphate deacetylase	Carbohydrate-related metabolism	ManD	BN194_02950	K0N1P4	0.28	0.26	1.19
apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	Tricarboxylic acid pathway	CitX	BN194_20300	K0N6A3	0.72	0.25	1.19
glucokinase	Central glycolytic/intermediary pathways	GlcK	BN194_18420	K0NB57	1.01	0.24	1.18
cysteinyl-tRNA synthetase	tRNA aminoacyl synthesis	CysS	BN194_24430	K0NAB2	0.14	0.23	1.17
PTS system HPr protein serine kinase	Phosphotransferase systems	HprK	BN194_10330	K0N6Y3	0.30	0.23	1.17
ribosomal RNA small subunit methyltransferase H	tRNA/Ribosome assembly/processing	RsmH	BN194_14680	K0N814	0.36	0.23	1.17
DUF161/DUF2179 superfamily protein	Unknown/uncharacterized		BN194_15780	K0N8E8	0.48	0.22	1.17
L-lactate dehydrogenase	Carbohydrate-related metabolism	Ldh	BN194_26560	K0N7J5	0.94	0.22	1.17
cell division ATP-binding protein FtsE	Cytokinesis	FtsE	BN194_10190	K0MTZ2	0.23	0.21	1.16
GMP synthase	Nucleic acid/nucleotide metabolism	GuaA	BN194_21070	K0NBJ2	0.69	0.21	1.15
asparagine--tRNA ligase	tRNA aminoacyl synthesis	AsnS	BN194_16760	K0N569	0.55	0.21	1.15
30S ribosomal protein S20	Ribosomal proteins	RpsT	BN194_15250	K0N4X9	0.23	0.21	1.15
elongation factor G	Protein translation (elongation)	Fus	BN194_26270	K0NCN8	0.30	0.19	1.14
3-oxoacyl-ACP reductase	Lipid-related metabolism	FabG	BN194_22560	K0N6N3	0.15	0.19	1.14
DNA-directed RNA polymerase subunit delta	RNA polymerase	RpoE	BN194_26810	K0N7L4	1.15	0.18	1.14
pyridoxine 5'-phosphate oxidase-like family protein	Cofactor-related metabolism		BN194_03700	K0N1T2	0.03	0.17	1.13
	Central glycolytic/intermediary pathways			K0N7I6;K0N4A6	0.50	0.17	1.13
Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (EC 2.7.7.12) (UDP-glucose--hexose-1-phosphate uridylyltransferase)	Carbohydrate-related metabolism	galT	BN194_07370	K0N8X1	0.42	0.17	1.12

glutamyl-tRNA(Gln) amidotransferase subunit A	tRNA aminoacyl synthesis	GatA	BN194_11960	K0N3Z6	0.91	0.16	1.12
alcohol dehydrogenase, MDR superfamily	General prediction only		BN194_07740	K0MTE1	0.21	0.15	1.11
30S ribosomal protein S6	Ribosomal proteins	RspF	BN194_00100	K0N0Z1	0.17	0.15	1.11
DUF1447 superfamily protein	Unknown/uncharacterized		BN194_15030	K0N856	0.18	0.14	1.10
signal recognition particle protein	Protein export	Ffh	BN194_17820	K0NB27	0.15	0.13	1.10
polar amino acid ABC-type importer, ATP-binding protein	ABC-type transporter systems	GlnQ4	BN194_29900	K0N971	0.42	0.13	1.09
peptidase S9 superfamily protein	Amino acid-related metabolism	YuxL	BN194_19910	K0N5X4	0.17	0.12	1.09
pyruvate kinase	Central glycolytic/intermediary pathways	Pyk	BN194_15580	K0N8B6	0.23	0.12	1.09
	Central glycolytic/intermediary pathways			K0N3R3	0.55	0.12	1.08
UDP-glucose 4-epimerase	Cell wall biogenesis	GalE2	BN194_21400	K0N6R1	0.17	0.11	1.08
adenine phosphoribosyltransferase	Nucleic acid/nucleotide metabolism	Apt	BN194_17380	K0N902	0.07	0.11	1.08
hypothetical protein BN194_29450	Unknown/uncharacterized		BN194_29450	K0N932	0.40	0.09	1.06
Cold shock-like protein CspLA	Transcription-associated proteins	CspLA	BN194_12460	K0N438	0.04	0.08	1.06
6-phospho-beta-galactosidase	Carbohydrate-related metabolism	LacG	BN194_07320	K0N8W7	0.07	0.07	1.05
ribose-phosphate pyrophosphokinase 1	Nucleic acid/nucleotide metabolism	Prs1	BN194_26930	K0NAT2	0.16	0.07	1.05
copper homeostasis protein	Cell defense/detoxification	CutC	BN194_09910	K0N3H0	0.17	0.07	1.05
PTS system beta-glucoside-specific transporter subunit IIBCA	Phosphotransferase systems	BglP	BN194_06940	K0MT60	0.12	0.06	1.04
ATP synthase subunit gamma	Membrane bioenergetics	AtpG	BN194_13610	K0N4D3	0.02	0.06	1.04
glutamate--tRNA ligase	tRNA aminoacyl synthesis	GltX	BN194_24470	K0NC38	0.03	0.04	1.03
DNA gyrase subunit A	DNA replication-related	GyrB	BN194_00070	K0N6S7	0.00	0.04	1.03
sugar/glycerol-3-phosphate uptake ABC-type importer, substrate-binding protein	ABC-type transporter systems		BN194_29810	K0N8H4	0.03	0.03	1.02
DNA-binding regulatory protein, YebC/PmpR family	Transcriptional regulation		BN194_11600	K0N3Z3	0.02	0.03	1.02
elongation factor Tu	Protein translation (elongation)	Tuf	BN194_15310	K0N4R1	0.07	0.02	1.01
serine--tRNA ligase	tRNA aminoacyl synthesis	SerS	BN194_20080	K0N9N4	0.01	0.01	1.01
23S rRNA methyltransferase, SpoU_sub_bind/SpoU_methylase superfamily	tRNA/Ribosome assembly/processing	YsgA	BN194_18610	K0N5M8	0.00	0.00	1.00
NH(3)-dependent NAD(+) synthetase	Cofactor-related metabolism	NadE	BN194_19840	K0MWF6	0.00	0.00	1.00
pyruvate, phosphate dikinase	Central glycolytic/intermediary pathways	PpdK	BN194_24730	K0NAC6	0.02	-0.01	1.00

RNA polymerase sigma factor A	RNA polymerase	RpoD/SigA	BN194_16920	K0NAV6	0.00	-0.01	1.00
50S ribosomal protein L30	Ribosomal proteins	RpmD	BN194_26040	K0MXS6	1.47	-3.83	-14.25
HD superfamily phosphohydrolase	General prediction only	YwfO	BN194_26840	K0MXZ5	0.69	-1.57	-2.97
NADH-flavin reductase, BVR-B_like_SDR_a family	General prediction only		BN194_07680	K0N6C4	2.14	-1.44	-2.71
30S ribosomal protein S15	Ribosomal proteins	RpsO	BN194_15260	K0N4Q6	2.30	-1.43	-2.70
cysteine synthase	Amino acid-related metabolism	CysK	BN194_05520	K0N8E6	2.56	-1.39	-2.62
aluminum resistance protein, AAT_I superfamily	Cell defense/detoxification	YnbB	BN194_18380	K0N9B7	2.00	-1.31	-2.48
cysteinyl aminopeptidase, peptidase C1 family	Amino acid-related metabolism	PepC	BN194_24670	K0NC50	2.58	-1.26	-2.40
class I heat-shock protein (chaperonin) small subunit	Protein folding/turnover	GroES	BN194_23760	K0N700	2.56	-1.26	-2.40
nucleic-acid-binding protein, YlxR family protein	General prediction only	YlxR	BN194_17570	K0NAZ6	0.47	-1.11	-2.16
30S ribosomal protein S12	Ribosomal proteins	RplL	BN194_26290	K0MXV0	2.84	-1.10	-2.14
preprotein translocase insertion/stabilisation protein	Protein export	YajC	BN194_08390	K0MTL6	0.90	-0.99	-1.99
ATP synthase subunit alpha	Membrane bioenergetics	AtpA	BN194_13600	K0N4K1	2.86	-0.98	-1.98
hydrolase, HAD_like superfamily	General prediction only		BN194_11320	K0N9U2	0.93	-0.94	-1.92
replicative DNA helicase	DNA replication-related	DnaC	BN194_01140	K0MRW2	2.66	-0.92	-1.89
ribonucleoside-diphosphate reductase subunit beta	Nucleic acid/nucleotide metabolism	NrdF	BN194_16610	K0N552	3.06	-0.92	-1.89
ATP synthase subunit beta	Membrane bioenergetics	AtpD	BN194_13620	K0NAB3	2.44	-0.92	-1.89
30S ribosomal protein S10	Ribosomal proteins	RpsJ	BN194_26230	K0NAM5	1.90	-0.90	-1.87
translation initiation factor IF-3	Protein translation (initiation)	InfC	BN194_18820	K0NB73	1.79	-0.86	-1.82
N-acetylated sugar-phosphate isomerase	Carbohydrate-related metabolism	AgaS	BN194_02940	K0MSD9	1.82	-0.85	-1.80
tagatose 1,6-diphosphate aldolase 2	Carbohydrate-related metabolism	LacD2	BN194_27060	K0N7P0	3.07	-0.85	-1.80
maltose phosphorylase	Carbohydrate-related metabolism	YvdK	BN194_11160	K0N3S7	0.93	-0.81	-1.75
inosine-5'-monophosphate dehydrogenase	Nucleic acid/nucleotide metabolism	GuaB	BN194_02100	K0N1G3	1.43	-0.80	-1.74
50S ribosomal protein L19	Ribosomal proteins	RplS	BN194_17770	K0NB12	0.73	-0.79	-1.73
HTH_XRE family transcriptional regulator	Transcriptional regulation		BN194_21960	K0N6F6	0.74	-0.78	-1.71
30S ribosomal protein S7	Ribosomal proteins	RpsG	BN194_26280	K0NAM9	2.84	-0.76	-1.69
30S ribosomal protein S8	Ribosomal proteins	RpsH	BN194_26080	K0NAL1	2.03	-0.75	-1.68
transcriptional repression of sugar metabolism, DeoR family	Transcriptional regulation	SrlR	BN194_28690	K0MYG3	0.65	-0.72	-1.64

cell-shape determining protein Mbl	Cytokinesis	Mbl	BN194_13650	K0N4K5	1.47	-0.70	-1.62
Cold shock protein 1	Transcription-associated proteins	Csp	BN194_06990	K0MT67	0.69	-0.70	-1.62
50S ribosomal protein L5	Ribosomal proteins	RplE	BN194_26100	K0N859	2.11	-0.68	-1.61
thioredoxin reductase	Posttranslational modification	TrxB	BN194_10360	K0N3L1	1.14	-0.68	-1.60
neutral endopeptidase	Amino acid-related metabolism	PepO2	BN194_16630	K0N8Q0	1.55	-0.67	-1.59
ATP-dependent Clp protease proteolytic subunit	Protein folding/turnover	ClpP2	BN194_10510	K0N3M4	2.22	-0.67	-1.59
isoleucine--tRNA ligase	tRNA aminoacyl synthesis	IleS	BN194_14810	K0N4L9	2.71	-0.65	-1.57
two-component system histidine kinase	Signal transduction	CiaH	BN194_07810	K0N319	0.37	-0.61	-1.53
glycine--tRNA ligase subunit beta	tRNA aminoacyl synthesis	GlyS	BN194_16950	K0N5D3	1.33	-0.61	-1.53
oligoendopeptidase F	Amino acid-related metabolism	YjbG	BN194_02530	K0N560	0.47	-0.61	-1.53
30S ribosomal protein S14 type Z	Ribosomal proteins	RpsZ	BN194_26090	K0MXS9	1.23	-0.61	-1.53
dTDP-4-dehydrorhamnose 3,5-epimerase	Cell wall biogenesis		BN194_21780	K0N6Q5	0.71	-0.57	-1.48
hypothetical protein BN194_11770	Unknown/uncharacterized		BN194_11770	K0N9Y6	0.62	-0.55	-1.47
oligopeptide ABC-type transporter, substrate-binding protein	ABC-type transporter systems	OppA2	BN194_20640	K0MWL6	0.29	-0.54	-1.46
50S ribosomal protein L3	Ribosomal proteins	RplC	BN194_26220	K0NCN1	1.63	-0.54	-1.45
DEAD/DEAH box helicase	tRNA/Ribosome assembly/processing	CshB	BN194_08460	K0N356	1.38	-0.52	-1.43
enolase	Central glycolytic/intermediary pathways	Eno	BN194_11040	K0MU67	1.83	-0.50	-1.41
asparagine synthetase [glutamine-hydrolyzing] 1	Amino acid-related metabolism	AsnB	BN194_22990	K0MX90	0.89	-0.50	-1.41
DUF1831 superfamily protein	Unknown/uncharacterized		BN194_14910	K0N4M6	1.26	-0.48	-1.39
glucosamine-6-phosphate deaminase	Carbohydrate-related metabolism	NagB	BN194_30440	K0MYW0	1.83	-0.46	-1.37
mannitol-1-phosphate 5-dehydrogenase	Carbohydrate-related metabolism	MtlD3	BN194_30400	K0N9C8	1.86	-0.46	-1.37
aminopeptidase C	Amino acid-related metabolism	PepC2	BN194_24680	K0NAC2	2.13	-0.45	-1.37
6-phosphofructokinase	Central glycolytic/intermediary pathways	Pfk	BN194_15570	K0NAK6	1.17	-0.45	-1.37
2,5-diketo-D-gluconic acid reductase B	Cell defense/detoxification	DkgB	BN194_08260	K0N347	1.45	-0.44	-1.36
trehalose-6-phosphate hydrolase	Carbohydrate-related metabolism	TreA	BN194_06930	K0N662	0.63	-0.44	-1.36
50S ribosomal protein L14	Ribosomal proteins	RplN	BN194_26120	K0NCL3	1.48	-0.44	-1.35
ABC-type transporter, ATP-binding component	ABC-type transporter systems		BN194_06850	K0N2J7	0.65	-0.43	-1.35
galactose mutarotase	Carbohydrate-related metabolism	LacX	BN194_27070	K0NCY0	1.04	-0.41	-1.33

tryptophan--tRNA ligase	tRNA aminoacyl synthesis	TrpS	BN194_27360	K0N7S4	0.24	-0.41	-1.33
polar amino acid ABC-type exporter, ATP-binding protein	ABC-type transporter systems	GlnQ3	BN194_21440	K0MWS9	1.46	-0.41	-1.33
50S ribosomal protein L31	Ribosomal proteins	RpmE	BN194_26770	K0NCV4	0.92	-0.40	-1.32
oligoendopeptidase F	Amino acid-related metabolism	PepF	BN194_11580	K0N779	1.25	-0.40	-1.32
50S ribosomal protein L6	Ribosomal proteins	RplF	BN194_26070	K0NCK5	0.90	-0.40	-1.32
30S ribosomal protein S2	Ribosomal proteins	RpsB	BN194_17680	K0N936	1.96	-0.39	-1.31
acetyltransferase GNAT family protein	General prediction only		BN194_03130	K0N5D9	0.41	-0.39	-1.31
nucleoside diphosphate kinase	Nucleic acid/nucleotide metabolism	Ndk	BN194_08160	K0N340	0.19	-0.38	-1.30
D-alanine--D-alanine ligase	Cell wall biogenesis	Ddl	BN194_01390	K0MRY4	1.78	-0.38	-1.30
[citrate (pro-3S)-lyase] ligase	Posttranslational modification	CitC	BN194_20340	K0MWJ1	0.32	-0.37	-1.30
PTS (Mannose/Fructose/Sorbose family) IID	Phosphotransferase systems	ManZ	BN194_29700	K0N954	1.81	-0.37	-1.29
signal recognition particle receptor	Protein export	FtsY	BN194_17850	K0N5R8	0.53	-0.36	-1.29
maltose/maltodextrin ABC-type transporter, substrate binding protein	ABC-type transporter systems	MdxE/MalE	BN194_11200	K0N3U4	0.96	-0.34	-1.26
50S ribosomal protein L13	Ribosomal proteins	RplM	BN194_25850	K0N828	1.22	-0.34	-1.26
chaperone protein DnaK	Protein folding/turnover	DnaK	BN194_17460	K0N5C7	0.76	-0.33	-1.26
oligoendopeptidase F	Amino acid-related metabolism	YjbG2	BN194_08130	K0N6H7	1.06	-0.32	-1.25
50S ribosomal protein L21	Ribosomal proteins	RplU	BN194_18290	K0MW61	0.13	-0.32	-1.25
phosphoglycerate kinase	Central glycolytic/intermediary pathways	Pgk	BN194_11020	K0N9R1	1.79	-0.32	-1.25
50S ribosomal protein L2	Ribosomal proteins	RplB	BN194_26190	K0MXU1	1.65	-0.32	-1.25
50S ribosomal protein L1	Ribosomal proteins	RplA	BN194_24150	K0N7M7	1.43	-0.31	-1.24
Proline--tRNA ligase	tRNA aminoacyl synthesis	ProS	BN194_17610	K0N5E2	0.81	-0.31	-1.24
30S ribosomal protein S4	Ribosomal proteins	RpsD	BN194_14440	K0MV63	1.23	-0.31	-1.24
manganese-dependent inorganic pyrophosphatase	Membrane bioenergetics	PpaC	BN194_16110	K0N4Z4	0.54	-0.29	-1.23
Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Phosphotransferase system, enzyme I)	Phosphotransferase systems	ptsI		K0N5T2	1.51	-0.27	-1.21
50S ribosomal protein L4	Ribosomal proteins	RplD	BN194_26210	K0N7H0	0.52	-0.26	-1.20
D-lactate dehydrogenase, putative	Carbohydrate-related metabolism		BN194_01410	K0N1L0	2.42	-0.24	-1.18
S-adenosylmethionine--tRNA ribosyltransferase-isomerase	tRNA/Ribosome assembly/processing	QueA	BN194_08370	K0N965	0.48	-0.24	-1.18

50S ribosomal protein L23	Ribosomal proteins	RplW	BN194_26200	K0N869	0.78	-0.23	-1.18
DUF1292 superfamily protein	Unknown/uncharacterized		BN194_08530	K0N6K6	0.40	-0.23	-1.17
UPF0154 superfamily protein	Unknown/uncharacterized	YneF	BN194_17740	K0MVY5	0.59	-0.23	-1.17
DNA-directed RNA polymerase subunit alpha	RNA polymerase	RpoA	BN194_25960	K0N7E5	0.60	-0.22	-1.16
dipeptidase B	Amino acid-related metabolism	PepDB	BN194_21110	K0N678	0.35	-0.22	-1.16
dTDP-glucose 4,6-dehydratase	Cell wall biogenesis	RmlB2	BN194_21770	K0NBN4	1.24	-0.22	-1.16
DNA-directed RNA polymerase subunit beta	RNA polymerase	RpoB	BN194_26340	K0MXV4	1.10	-0.21	-1.16
NIF3 superfamily protein	Unknown/uncharacterized		BN194_16900	K0N5C6	0.58	-0.21	-1.15
DNA-directed RNA polymerase subunit beta'	RNA polymerase	RpoC	BN194_26330	K0NAN3	0.96	-0.21	-1.15
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	Central glycolytic/intermediary pathways	GpmA2	BN194_22740	K0MX58	0.28	-0.20	-1.15
>tr|K0N699|K0N699_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA PE=3 SV=1;>tr|K0MWW4|K0MWW4_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA_2 PE=3 SV=1	Cell wall biogenesis	rmlA		K0N699;K0MWW4	0.29	-0.19	-1.14
hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	0.99	-0.19	-1.14
DL-methionine uptake ABC transporter, substrate binding protein	ABC-type transporter systems	MetN	BN194_13740	K0MV23	0.27	-0.18	-1.13
oligopeptide-binding protein OppA	ABC-type transporter systems	OppA	BN194_17880	K0N983	0.35	-0.17	-1.13
dipeptidase, peptidase C69 family	Amino acid-related metabolism	PepD	BN194_13380	K0N7S0	0.85	-0.17	-1.12
maltose/maltodextrin ABC-type transporter, ATP-binding protein	ABC-type transporter systems	MsmK	BN194_11180	K0N747	0.25	-0.17	-1.12
galactokinase	Carbohydrate-related metabolism	GalK	BN194_07340	K0MTA3	0.31	-0.16	-1.12
bifunctional phosphatase/peptidyl-prolyl cis-trans isomerase	Protein folding/turnover	PpiB	BN194_08960	K0N387	0.24	-0.16	-1.12
oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	OppD	BN194_17920	K0NB35	0.29	-0.14	-1.10
promiscuous ribonucleotide (NMP) phosphatase	Nucleic acid/nucleotide metabolism	YutF	BN194_08910	K0N383	0.54	-0.13	-1.09
nitroreductase family protein	General prediction only		BN194_16550	K0N597	0.17	-0.13	-1.09
30S ribosomal protein S1	Ribosomal proteins	RpsA	BN194_15720	K0NAL9	0.23	-0.13	-1.09
3-hydroxyisobutyrate dehydrogenase family protein	General prediction only		BN194_30100	K0N992	0.14	-0.12	-1.09
ribose ABC-type transport system, substrate=binding protein	ABC-type transporter systems	RsbB	BN194_03290	K0MSF6	0.12	-0.12	-1.09
30S ribosomal protein S13	Ribosomal proteins	RpsM	BN194_25980	K0NAK3	0.11	-0.12	-1.09

50S ribosomal protein L15	Ribosomal proteins	RplO	BN194_26030	K0NAK7	0.17	-0.11	-1.08
xylulose-5-phosphate phosphoketolase	Central glycolytic/intermediary pathways	XpaK	BN194_01710	K0N1M9	0.65	-0.11	-1.08
divergent methyl-accepting chemotaxis-like domain, DUF948 superfamily	Signal transduction	YtxG	BN194_08710	K0N365	0.23	-0.10	-1.07
fructose-bisphosphate aldolase	Central glycolytic/intermediary pathways	Fba2	BN194_05060	K0N2C9	0.47	-0.10	-1.07
30S ribosomal protein S16	Ribosomal proteins	RpsP	BN194_17810	K0N5H1	0.26	-0.09	-1.06
acetyltransferase (GNAT) family protein	General prediction only		BN194_08200	K0N2Z8	0.07	-0.08	-1.06
succinate-semialdehyde dehydrogenase [NADP(+)]	Amino acid-related metabolism	GabD	BN194_24140	K0MXE0	0.41	-0.08	-1.06
ribosome stabilisation protein, Iojap_YbeB family	tRNA/Ribosome assembly/processing	YqeL	BN194_18710	K0N5N6	0.02	-0.07	-1.05
30S ribosomal protein S18	Ribosomal proteins	RspR	BN194_00120	K0N6T2	0.02	-0.05	-1.04
Pur operon repressor	Transcriptional regulation	PurR2	BN194_26960	K0N7M9	0.03	-0.05	-1.03
6-phosphogluconate dehydrogenase	Central glycolytic/intermediary pathways	Gnd	BN194_18660	K0N5N2	0.11	-0.04	-1.03
adenylate kinase	Nucleic acid/nucleotide metabolism	Adk	BN194_26010	K0N7F0	0.03	-0.04	-1.03
L-2-hydroxyisocaproate dehydrogenase	Carbohydrate-related metabolism		BN194_27170	K0NCZ6	0.28	-0.04	-1.03
30S ribosomal protein S3	Ribosomal proteins	RpsC	BN194_26160	K0N7G5	0.03	-0.04	-1.02
pyruvate carboxylase	Tricarboxylic acid pathway	Pyc	BN194_15170	K0NAI2	0.04	-0.03	-1.02
ABM/COG1359 superfamily protein YcnE/LsrG	General prediction only	YcnE	BN194_13230	K0N7R3	0.03	-0.03	-1.02
CTP synthase	Nucleic acid/nucleotide metabolism	PyrG	BN194_26790	K0MXZ1	0.07	-0.03	-1.02
CBS pair domain superfamily protein	Unknown/uncharacterized		BN194_26610	K0N7J7	0.02	-0.02	-1.01
adenylosuccinate lyase	Nucleic acid/nucleotide metabolism	PurB	BN194_12520	K0NA41	0.01	-0.01	-1.01

(2e) Protein FC >2 Tween 80 Vs citrate P2

Protein name	Functional Class	Gene/protein symbol	Gene Locus	Protein IDs	-Log t-test p-value	t t-test Difference	Fold change
two-component system histidine kinase	Signal transduction	CiaH	BN194_07810	K0N319	1.53	3.91	15.04
pyridoxine 5'-phosphate oxidase-like family protein	Cofactor-related metabolism		BN194_03700	K0N1T2	0.66	2.25	4.75
30S ribosomal protein S3	Ribosomal proteins	RpsC	BN194_26160	K0N7G5	1.31	2.15	4.43
50S ribosomal protein L30	Ribosomal proteins	RpmD	BN194_26040	K0MXS6	0.45	1.80	3.49
ATP synthase subunit gamma	Membrane bioenergetics	AtpG	BN194_13610	K0N4D3	3.65	1.80	3.47
ribosome stabilisation protein, Iojap_YbeB family	tRNA/Ribosome assembly/processing	YqeL	BN194_18710	K0N5N6	0.81	1.69	3.23
30S ribosomal protein S11	Ribosomal proteins	RpsK	BN194_25970	K0NCJ0	3.39	1.65	3.14
30S ribosomal protein S18	Ribosomal proteins	RspR	BN194_00120	K0N6T2	0.70	1.57	2.97
30S ribosomal protein S13	Ribosomal proteins	RpsM	BN194_25980	K0NAK3	1.38	1.47	2.78
30S ribosomal protein S15	Ribosomal proteins	RpsO	BN194_15260	K0N4Q6	1.58	1.39	2.62
50S ribosomal protein L19	Ribosomal proteins	RplS	BN194_17770	K0NB12	3.86	1.36	2.57
50S ribosomal protein L16	Ribosomal proteins	RplP	BN194_26150	K0N863	1.50	1.32	2.49
50S ribosomal protein L21	Ribosomal proteins	RplU	BN194_18290	K0MW61	0.66	1.28	2.43
30S ribosomal protein S12	Ribosomal proteins	RplL	BN194_26290	K0MXV0	3.01	1.28	2.42
50S ribosomal protein L17	Ribosomal proteins	RpsQ	BN194_25950	K0N841	1.53	1.23	2.35
fatty acid hydratase/isomerase (oleate hydratase, linoleate isomerase)	Lipid-related metabolism	Sph	BN194_04930	K0N5Q0	1.91	1.23	2.35
Cold shock protein 1	Transcription-associated proteins	Csp	BN194_06990	K0MT67	0.38	1.23	2.34
DUF1447 superfamily protein	Unknown/uncharacterized		BN194_15030	K0N856	3.15	1.10	2.14
50S ribosomal protein L20	Ribosomal proteins	RplT	BN194_18800	K0N5Y4	2.31	1.05	2.07
nucleic-acid-binding protein, YlxR family protein	General prediction only	YlxR	BN194_17570	K0NAZ6	0.44	1.05	2.07
pyruvate, phosphate dikinase	Central glycolytic/intermediary pathways	PpdK	BN194_24730	K0NAC6	4.28	1.04	2.06

(2f) Protein FC<2 Tween 80 Vs citrate P2

Protein name	Functional Class	Gene/protein symbol	Gene Locus	Protein IDs	-Log t-test p-value	t t-test Difference	Fold change
HD superfamily phosphohydrolase	General prediction only	YwfO	BN194_26840	K0MXZ5	0.46	0.99	1.99
aminopeptidase N	Amino acid-related metabolism	PepN	BN194_05410	K0N2F5	2.06	0.98	1.97
elongation factor G	Protein translation (elongation)	Fus	BN194_26270	K0NCN8	1.65	0.98	1.97
50S ribosomal protein L11	Ribosomal proteins	RplK	BN194_24160	K0N724	2.97	0.96	1.95
fructose-bisphosphate aldolase	Central glycolytic/intermediary pathways	Fba2	BN194_05060	K0N2C9	3.41	0.93	1.91
maltose phosphorylase	Carbohydrate-related metabolism	YvdK	BN194_11160	K0N3S7	3.02	0.93	1.91
glucosamine-6-phosphate deaminase	Carbohydrate-related metabolism	NagB	BN194_30440	K0MYW0	3.33	0.93	1.91
50S ribosomal protein L3	Ribosomal proteins	RplC	BN194_26220	K0NCN1	2.56	0.88	1.84
30S ribosomal protein S20	Ribosomal proteins	RpsT	BN194_15250	K0N4X9	0.83	0.88	1.84
50S ribosomal protein L31	Ribosomal proteins	RpmE	BN194_26770	K0NCV4	1.53	0.87	1.83
Pur operon repressor	Transcriptional regulation	PurR2	BN194_26960	K0N7M9	0.68	0.84	1.79
50S ribosomal protein L22	Ribosomal proteins	RplV	BN194_26170	K0NCM1	1.87	0.82	1.77
nucleoside diphosphate kinase	Nucleic acid/nucleotide metabolism	Ndk	BN194_08160	K0N340	0.56	0.82	1.76
maltogenic amylase	Carbohydrate-related metabolism	BbmA	BN194_11150	K0N3T4	1.98	0.82	1.76
50S ribosomal protein L29	Ribosomal proteins	RpmC	BN194_26140	K0MXT6	2.66	0.81	1.76
50S ribosomal protein L6	Ribosomal proteins	RplF	BN194_26070	K0NCK5	1.31	0.81	1.76
xanthine phosphoribosyltransferase	Nucleic acid/nucleotide metabolism	Xpt	BN194_12490	K0MUR6	0.25	0.80	1.74
6-phosphofructokinase	Central glycolytic/intermediary pathways	Pfk	BN194_15570	K0NAK6	3.12	0.79	1.73
50S ribosomal protein L1	Ribosomal proteins	RplA	BN194_24150	K0N7M7	3.62	0.78	1.72
30S ribosomal protein S19	Ribosomal proteins	RpsS	BN194_26180	K0NAM1	1.49	0.76	1.70
aspartate racemase	Amino acid-related metabolism		BN194_02170	K0N7H2	0.71	0.76	1.70
glycine--tRNA ligase subunit beta	tRNA aminoacyl synthesis	GlyS	BN194_16950	K0N5D3	2.27	0.76	1.70
50S ribosomal protein L4	Ribosomal proteins	RplD	BN194_26210	K0N7H0	3.08	0.74	1.67

phosphocarrier protein HPr	Phosphotransferase systems	PtsH	BN194_19430	K0N9I2	0.41	0.73	1.66
aluminum resistance protein, AAT_I superfamily	Cell defense/detoxification	YnbB	BN194_18380	K0N9B7	1.58	0.72	1.65
30S ribosomal protein S4	Ribosomal proteins	RpsD	BN194_14440	K0MV63	1.61	0.72	1.64
50S ribosomal protein L14	Ribosomal proteins	RplN	BN194_26120	K0NCL3	1.72	0.70	1.63
50S ribosomal protein L5	Ribosomal proteins	RplE	BN194_26100	K0N859	2.48	0.69	1.62
30S ribosomal protein S9	Ribosomal proteins	RpsI	BN194_25840	K0MXR0	1.65	0.69	1.61
elongation factor Tu	Protein translation (elongation)	Tuf	BN194_15310	K0N4R1	1.88	0.68	1.60
DNA-directed RNA polymerase subunit delta	RNA polymerase	RpoE	BN194_26810	K0N7L4	2.97	0.66	1.58
pyruvate kinase	Central glycolytic/intermediary pathways	Pyk	BN194_15580	K0N8B6	2.87	0.65	1.57
50S ribosomal protein L2	Ribosomal proteins	RplB	BN194_26190	K0MXU1	3.54	0.65	1.56
50S ribosomal protein L18	Ribosomal proteins	RplR	BN194_26060	K0N7F4	1.53	0.64	1.56
50S ribosomal protein L23	Ribosomal proteins	RplW	BN194_26200	K0N869	2.29	0.63	1.55
ATP synthase subunit alpha	Membrane bioenergetics	AtpA	BN194_13600	K0N4K1	2.42	0.62	1.54
uracil phosphoribosyltransferase	Nucleic acid/nucleotide metabolism	Upp	BN194_13550	K0N4J8	2.56	0.62	1.54
50S ribosomal protein L15	Ribosomal proteins	RplO	BN194_26030	K0NAK7	2.05	0.62	1.53
30S ribosomal protein S2	Ribosomal proteins	RpsB	BN194_17680	K0N936	2.97	0.60	1.52
CTP synthase	Nucleic acid/nucleotide metabolism	PyrG	BN194_26790	K0MXZ1	2.32	0.59	1.50
isoleucine--tRNA ligase	tRNA aminoacyl synthesis	IleS	BN194_14810	K0N4L9	2.59	0.59	1.50
Cold shock-like protein CspLA	Transcription-associated proteins	CspLA	BN194_12460	K0N438	0.22	0.58	1.49
dipeptidase, peptidase C69 family	Amino acid-related metabolism	PepD	BN194_13380	K0N7S0	2.83	0.57	1.48
DNA-directed RNA polymerase subunit beta	RNA polymerase	RpoB	BN194_26340	K0MXV4	2.99	0.57	1.48
30S ribosomal protein S1	Ribosomal proteins	RpsA	BN194_15720	K0NAL9	1.59	0.57	1.48
glutamine synthetase	Amino acid-related metabolism	GlnA	BN194_18340	K0MW64	3.13	0.57	1.48
oligoendopeptidase F	Amino acid-related metabolism	YjbG	BN194_02530	K0N560	2.62	0.56	1.47
galactose-6-phosphate isomerase subunit LacA	Carbohydrate-related metabolism	LacA	BN194_07500	K0N2T4	0.88	0.56	1.47
30S ribosomal protein S10	Ribosomal proteins	RpsJ	BN194_26230	K0NAM5	1.72	0.55	1.47
ATP synthase subunit beta	Membrane bioenergetics	AtpD	BN194_13620	K0NAB3	1.82	0.55	1.46

inosine-5'-monophosphate dehydrogenase	Nucleic acid/nucleotide metabolism	GuaB	BN194_02100	K0N1G3	1.77	0.54	1.46
chaperone protein ClpB	Protein folding/turnover	ClpB	BN194_15500	K0N4Z8	1.26	0.53	1.44
D-lactate dehydrogenase, putative	Carbohydrate-related metabolism		BN194_01410	K0N1L0	1.76	0.52	1.44
30S ribosomal protein S7	Ribosomal proteins	RpsG	BN194_26280	K0NAM9	2.40	0.52	1.43
GMP synthase	Nucleic acid/nucleotide metabolism	GuaA	BN194_21070	K0NBJ2	4.49	0.51	1.42
2-dehydropantoate 2-reductase	Cofactor-related metabolism	PanE	BN194_16370	K0NAS0	1.82	0.51	1.42
nitroreductase family protein	General prediction only		BN194_16550	K0N597	1.38	0.50	1.41
50S ribosomal protein L24	Ribosomal proteins	RpsX	BN194_26110	K0N7F9	0.83	0.49	1.41
30S ribosomal protein S8	Ribosomal proteins	RpsH	BN194_26080	K0NAL1	1.19	0.49	1.40
aspartate aminotransferase	Amino acid-related metabolism	AspC	BN194_16770	K0NAU6	2.68	0.48	1.39
D-alanyl-D-alanine carboxypeptidase dacA	Cell wall biogenesis	DacA	BN194_02140	K0MS53	2.23	0.47	1.38
DNA-directed RNA polymerase subunit alpha	RNA polymerase	RpoA	BN194_25960	K0N7E5	1.71	0.47	1.38
promiscuous ribonucleotide (NMP) phosphatase	Nucleic acid/nucleotide metabolism	YutF	BN194_08910	K0N383	1.15	0.46	1.38
Xaa-Pro aminopeptidase, APP_like family	Amino acid-related metabolism	PepQ	BN194_08740	K0MTP0	1.88	0.46	1.37
30S ribosomal protein S14 type Z	Ribosomal proteins	RpsZ	BN194_26090	K0MXS9	0.34	0.44	1.36
ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	YkpA	BN194_07220	K0N8V6	2.44	0.42	1.34
50S ribosomal protein L13	Ribosomal proteins	RplM	BN194_25850	K0N828	1.32	0.42	1.33
PTS(Glucose/Mannose family) IIA	Phosphotransferase systems	LevD/ManX	BN194_03000	K0N1P6	0.58	0.41	1.33
>tr|K0N9X8|K0N9X8_LACCA SpsK protein OS=Lactobacillus casei W56 GN=spsK PE=4 SV=1;>tr|K0N6D6|K0N6D6_LACCA SpsK_2 protein OS=Lactobacillus casei W56 GN=spsK_2 PE=4 SV=1	Cell wall biogenesis	spsK		K0N9X8;K0N6D6	1.01	0.41	1.33
Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Phosphotransferase system, enzyme I)	Phosphotransferase systems	ptsI		K0N5T2	2.25	0.41	1.33
response regulator ArlR	Signal transduction	ArlR	BN194_18650	K0N5X3	0.26	0.40	1.32
L-lactate dehydrogenase	Carbohydrate-related metabolism	Ldh	BN194_26560	K0N7J5	1.21	0.39	1.31
DEAD/DEAH box helicase	tRNA/Ribosome assembly/processing	CshA	BN194_26700	K0N8C7	0.76	0.39	1.31
glutamate--tRNA ligase	tRNA aminoacyl synthesis	GltX	BN194_24470	K0NC38	1.85	0.39	1.31
translation initiation factor IF-2	Protein translation (initiation)	InfB	BN194_17550	K0N5K7	1.22	0.38	1.30
hypothetical protein BN194_24780	Unknown/uncharacterized		BN194_24780	K0NAC8	2.25	0.35	1.28

RNA polymerase sigma factor A	RNA polymerase	RpoD/SigA	BN194_16920	K0NAV6	0.36	0.35	1.28
trigger factor Tig	Protein folding/turnover	Tig	BN194_15330	K0N884	0.97	0.35	1.28
NH(3)-dependent NAD(+) synthetase	Cofactor-related metabolism	NadE	BN194_19840	K0MWF6	1.99	0.35	1.27
butyrate kinase	Lipid-related metabolism	Buk	BN194_16410	K0N529	1.19	0.35	1.27
preprotein translocase insertion/stabilisation protein	Protein export	YajC	BN194_08390	K0MTL6	0.27	0.35	1.27
adenylosuccinate lyase	Nucleic acid/nucleotide metabolism	PurB	BN194_12520	K0NA41	0.75	0.34	1.26
adenylate kinase	Nucleic acid/nucleotide metabolism	Adk	BN194_26010	K0N7F0	0.32	0.33	1.26
DNA-directed RNA polymerase subunit beta'	RNA polymerase	RpoC	BN194_26330	K0NAN3	2.68	0.33	1.26
trehalose-6-phosphate hydrolase	Carbohydrate-related metabolism	TreA	BN194_06930	K0N662	1.02	0.33	1.26
neutral endopeptidase	Amino acid-related metabolism	PepO2	BN194_16630	K0N8Q0	1.02	0.32	1.25
30S ribosomal protein S6	Ribosomal proteins	RspF	BN194_00100	K0N0Z1	0.58	0.32	1.25
ribonuclease J1	RNA degradation	RnjA	BN194_15020	K0NAH6	1.27	0.32	1.25
30S ribosomal protein S5	Ribosomal proteins	RpsE	BN194_26050	K0N853	0.92	0.31	1.24
elongation factor Ts	Protein translation (elongation)	Tsf	BN194_17670	K0NB01	0.47	0.31	1.24
cysteinyl aminopeptidase, peptidase C1 family	Amino acid-related metabolism	PepC	BN194_24670	K0NC50	0.18	0.31	1.24
DNA-binding regulatory protein, YebC/PmpR family	Transcriptional regulation		BN194_11600	K0N3Z3	0.26	0.31	1.24
peptidase S9 superfamily protein	Amino acid-related metabolism	YuxL	BN194_19910	K0N5X4	0.62	0.30	1.23
DNA gyrase subunit A	DNA replication-related	GyrB	BN194_00070	K0N6S7	1.17	0.29	1.22
HTH_XRE family transcriptional regulator	Transcriptional regulation		BN194_21960	K0N6F6	0.25	0.28	1.22
DEAD/DEAH box helicase	tRNA/Ribosome assembly/processing	CshB	BN194_08460	K0N356	0.14	0.27	1.21
Proline--tRNA ligase	tRNA aminoacyl synthesis	ProS	BN194_17610	K0N5E2	0.96	0.26	1.20
oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	OppD	BN194_17920	K0NB35	0.73	0.26	1.20
pyruvate carboxylase	Tricarboxylic acid pathway	Pyc	BN194_15170	K0NAI2	0.59	0.26	1.19
glucokinase	Central glycolytic/intermediary pathways	GlcK	BN194_18420	K0NB57	1.88	0.25	1.19
translation initiation factor IF-3	Protein translation (initiation)	InfC	BN194_18820	K0NB73	1.03	0.25	1.19
UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2	Cell wall biogenesis	MurA2	BN194_26780	K0NAR9	1.29	0.25	1.19
UPF0154 superfamily protein	Unknown/uncharacterized	YneF	BN194_17740	K0MVY5	0.60	0.25	1.19

phosphoglucosamine mutase	Cell wall biogenesis	GlmM	BN194_11550	K0N3Y7	0.44	0.24	1.18
galactokinase	Carbohydrate-related metabolism	GalK	BN194_07340	K0MTA3	0.35	0.23	1.17
oligoendopeptidase F	Amino acid-related metabolism	PepF	BN194_11580	K0N779	0.90	0.23	1.17
mannitol-1-phosphate 5-dehydrogenase	Carbohydrate-related metabolism	MtlD3	BN194_30400	K0N9C8	1.01	0.23	1.17
DNA helicase IV	DNA repair/recombination	PcrA	BN194_21130	K0N9W3	0.51	0.22	1.17
deoxyuridine 5'-triphosphate nucleotidohydrolase	Nucleic acid/nucleotide metabolism	Dut	BN194_24640	K0MXG3	0.52	0.22	1.17
glucose-6-phosphate 1-dehydrogenase	Central glycolytic/intermediary pathways	Zwf	BN194_08420	K0N966	0.52	0.22	1.17
ribonuclease R	tRNA/Ribosome assembly/processing	Rnr	BN194_11100	K0N3S4	0.98	0.22	1.16
tagatose 1,6-diphosphate aldolase 2	Carbohydrate-related metabolism	LacD2	BN194_07480	K0N6A8	1.10	0.21	1.16
50S ribosomal protein L10	Ribosomal proteins	RplJ	BN194_24090	K0MXD8	1.56	0.21	1.15
serine--tRNA ligase	tRNA aminoacyl synthesis	SerS	BN194_20080	K0N9N4	0.39	0.20	1.15
hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	MvaS	BN194_19680	K0N9K3	0.48	0.19	1.14
mannose-6-phosphate isomerase	Carbohydrate-related metabolism	Pmi/ManA	BN194_02920	K0N7U2	0.94	0.18	1.14
maltose/maltodextrin ABC-type transporter, ATP-binding protein	ABC-type transporter systems	MsmK	BN194_11180	K0N747	0.54	0.18	1.13
tagatose 1,6-diphosphate aldolase 2	Carbohydrate-related metabolism	LacD2	BN194_27060	K0N7P0	1.02	0.17	1.13
hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	0.39	0.16	1.12
copper homeostasis protein	Cell defense/detoxification	CutC	BN194_09910	K0N3H0	0.45	0.16	1.11
aminopeptidase C	Amino acid-related metabolism	PepC2	BN194_24680	K0NAC2	0.52	0.15	1.11
dTDP-glucose 4,6-dehydratase	Cell wall biogenesis	RmlB2	BN194_21770	K0NBN4	0.48	0.14	1.10
class I heat-shock protein (chaperonin) large subunit	Protein folding/turnover	GroEL	BN194_23750	K0N7K7	0.14	0.14	1.10
N-acetylated sugar-phosphate isomerase	Carbohydrate-related metabolism	AgaS	BN194_02940	K0MSD9	0.38	0.13	1.10
phosphopentomutase	Nucleic acid/nucleotide metabolism	DeoB	BN194_02800	K0N1N0	0.21	0.11	1.08
chaperone protein DnaK	Protein folding/turnover	DnaK	BN194_17460	K0N5C7	0.33	0.11	1.08
	Central glycolytic/intermediary pathways			K0N3R3	0.28	0.11	1.08
N-acetylglucosamine-6-phosphate deacetylase	Carbohydrate-related metabolism	NagA	BN194_19890	K0MWF9	0.22	0.09	1.06
peptidoglycan-binding lysin	General prediction only	BacA	BN194_00330	K0N4B3	0.26	0.08	1.06
phosphoglycerate kinase	Central glycolytic/intermediary pathways	Pgk	BN194_11020	K0N9R1	0.31	0.08	1.06

oligopeptide-binding protein OppA	ABC-type transporter systems	OppA	BN194_17880	K0N983	0.05	0.07	1.05
spermidine/putrescine import ATP-binding protein PotA	ABC-type transporter systems	PotA	BN194_11290	K0MU90	0.09	0.07	1.05
enolase	Central glycolytic/intermediary pathways	Eno	BN194_11040	K0MU67	0.46	0.06	1.05
hydroquinone dioxygenase-like GLO_EDI_BRP_like superfamily protein	General prediction only	MqhA	BN194_18760	K0N5N7	0.10	0.06	1.04
Galactose-6-phosphate isomerase subunit lacB	Carbohydrate-related metabolism	LacB	BN194_07490	K0MTB7	0.04	0.04	1.03
UDP-glucose 4-epimerase	Cell wall biogenesis	GalE2	BN194_21400	K0N6R1	0.10	0.04	1.03
uridylate kinase	Nucleic acid/nucleotide metabolism	PyrH	BN194_17660	K0N5E6	0.04	0.04	1.03
ribose ABC-type transport system, substrate=binding protein	ABC-type transporter systems	RsbB	BN194_03290	K0MSF6	0.05	0.02	1.02
asparagine--tRNA ligase	tRNA aminoacyl synthesis	AsnS	BN194_16760	K0N569	0.04	0.02	1.02
threonine--tRNA ligase	tRNA aminoacyl synthesis	ThrS	BN194_18860	K0N5P5	0.04	0.01	1.01
Protein translocase subunit SecA	Protein export	SecA	BN194_10170	K0N9J2	0.02	0.01	1.01
ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	ClpC	BN194_21680	K0N9Z7	0.01	0.01	1.00
bifunctional phosphatase/peptidyl-prolyl cis-trans isomerase	Protein folding/turnover	PpiB	BN194_08960	K0N387	0.00	0.00	1.00
lysine--tRNA ligase	tRNA aminoacyl synthesis	LysS	BN194_26380	K0NAN7	0.00	0.00	1.00
asparagine synthetase [glutamine-hydrolyzing] 1	Amino acid-related metabolism	AsnB	BN194_22990	K0MX90	0.01	0.00	1.00
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	3.94	-7.25	-152.29
(3R)-hydroxymyristoyl-ACP dehydratase	Lipid-related metabolism	FabZ	BN194_22520	K0NBS8	4.11	-7.06	-133.61
3-oxoacyl-ACP synthase I/II	Lipid-related metabolism	FabF	BN194_22540	K0MX40	3.89	-6.51	-90.83
malonyl CoA-acyl carrier protein transacylase	Lipid-related metabolism	FabD	BN194_22570	K0NBT1	4.13	-5.75	-53.93
enoyl-[acyl-carrier protein] reductase II	Lipid-related metabolism	FabK	BN194_22580	K0NA38	4.04	-5.38	-41.58
(3R)-hydroxymyristoyl-ACP dehydratase	Lipid-related metabolism	FabZ	BN194_22620	K0NBT3	4.91	-5.30	-39.47
acyl carrier protein	Lipid-related metabolism	AcpP2	BN194_22590	K0MX45	4.03	-5.23	-37.64
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)	Lipid-related metabolism	accC		K0N6M5	5.08	-4.73	-26.50
3-oxoacyl-[acyl-carrier-protein] reductase 4	Lipid-related metabolism	Bkr4	BN194_22550	K0N799	2.54	-4.30	-19.71
3-oxoacyl-ACP reductase	Lipid-related metabolism	FabG	BN194_22560	K0N6N3	2.27	-3.55	-11.67
oxaloacetate decarboxylase, alpha subunit	Tricarboxylic acid pathway	OadA	BN194_20290	K0MWI8	5.08	-3.46	-11.04
	Uncharacterized protein		BN194_22500	K0N788	2.40	-3.45	-10.96
NADPH-dependent FMN reductase with a PAS domain	General prediction only		BN194_06540	K0MT25	4.56	-3.45	-10.92

acetyl-CoA carboxylase biotin carboxyl carrier protein	Lipid-related metabolism	AccB	BN194_22530	K0NA35	3.04	-3.29	-9.79
phosphate transport system regulatory protein phoU	Transcriptional regulation	PhoU	BN194_10290	K0MTZ9	2.79	-3.01	-8.08
3-oxoacyl-ACP synthase III	Lipid-related metabolism	FabH	BN194_22600	K0N7B0	2.08	-2.97	-7.81
acetate kinase	Carbohydrate-related metabolism	AckA	BN194_01620	K0N7B1	2.17	-2.75	-6.75
glycogen/starch synthase	Carbohydrate-related metabolism	GlgA	BN194_21580	K0N9Z2	4.22	-2.67	-6.38
DUF322 superfamily protein	Unknown/uncharacterized	YqhY	BN194_18230	K0N9A7	1.28	-2.63	-6.19
purine nucleoside phosphoramidase, putative	tRNA aminoacyl synthesis	HinT2	BN194_19040	K0MWA8	2.94	-2.59	-6.02
citrate lyase acyl carrier protein	Tricarboxylic acid pathway	CitD	BN194_20330	K0N9Q5	3.06	-2.47	-5.56
transcriptional repression of sugar metabolism, DeoR family	Transcriptional regulation	SrlR	BN194_28690	K0MYG3	0.52	-2.33	-5.02
citrate lyase alpha subunit	Tricarboxylic acid pathway	CitF	BN194_20310	K0N607	5.17	-2.32	-4.99
hypothetical protein BN194_29450	Unknown/uncharacterized		BN194_29450	K0N932	1.16	-2.15	-4.43
DL-methionine uptake ABC transporter, substrate binding protein	ABC-type transporter systems	MetN	BN194_13740	K0MV23	3.33	-2.13	-4.38
acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase	Carbohydrate-related metabolism	AdhE	BN194_08400	K0N307	4.60	-2.09	-4.26
LysR family transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	3.48	-2.08	-4.24
ADP-glucose pyrophosphorylase	Carbohydrate-related metabolism	GlgC	BN194_21600	K0N6T3	4.00	-2.05	-4.15
hydrolase, HAD superfamily	General prediction only	YidA	BN194_28520	K0NDD5	4.44	-2.04	-4.12
3-hydroxyisobutyrate dehydrogenase family protein	General prediction only		BN194_02520	K0N7M3	1.11	-2.01	-4.03
citrate lyase beta subunit	Tricarboxylic acid pathway	CitE	BN194_20320	K0NBF4	3.06	-1.99	-3.97
coenzyme A disulfide reductase	Cell defense/detoxification		BN194_02850	K0N1N9	3.11	-1.97	-3.91
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	Central glycolytic/intermediary pathways	PdhC	BN194_15100	K0N4W5	4.59	-1.93	-3.82
Pyruvate dehydrogenase E1 component subunit alpha	Central glycolytic/intermediary pathways	PdhA	BN194_15080	K0N860	3.26	-1.90	-3.73
hypothetical protein BN194_24010	Unknown/uncharacterized		BN194_24010	K0N715	4.34	-1.90	-3.72
ribonuclease III	tRNA/Ribosome assembly/processing	Rnc	BN194_17870	K0NB31	4.93	-1.86	-3.63
hypothetical protein BN194_07660	Unknown/uncharacterized		BN194_07660	K0N2Y6	1.50	-1.83	-3.56
dihydrolipoyl dehydrogenase	Central glycolytic/intermediary pathways	PdhD	BN194_15110	K0N4P1	2.58	-1.80	-3.49
thiamine biosyn. ATP pyrophosphatase/tRNA sulfurtransferase	Cofactor-related metabolism	ThiI	BN194_14480	K0N7Z7	0.54	-1.79	-3.45
Nad(P)H-dependent nitroreductase family protein	General prediction only		BN194_16210	K0N508	3.74	-1.77	-3.42

methionine--tRNA ligase	tRNA aminoacyl synthesis	MetS	BN194_27130	K0NAU5	3.52	-1.74	-3.35
YbjQ_1 superfamily protein	Unknown/uncharacterized		BN194_07140	K0MT82	0.98	-1.70	-3.25
aldose 1-epimerase	Central glycolytic/intermediary pathways	Ald 1 epim	BN194_16020	K0NAP4	4.51	-1.65	-3.14
glucose-1-phosphate adenylyltransferase	Carbohydrate-related metabolism	GlgD	BN194_21590	K0MWU4	2.89	-1.62	-3.08
pyruvate dehydrogenase E1 component subunit beta	Central glycolytic/intermediary pathways	PdhB	BN194_15090	K0MVA7	4.92	-1.61	-3.06
UDP-N-acetylmuramoylalanine--D-glutamate ligase	Cell wall biogenesis	MurD	BN194_14720	K0NAG5	0.69	-1.61	-3.05
ATP-dependent chaperone/Clp protease	Protein folding/turnover	ClpB	BN194_19460	K0N5T8	2.65	-1.60	-3.03
DegV superfamily protein	Unknown/uncharacterized		BN194_14170	K0NAD8	2.07	-1.56	-2.95
N-acetylglucosamine-6-phosphate deacetylase	Carbohydrate-related metabolism	ManD	BN194_02950	K0N1P4	2.51	-1.56	-2.95
hypothetical protein BN194_08190	Unknown/uncharacterized		BN194_08190	K0MTK3	2.66	-1.56	-2.95
phosphatidylethanolamine-binding protein, putative	General prediction only		BN194_27230	K0NAV1	1.07	-1.55	-2.93
Proline iminopeptidase	Amino acid-related metabolism	FpaP3	BN194_21160	K0N682	1.59	-1.55	-2.92
glycogen/starch phosphorylase	Carbohydrate-related metabolism	GlgP	BN194_21570	K0NBM1	1.36	-1.54	-2.91
[citrate (pro-3S)-lyase] ligase	Posttranslational modification	CitC	BN194_20340	K0MWJ1	1.72	-1.49	-2.81
hypothetical protein BN194_23460	Unknown/uncharacterized		BN194_23460	K0N6Y5	3.39	-1.46	-2.74
Dak2 domain fusion protein	Unknown/uncharacterized		BN194_17960	K0N5I6	3.84	-1.42	-2.68
polyphosphate kinase	Membrane bioenergetics	Ppk	BN194_27270	K0ND10	1.55	-1.39	-2.61
formate acetyltransferase	Carbohydrate-related metabolism	PflB	BN194_16080	K0N8I5	3.26	-1.39	-2.61
phosphotransferase activator of gluconeogenesis	Transcriptional regulation	YqfL	BN194_17060	K0N598	2.23	-1.38	-2.60
DUF964 superfamily protein	Unknown/uncharacterized		BN194_19080	K0N9F7	1.01	-1.37	-2.59
apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	Tricarboxylic acid pathway	CitX	BN194_20300	K0N6A3	0.97	-1.37	-2.59
Valine--tRNA ligase	tRNA aminoacyl synthesis	ValS	BN194_14510	K0N4J6	3.45	-1.34	-2.54
foldase protein prsA	Protein folding/turnover	PrsA	BN194_19060	K0N5Q8	3.59	-1.32	-2.50
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	ClpE	BN194_19450	K0N644	1.88	-1.32	-2.49
fatty acid methyltransferase (cyclopropane fatty acid acyl synthase)	Lipid-related metabolism	fa methyl tranf	BN194_22460	K0N6M0	3.27	-1.30	-2.47
leucine--tRNA ligase	tRNA aminoacyl synthesis	LeuS	BN194_09210	K0N3A9	2.72	-1.29	-2.44
1,4-alpha-glucan branching enzyme	Carbohydrate-related metabolism	GlgB	BN194_21610	K0N6B8	2.98	-1.25	-2.37
aspartyl/glutamyl-tRNA amidotransferase subunit C	tRNA aminoacyl synthesis	GatC	BN194_11950	K0N436	0.52	-1.22	-2.33

penicillin acylase family protein	Cell defense/detoxification		BN194_04910	K0N2B8	2.08	-1.22	-2.33
dihydroxyacetone kinase, N-terminal domain	Central glycolytic/intermediary pathways	DhaK	BN194_04980	K0N5Q3	1.75	-1.21	-2.32
NIF3 superfamily protein	Unknown/uncharacterized		BN194_16900	K0N5C6	0.61	-1.21	-2.31
DUF3800 superfamily protein	Unknown/uncharacterized		BN194_07060	K0N2T7	1.27	-1.21	-2.31
pyruvate oxidase	Carbohydrate-related metabolism	Pox5	BN194_19670	K0NBB6	3.95	-1.20	-2.30
sex pheromone lipoprotein (similar to cAD1 in E. faecalis)	General prediction only		BN194_24320	K0NC29	1.69	-1.20	-2.29
PTS (Mannose/Fructose/Sorbose family) IIC	Phosphotransferase systems	ManY	BN194_29710	K0N8G4	0.62	-1.14	-2.20
lipoate-protein ligase LplJ	Cofactor-related metabolism	LplJ	BN194_16640	K0MVN0	3.74	-1.13	-2.19
PspC domain-containing protein	Unknown/uncharacterized		BN194_10300	K0N3H5	1.79	-1.13	-2.19
GntR family transcriptional regulator	Transcriptional regulation	YvoA	BN194_19880	K0N9L8	0.77	-1.12	-2.17
phosphate acetyltransferase	Carbohydrate-related metabolism	Pta	BN194_11340	K0MU95	3.10	-1.09	-2.13
signal recognition particle protein	Protein export	Ffh	BN194_17820	K0NB27	1.87	-1.09	-2.13
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-2,6-diaminopimelate ligase	Cell wall biogenesis	MurE	BN194_02160	K0N1S5	2.46	-1.08	-2.11
PTS (Mannose/Fructose/Sorbose family) IIAB	Phosphotransferase systems	ManX	BN194_29720	K0NDL4	2.33	-1.06	-2.09
branched-chain amino acid aminotransferase	Lipid-related metabolism	IlvE	BN194_21620	K0NBM4	2.43	-1.06	-2.08
universal stress protein, UspA superfamily	Signal transduction		BN194_13870	K0NAC5	2.86	-1.05	-2.07
DNA polymerase III subunit beta	DNA replication-related	DnaN	BN194_00020	K0N6S3	3.28	-1.04	-2.05
pyruvate formate-lyase activating enzyme	Carbohydrate-related metabolism	PflA	BN194_16090	K0MVI3	1.26	-1.02	-2.02
myo-inositol catabolism protein IolS	Carbohydrate-related metabolism	IolS	BN194_29680	K0NB94	3.17	-1.01	-2.02
DUF965 superfamily protein	Unknown/uncharacterized		BN194_08510	K0N358	1.83	-1.00	-2.00
two-component system response regulator	Signal transduction		BN194_11790	K0MUE5	1.24	-1.00	-2.00
glucosamine-1-phosphate N-acetyltransferase / UDP-N-acetylglucosamine pyrophosphorylase	Cell wall biogenesis	GlmU	BN194_26940	K0MY10	2.07	-0.99	-1.99
cell wall integrity sensing response regulator CesR	Signal transduction	CesR	BN194_02120	K0N7G4	2.83	-0.99	-1.98
alpha-acetolactate decarboxylase	Carbohydrate-related metabolism	AlsD	BN194_20140	K0MWH5	0.43	-0.97	-1.96
ribose-phosphate pyrophosphokinase 1	Nucleic acid/nucleotide metabolism	Prs2	BN194_30370	K0NDQ5	2.78	-0.97	-1.95
glycerol-3-phosphate ABC transporter substrate-binding protein	ABC-type transporter systems	UgpB	BN194_11260	K0N3T6	4.07	-0.93	-1.91
signal recognition particle receptor	Protein export	FtsY	BN194_17850	K0N5R8	0.27	-0.92	-1.89

2,5-diketo-D-gluconic acid reductase B	Cell defense/detoxification	DkgB	BN194_08260	K0N347	3.91	-0.89	-1.86
glycerol-3-phosphate dehydrogenase	Lipid-related metabolism	GpsA	BN194_10350	K0N3I2	3.10	-0.87	-1.83
YcaC related amidohydrolase family protein	General prediction only		BN194_29650	K0N948	2.24	-0.87	-1.83
S-adenosylmethionine--tRNA ribosyltransferase-isomerase	tRNA/Ribosome assembly/processing	QueA	BN194_08370	K0N965	0.38	-0.86	-1.82
hypothetical protein BN194_17400	Unknown/uncharacterized		BN194_17400	K0N5I7	1.39	-0.86	-1.82
hypothetical protein BN194_25890	Unknown/uncharacterized		BN194_25890	K0MXR4	0.48	-0.86	-1.81
peptide chain release factor 3	Protein translation (peptide release)	PrfC	BN194_19480	K0N9I7	0.98	-0.85	-1.80
ribonucleoside-diphosphate reductase subunit alpha 2	Nucleic acid/nucleotide metabolism	NrdE2	BN194_16600	K0N5A1	2.68	-0.84	-1.79
alanine--tRNA ligase	tRNA aminoacyl synthesis	AlaS	BN194_08480	K0N6K2	2.71	-0.83	-1.78
chromosome partitioning regulatory protein	Cytokinesis	ParB	BN194_02050	K0N1F9	1.46	-0.83	-1.78
Clp endopeptidase ATP-binding subunit	Protein folding/turnover	ClpB2	BN194_26350	K0N887	4.36	-0.83	-1.77
formate--tetrahydrofolate ligase	Cofactor-related metabolism	Fhs	BN194_16520	K0NAT0	2.70	-0.82	-1.76
Cys-based peroxiredoxin, OsmC superfamily	Cell defense/detoxification		BN194_07010	K0N2T5	0.85	-0.81	-1.76
deoxyribose-phosphate aldolase	Nucleic acid/nucleotide metabolism	DeoC	BN194_00080	K0N486	1.30	-0.81	-1.75
dihydroorotate dehydrogenase A	Nucleic acid/nucleotide metabolism	PyrDA	BN194_19150	K0N623	0.44	-0.80	-1.75
hydrolase, HAD_like superfamily	General prediction only		BN194_11320	K0N9U2	0.88	-0.80	-1.74
short chain dehydrogenase/reductase family protein	General prediction only	YqjQ	BN194_15480	K0N8A1	0.87	-0.80	-1.74
3-hydroxyisobutyrate dehydrogenase family protein	General prediction only		BN194_30100	K0N992	1.46	-0.80	-1.74
PTS(Glucose/Mannose family) IIB	Phosphotransferase systems	LevE/ManX	BN194_02970	K0N7U7	1.53	-0.79	-1.73
ribose-5-phosphate isomerase A	Central glycolytic/intermediary pathways	RpiA2	BN194_28600	K0N8W9	2.75	-0.79	-1.73
glucosamine--fructose-6-phosphate aminotransferase	Cell wall biogenesis	GlmS	BN194_11560	K0N3V9	2.62	-0.79	-1.73
cysteinyl-tRNA synthetase	tRNA aminoacyl synthesis	CysS	BN194_24430	K0NAB2	0.86	-0.79	-1.73
aldo_keto_reductase superfamily protein	General prediction only		BN194_27510	K0N7U8	2.28	-0.75	-1.68
>tr|K0N699|K0N699_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA PE=3 SV=1;>tr|K0MWW4|K0MWW4_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA_2 PE=3 SV=1	Cell wall biogenesis	rmlA		K0N699;K0MWW4	1.64	-0.74	-1.67

23S rRNA methyltransferase, SpoU_sub_bind/SpoU_methylase superfamily	tRNA/Ribosome assembly/processing	YsgA	BN194_18610	K0N5M8	0.53	-0.73	-1.65
cell division protein FtsA	Cytokinesis	FtsA	BN194_14750	K0N4T3	0.95	-0.72	-1.64
transcription elongation protein NusA	Transcription-associated proteins	NusA	BN194_17580	K0N927	2.39	-0.70	-1.63
serine hydroxymethyltransferase	Amino acid-related metabolism	GlyA	BN194_13540	K0MV12	1.82	-0.70	-1.62
Dyp-type iron-dependent peroxidase	Cell defense/detoxification	YfeX	BN194_07170	K0N8U9	0.94	-0.69	-1.61
glutathione peroxidase	Cell defense/detoxification	Gpo	BN194_09780	K0N6T6	2.27	-0.68	-1.61
NAD(P)H-disulfide dehydrogenase, pyr_redox superfamily	Membrane bioenergetics	YumB	BN194_24330	K0NAA7	0.96	-0.68	-1.60
adenine phosphoribosyltransferase	Nucleic acid/nucleotide metabolism	Apt	BN194_17380	K0N902	0.79	-0.67	-1.59
PTS (fructose family) subunit IIABC	Phosphotransferase systems	FruA	BN194_27690	K0MY77	1.15	-0.66	-1.58
purine nucleoside phosphorylase	Nucleic acid/nucleotide metabolism	DeoD	BN194_02810	K0N1Z0	1.43	-0.66	-1.58
ribosome-recycling factor	Protein translation (peptide release)	Frr	BN194_17650	K0N5M3	2.65	-0.66	-1.58
CBS pair domain superfamily protein	Unknown/uncharacterized		BN194_26610	K0N7J7	0.87	-0.63	-1.54
acetyltransferase GNAT family protein	General prediction only		BN194_03130	K0N5D9	0.68	-0.61	-1.52
hypothetical protein BN194_11770	Unknown/uncharacterized		BN194_11770	K0N9Y6	1.93	-0.60	-1.52
ribosomal RNA small subunit methyltransferase H	tRNA/Ribosome assembly/processing	RsmH	BN194_14680	K0N814	0.60	-0.60	-1.52
arginine--tRNA ligase	tRNA aminoacyl synthesis	ArgS	BN194_19120	K0NB86	4.41	-0.59	-1.51
succinate-semialdehyde dehydrogenase [NADP(+)]	Amino acid-related metabolism	GabD	BN194_24140	K0MXE0	2.60	-0.58	-1.50
histidine--tRNA ligase	tRNA aminoacyl synthesis	HisS	BN194_17110	K0N5A0	1.88	-0.57	-1.49
glutathione amide reductase	Cofactor-related metabolism	GarB	BN194_27400	K0N8K3	2.47	-0.57	-1.48
DegV superfamily protein	Unknown/uncharacterized		BN194_16330	K0N8L5	1.50	-0.56	-1.48
DUF1292 superfamily protein	Unknown/uncharacterized		BN194_08530	K0N6K6	1.09	-0.56	-1.48
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	Cofactor-related metabolism	ThiD2	BN194_07650	K0N2U9	2.41	-0.54	-1.45
tRNA-binding protein, tRNA_domain_binding superfamily	General prediction only	YtpR	BN194_18970	K0NB80	0.89	-0.53	-1.45
rod shape-determining protein MreB	Cytokinesis	MreB	BN194_14550	K0N4R7	1.66	-0.53	-1.44
PTS (Mannose/Fructose/Sorbose family) IID	Phosphotransferase systems	ManZ	BN194_29700	K0N954	2.27	-0.52	-1.44
multifunctional methylglyoxal reductase, putative	Cell defense/detoxification		BN194_02180	K0N513	2.88	-0.52	-1.44
cysteine desulfurase IscS 1	Cofactor-related metabolism	IscS	BN194_14900	K0N4U8	1.92	-0.51	-1.43

RNA-binding protein, ASCH superfamily	General prediction only		BN194_17420	K0NAY8	1.58	-0.51	-1.42
oligo-1,6-glucosidase	Carbohydrate-related metabolism		BN194_27950	K0N8T1	2.98	-0.50	-1.42
UDP-glucose 4-epimerase	Cell wall biogenesis	GalE	BN194_07350	K0N2R3	1.57	-0.50	-1.41
XRE family transcriptional regulator	Transcriptional regulation		BN194_23510	K0N6Y7	1.13	-0.50	-1.41
cell-shape determining protein Mbl	Cytokinesis	Mbl	BN194_13650	K0N4K5	1.06	-0.49	-1.41
aspartate--tRNA ligase	tRNA aminoacyl synthesis	AspS	BN194_17100	K0N5F3	2.06	-0.49	-1.40
dihydrolipoyl dehydrogenase	Lipid-related metabolism	BFmBC	BN194_16400	K0N582	0.46	-0.49	-1.40
DUF1831 superfamily protein	Unknown/uncharacterized		BN194_14910	K0N4M6	1.25	-0.47	-1.39
dipeptidase, peptidase C69 family	Amino acid-related metabolism	PepD	BN194_23190	K0MXA1	1.33	-0.46	-1.38
oligopeptide ABC-type transporter, substrate-binding protein	ABC-type transporter systems	OppA2	BN194_20640	K0MWL6	0.70	-0.46	-1.37
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	HslU	BN194_16010	K0N4Y1	0.60	-0.45	-1.36
aspartate-semialdehyde dehydrogenase	Amino acid-related metabolism	Asd	BN194_01060	K0N1I5	0.92	-0.43	-1.35
	Uncharacterized protein		BN194_07360	K0N2W3	0.99	-0.43	-1.35
cysteine synthase	Amino acid-related metabolism	CysK	BN194_05520	K0N8E6	0.54	-0.43	-1.34
alcohol dehydrogenase, MDR superfamily	General prediction only		BN194_07740	K0MTE1	0.55	-0.43	-1.34
polar amino acid ABC-type exporter, ATP-binding protein	ABC-type transporter systems	GlnQ3	BN194_21440	K0MWS9	0.51	-0.42	-1.34
galactose 1-epimerase, aldos_epim superfamily	Central glycolytic/intermediary pathways	GalM	BN194_07390	K0MTA8	1.00	-0.41	-1.33
Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (EC 2.7.7.12) (UDP-glucose--hexose-1-phosphate uridylyltransferase)	Carbohydrate-related metabolism	galT	BN194_07370	K0N8X1	1.60	-0.41	-1.33
6-phosphogluconate dehydrogenase	Central glycolytic/intermediary pathways	Gnd	BN194_18660	K0N5N2	1.23	-0.41	-1.33
ABM/COG1359 superfamily protein YcnE/LsrG	General prediction only	YcnE	BN194_13230	K0N7R3	1.10	-0.38	-1.30
fructose-1,6-bisphosphatase class 3	Central glycolytic/intermediary pathways	Fpb	BN194_21660	K0N6C3	0.34	-0.38	-1.30
hypothetical protein BN194_01760	Unknown/uncharacterized		BN194_01760	K0N1N3	0.77	-0.38	-1.30
divergent methyl-accepting chemotaxis-like domain, DUF948 superfamily	Signal transduction	YtxG	BN194_08710	K0N365	2.30	-0.38	-1.30
amidase superfamily protein	General prediction only		BN194_24180	K0NAA2	1.71	-0.36	-1.29
50S ribosomal protein L9	Ribosomal proteins	RplI	BN194_01130	K0N4K3	1.69	-0.36	-1.28
GTP-binding protein TypA/BipA	Protein translation (elongation)	TypA/BipA	BN194_15150	K0N4W9	1.57	-0.36	-1.28

DUF1341 superfamily protein	Unknown/uncharacterized		BN194_28350	K0N8V3	0.82	-0.35	-1.27
DUF161/DUF2179 superfamily protein	Unknown/uncharacterized		BN194_15780	K0N8E8	1.03	-0.33	-1.26
tRNA-dihydrouridine synthase 1	tRNA/Ribosome assembly/processing	Dus1	BN194_26390	K0MXV9	1.23	-0.33	-1.26
catabolite control protein A	Transcriptional regulation	CcpA	BN194_08750	K0N323	0.65	-0.32	-1.25
NADH-flavin reductase, BVR-B_like_SDR_a family	General prediction only		BN194_07680	K0N6C4	0.23	-0.32	-1.25
triosephosphate isomerase	Central glycolytic/intermediary pathways	Tpi	BN194_11030	K0N736	0.47	-0.31	-1.24
xylulose-5-phosphate phosphoketolase	Central glycolytic/intermediary pathways	XpaK	BN194_01710	K0N1M9	2.76	-0.30	-1.24
maltose/maltodextrin ABC-type transporter, substrate binding protein	ABC-type transporter systems	MdxE/MalE	BN194_11200	K0N3U4	1.03	-0.30	-1.23
L-lactate dehydrogenase	Carbohydrate-related metabolism		BN194_06970	K0N8S5	0.65	-0.29	-1.22
cell division ATP-binding protein FtsE	Cytokinesis	FtsE	BN194_10190	K0MTZ2	0.70	-0.28	-1.21
NADH peroxidase	Cell defense/detoxification	Npr	BN194_04740	K0MSP8	1.20	-0.28	-1.21
tryptophan--tRNA ligase	tRNA aminoacyl synthesis	TrpS	BN194_27360	K0N7S4	0.26	-0.28	-1.21
PTS system HPr protein serine kinase	Phosphotransferase systems	HprK	BN194_10330	K0N6Y3	1.03	-0.27	-1.20
ABC-type transporter, ATP-binding component	ABC-type transporter systems		BN194_06850	K0N2J7	1.36	-0.26	-1.19
dTDP-glucose 4,6-dehydratase	Cell wall biogenesis	RmlB	BN194_21340	K0MWS0	0.75	-0.25	-1.19
deoxyribose-phosphate aldolase	Nucleic acid/nucleotide metabolism	DeoC	BN194_02790	K0MSB5	0.43	-0.25	-1.19
phosphate butyryltransferase	Lipid-related metabolism	Ptb	BN194_16420	K0NAS3	0.77	-0.24	-1.18
class I heat-shock protein (chaperonin) small subunit	Protein folding/turnover	GroES	BN194_23760	K0N700	0.23	-0.24	-1.18
ABC transporter, ATP-binding component	ABC-type transporter systems		BN194_07730	K0N6C9	0.08	-0.23	-1.17
ATP-dependent Clp protease proteolytic subunit	Protein folding/turnover	ClpP2	BN194_10510	K0N3M4	0.75	-0.23	-1.17
glutamyl-tRNA(Gln) amidotransferase subunit A	tRNA aminoacyl synthesis	GatA	BN194_11960	K0N3Z6	1.27	-0.22	-1.17
dipeptidase B	Amino acid-related metabolism	PepDB	BN194_21110	K0N678	0.09	-0.22	-1.16
ribosome-associated sigma 54 modulation protein	tRNA/Ribosome assembly/processing	Hpf	BN194_10150	K0N3F2	0.69	-0.21	-1.15
NADH-dependent butanol dehydrogenase A	Carbohydrate-related metabolism	BdhA	BN194_22640	K0MX50	0.56	-0.20	-1.15
replicative DNA helicase	DNA replication-related	DnaC	BN194_01140	K0MRW2	1.48	-0.20	-1.15
D-alanine-poly(phosphoribitol) ligase	Cell wall biogenesis	DltA	BN194_08590	K0MTN0	0.27	-0.20	-1.15
DUF711 (RNR_PFL-like) superfamily protein	Unknown/uncharacterized		BN194_09830	K0N6U0	0.59	-0.20	-1.14

phenylalanine--tRNA ligase subunit beta	tRNA aminoacyl synthesis	PheS	BN194_18560	K0N5M4	1.29	-0.20	-1.14
aspartyl/glutamyl-tRNA amidotransferase subunit B	tRNA aminoacyl synthesis	GatB	BN194_11970	K0NA01	0.65	-0.20	-1.14
ribose-phosphate pyrophosphokinase 1	Nucleic acid/nucleotide metabolism	Prs1	BN194_26930	K0NAT2	0.60	-0.19	-1.14
redox (NADH)-sensing transcriptional repressor	Transcriptional regulation	Rex	BN194_23820	K0NBZ5	0.58	-0.19	-1.14
adenylosuccinate synthetase	Nucleic acid/nucleotide metabolism	PurA	BN194_01160	K0N1J0	0.35	-0.19	-1.14
beta-Ala-Xaa dipeptidase	Amino acid-related metabolism	PepV	BN194_08800	K0N324	0.68	-0.19	-1.14
lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex	Lipid-related metabolism	BfmBB	BN194_16380	K0N8M3	0.27	-0.19	-1.14
dTDP-4-dehydrorhamnose 3,5-epimerase	Cell wall biogenesis		BN194_21780	K0N6Q5	0.22	-0.18	-1.14
lactaldehyde dehydrogenase/glycolaldehyde dehydrogenase	Cell defense/detoxification		BN194_25470	K0NCB9	0.38	-0.18	-1.13
thioredoxin reductase	Posttranslational modification	TrxB	BN194_10360	K0N3L1	0.33	-0.16	-1.11
manganese-dependent inorganic pyrophosphatase	Membrane bioenergetics	PpaC	BN194_16110	K0N4Z4	0.31	-0.15	-1.11
ssDNA-binding protein	DNA replication-related	Ssb	BN194_00110	K0N1C2	0.19	-0.14	-1.11
DNA-binding protein HU	DNA replication-related	Hup/Hbs	BN194_15740	K0MVF4	0.39	-0.13	-1.10
	Central glycolytic/intermediary pathways			K0N7I6;K0N4A6	0.30	-0.12	-1.09
D-alanine--D-alanine ligase	Cell wall biogenesis	Ddl	BN194_01390	K0MRY4	0.42	-0.12	-1.09
phosphoglucomutase	Central glycolytic/intermediary pathways	PgcA	BN194_10370	K0N9K8	0.54	-0.11	-1.08
peptide chain release factor 1	Protein translation (peptide release)	PrfA	BN194_13510	K0N4C6	0.31	-0.11	-1.08
lipid peroxide thiol-specific peroxidase	Cell defense/detoxification	Tpx	BN194_08090	K0MTJ5	0.31	-0.11	-1.08
translation initiation factor IF-1	Protein translation (initiation)	InfA	BN194_26000	K0N847	0.35	-0.10	-1.07
quinone-oxidoreductase	Membrane bioenergetics	YogA	BN194_18780	K0N9E0	0.78	-0.10	-1.07
ATP-dependent zinc metalloprotease FtsH	Protein folding/turnover	FtsH	BN194_26460	K0N7I8	0.94	-0.09	-1.07
polar amino acid ABC-type importer, ATP-binding protein	ABC-type transporter systems	GlnQ4	BN194_29900	K0N971	0.41	-0.09	-1.06
PTS system beta-glucoside-specific transporter subunit IIBCA	Phosphotransferase systems	BglP	BN194_06940	K0MT60	0.32	-0.09	-1.06
acetyltransferase (GNAT) family protein	General prediction only		BN194_08200	K0N2Z8	0.35	-0.09	-1.06
6-phosphogluconolactonase	Carbohydrate-related metabolism	YwcC	BN194_09930	K0N6V0	0.35	-0.08	-1.06
PTS (Fructose/Mannitol family) subunit IIA	Phosphotransferase systems	MtlA	BN194_30410	K0N8N0	0.33	-0.08	-1.06
oligoendopeptidase F	Amino acid-related metabolism	YjbG2	BN194_08130	K0N6H7	0.28	-0.08	-1.06

galactose mutarotase	Carbohydrate-related metabolism	LacX	BN194_27070	K0NCY0	0.21	-0.08	-1.05
ribonucleoside-diphosphate reductase subunit beta	Nucleic acid/nucleotide metabolism	NrdF	BN194_16610	K0N552	0.19	-0.07	-1.05
PTS(Glucose/Mannose family) IID	Phosphotransferase systems	LevG/ManZ	BN194_02990	K0MSE1	0.09	-0.07	-1.05
DNA polymerase I	DNA repair/recombination	PolA	BN194_18930	K0N9E7	0.06	-0.05	-1.04
50S ribosomal protein L7/L12	Ribosomal proteins	RplL	BN194_24080	K0NA98	0.09	-0.05	-1.04
phosphonate ABC transporter substrate-binding protein	ABC-type transporter systems	PhnD	BN194_25680	K0NAI1	0.12	-0.05	-1.04
glycine cleavage system H protein	Amino acid-related metabolism	GcvH	BN194_13700	K0N4K8	0.17	-0.05	-1.03
2-oxoisovalerate dehydrogenase subunit beta	Lipid-related metabolism	BfmBA	BN194_16390	K0MVK8	0.13	-0.05	-1.03
sugar/glycerol-3-phosphate uptake ABC-type importer, substrate-binding protein	ABC-type transporter systems		BN194_29810	K0N8H4	0.18	-0.05	-1.03
bifunctional oligoribonuclease and PAP phosphatase nrnA	RNA degradation	NrnA	BN194_08450	K0N309	0.27	-0.03	-1.02
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	Central glycolytic/intermediary pathways	GpmA2	BN194_22740	K0MX58	0.03	-0.02	-1.01
30S ribosomal protein S16	Ribosomal proteins	RpsP	BN194_17810	K0N5H1	0.01	-0.01	-1.01
6-phospho-beta-galactosidase	Carbohydrate-related metabolism	LacG	BN194_07320	K0N8W7	0.01	-0.01	-1.01
L-2-hydroxyisocaproate dehydrogenase	Carbohydrate-related metabolism		BN194_27170	K0NCZ6	0.07	-0.01	-1.01

Annexure 03: Master table CFE containing –log p values, t test difference and fold change of all conditions of Experiment P1

Protein names	**Functional Class**	**Gene**	**Protein IDs**	**Tween 80 Vs control**			**Citrate Vs control**			**Tween 80 citrate Vs control**			**Tween 80 dosed Vs control**			**Tween 80 Vs citrate**		
				-Log t test p	t-test Difference	Fold change	-Log t test p	t-test Difference	Fold change	-Log t test p	t-test Difference	Fold change	-Log t test p	t-test Difference	Fold change	-Log t test p	t-test Difference	Fold change

				value			value			value			value			value		
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	Cell wall biogenesis	glmS	K0N3V9	1.27	0.68	1.60	3.50	1.96	3.90	5.25	2.87	7.34	1.59	-4.93	0.03	1.93	-1.28	0.41
Bifunctional protein GlmU	Cell wall biogenesis	glmU	K0MY10	1.03	-0.51	0.70	0.74	-0.51	0.70	0.77	-0.49	0.71	3.95	-4.68	0.04	0.00	0.00	1.00
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	murE	K0N1S5	1.26	-0.25	0.84	0.73	0.15	1.11	0.65	0.20	1.15	4.18	-3.28	0.10	2.90	-0.41	0.75
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	ddl	K0MRY4	0.73	0.55	1.46	0.29	0.24	1.18	0.31	-0.35	0.79	1.33	-2.89	0.14	0.48	0.30	1.23
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		K0N6R1	0.44	0.20	1.15	1.38	0.48	1.39	1.42	0.56	1.47	1.77	-2.75	0.15	0.97	-0.28	0.83
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	glmM	K0N3Y7	0.09	-0.02	0.99	0.48	0.09	1.07	0.01	0.00	1.00	4.16	-2.71	0.15	0.71	-0.11	0.93
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	murC	K0N600	0.66	0.25	1.19	0.27	-0.09	0.94	0.39	-0.20	0.87	3.80	-2.27	0.21	1.37	0.34	1.27
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	murF	K0NCU5	0.29	0.16	1.12	0.52	-0.27	0.83	0.94	-0.44	0.74	0.50	-1.92	0.26	1.01	0.44	1.36
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	murI	K0MTN4	0.18	-0.06	0.96	0.83	0.32	1.25	0.02	-0.01	0.99	2.15	-1.90	0.27	1.26	-0.38	0.77
Glycosyl transferase family protein	Cell wall biogenesis		K0N7L2	0.01	0.01	1.01	0.24	0.23	1.17	0.92	0.78	1.71	1.01	-1.38	0.38	0.23	-0.22	0.86
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	cap4C	K0N7E3	2.31	-0.59	0.66	2.26	-0.55	0.68	1.78	-0.43	0.74	3.14	-1.13	0.46	0.19	-0.04	0.97
Penicillin-binding protein 1A	Cell wall biogenesis	ponA	K0NAU3	0.40	-0.31	0.81	0.39	-0.31	0.81	0.25	0.24	1.18	0.21	-1.12	0.46	0.01	0.00	1.00
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-	Cell wall biogenesis	murA2,murA	K0NAR9	0.57	-0.80	0.57	0.24	-0.13	0.92	0.38	-0.15	0.90	1.70	-1.10	0.47	0.46	-0.67	0.63

acetylglucosamine enolpyruvyl transferase)																		
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	rmlB	K0MWS0	1.28	0.41	1.32	0.29	-0.15	0.90	0.32	-0.24	0.85	0.96	-0.51	0.70	1.57	0.56	1.47
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	murD	K0NAG5	0.14	-0.05	0.96	0.78	-0.24	0.85	0.24	-0.08	0.95	0.06	-0.04	0.97	0.44	0.18	1.14
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	dltA	K0MTN0	1.37	0.53	1.44	0.74	-0.26	0.84	0.01	-0.01	1.00	0.09	0.06	1.04	2.78	0.78	1.72
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	dacA	K0MS53	0.62	-0.21	0.86	0.35	-0.09	0.94	2.13	0.49	1.41	0.91	0.18	1.13	0.30	-0.12	0.92
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	galE	K0N2R3	0.63	0.20	1.15	4.06	1.76	3.38	3.68	1.89	3.71	0.36	0.19	1.14	3.97	-1.56	0.34
Putative secreted protein	cell wall biogenesis		K0N7S8	0.17	-0.20	0.87	0.13	-0.16	0.90	1.23	1.64	3.12	0.81	0.93	1.91	0.10	-0.04	0.97
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	BN194_21350	K0N6Q5	2.95	0.45	1.36	0.22	-0.06	0.96	1.33	0.18	1.13	2.61	1.10	2.15	1.96	0.51	1.42
>tr|K0N699|K0N699_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA PE=3 SV=1;>tr|K0MWW4|K0MWW4_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA_2 PE=3 SV=1	Cell wall biogenesis	rmlA	K0N699;K0MWW4	0.01	0.00	1.00	1.17	0.40	1.32	0.64	0.30	1.23	2.10	-3.14	0.11	1.57	-0.40	0.76
>tr|K0N9X8|K0N9X8_LACCA SpsK protein OS=Lactobacillus casei W56 GN=spsK PE=4 SV=1;>tr|K0N6D6|K0N6D6_LACCA SpsK_2 protein OS=Lactobacillus casei W56 GN=spsK_2 PE=4 SV=1	Cell wall biogenesis	spsK_2	K0N9X8;K0N6D6	1.92	0.57	1.49	0.01	0.00	1.00	0.39	0.11	1.08	1.92	-3.69	0.08	2.06	0.57	1.49
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		K0NBU7	1.38	-0.20	0.87	1.13	-0.14	0.91	3.19	-0.41	0.75	3.30	-2.55	0.17	0.33	-0.06	0.96
Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	phoP	K0N9J6	0.44	-0.14	0.91	1.07	0.47	1.39	1.29	0.58	1.50	1.56	-1.57	0.34	1.34	-0.61	0.65

Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	yclJ	K0MUE5	0.11	-0.04	0.97	2.46	0.85	1.80	1.64	0.35	1.27	0.59	-1.16	0.45	2.46	-0.88	0.54
Protein ytsP	Signal transduction	ytsP	K0N4Q9	0.14	-0.21	0.86	0.19	-0.10	0.93	0.22	-0.25	0.84	0.60	-0.94	0.52	0.07	-0.12	0.92
Universal stress protein	Signal transduction		K0N7J0	0.66	0.21	1.16	1.89	0.84	1.79	1.90	0.66	1.58	2.00	-0.81	0.57	1.58	-0.64	0.64
Regulatory protein vanR	Signal transduction	vanR	K0N7G4	0.14	-0.09	0.94	1.94	0.47	1.39	0.69	0.20	1.14	2.20	-0.71	0.61	1.21	-0.56	0.68
UPF0478 protein SAOUHSC_01855	Signal transduction		K0N365	0.04	0.02	1.01	1.20	0.64	1.56	2.23	1.04	2.06	0.49	-0.40	0.76	1.10	-0.62	0.65
Transcriptional regulatory protein spaR	Signal transduction	spaR	K0N5S9	0.67	-1.56	0.34	0.49	1.04	2.06	0.26	-0.68	0.62	0.10	-0.26	0.84	2.16	-2.60	0.16
Universal stress protein	Signal transduction		K0NAC5	0.46	-0.22	0.86	0.94	0.31	1.24	0.25	0.10	1.07	0.71	-0.21	0.87	1.17	-0.53	0.69
Response regulator ArlR	Signal transduction	arlR	K0N5X3	0.53	0.31	1.24	0.03	0.02	1.01	0.43	-0.24	0.85	1.88	1.10	2.15	0.88	0.29	1.22
Transcriptional regulatory protein YycF	Signal transduction	yycF_2	K0N8E4	0.75	-0.27	0.83	3.29	-0.77	0.59	1.80	-0.70	0.61	2.50	1.42	2.67	1.48	0.50	1.41
ATP synthase epsilon chain (ATP synthase F1 sector epsilon subunit) (F-ATPase epsilon subunit)	Membrane bioenergetics	atpC	K0N7T2	0.79	-1.18	0.44	0.15	-0.27	0.83	0.14	-0.25	0.84	0.94	-1.41	0.38	1.46	-0.91	0.53
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	atpD	K0NAB3	1.56	-0.27	0.83	2.33	-0.34	0.79	2.28	-0.35	0.79	4.40	-1.28	0.41	0.32	0.07	1.05
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		K0N9E0	0.13	-0.22	0.86	1.71	1.45	2.73	1.24	0.95	1.93	0.81	-0.79	0.58	1.39	-1.67	0.31
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	atpA	K0N4K1	1.78	-0.47	0.72	2.76	-0.58	0.67	1.98	-0.55	0.68	0.50	-0.65	0.64	0.51	0.11	1.08
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	yjlD	K0NAA7	0.26	0.14	1.10	0.03	0.02	1.02	1.25	1.19	2.27	1.24	-0.63	0.65	0.18	0.11	1.08
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	atpG	K0N4D3	0.37	-0.25	0.84	0.85	-0.36	0.78	0.96	-0.43	0.74	0.21	0.07	1.05	0.12	0.11	1.08
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	atpH	K0MV16	1.38	-0.23	0.85	0.18	0.04	1.03	0.21	-0.08	0.94	1.91	0.18	1.13	1.15	-0.27	0.83
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	ppaC	K0N4Z4	0.60	0.13	1.10	2.08	-0.16	0.90	0.06	-0.02	0.99	1.53	0.30	1.23	1.36	0.29	1.22
ATP synthase subunit b (ATP synthase F(0) sector subunit b)	Membrane bioenergetics	atpF	K0N7S9	1.15	-1.01	0.50	0.01	0.01	1.01	1.25	1.23	2.35	2.23	2.18	4.52	1.23	-1.02	0.49

(ATPase subunit I) (F-type ATPase subunit b)																		
Signal recognition particle protein (Fifty-four homolog)	Protein export	ffh	K0NB27	0.63	-0.31	0.81	2.85	0.49	1.40	1.33	0.49	1.41	3.72	-3.75	0.07	1.59	-0.80	0.57
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	ftsY	K0N5R8	0.10	-0.05	0.96	0.43	-0.12	0.92	0.67	-0.25	0.84	1.51	-1.13	0.46	0.15	0.07	1.05
Protein translocase subunit SecA	Protein export	secA	K0N9J2	1.61	-0.74	0.60	2.63	-0.61	0.65	1.55	-0.38	0.77	0.97	-1.10	0.47	0.23	-0.13	0.92
UPF0092 membrane protein yrbF	Protein export	yrbF	K0MTL6	0.36	0.83	1.78	0.42	0.97	1.96	0.47	1.06	2.08	1.11	2.29	4.90	0.12	-0.14	0.91
Rod shape-determining protein MreB	Cytokinesis	mreB	K0N4R7	0.20	-0.23	0.85	0.36	0.30	1.23	0.85	0.58	1.49	2.90	-4.88	0.03	0.71	-0.53	0.69
MreB-like protein	Cytokinesis	mbl	K0N4K5	0.04	-0.01	0.99	0.29	-0.08	0.95	0.21	-0.08	0.95	2.97	-4.87	0.03	0.41	0.07	1.05
Cell division protein FtsA	Cytokinesis	ftsA	K0N4T3	1.85	-0.69	0.62	1.23	0.50	1.41	0.00	0.00	1.00	1.90	-2.37	0.19	2.93	-1.19	0.44
Stage 0 sporulation protein J	Cytokinesis	spo0J	K0N1F9	0.27	-0.07	0.95	1.42	0.42	1.34	1.94	0.72	1.65	1.66	-2.05	0.24	1.54	-0.49	0.71
Cell division ATP-binding protein FtsE	Cytokinesis	ftsE	K0MTZ2	1.46	-0.38	0.77	2.46	0.72	1.64	3.21	1.23	2.34	1.39	-1.28	0.41	3.68	-1.10	0.47
Cell division protein FtsZ	Cytokinesis	ftsZ	K0N4L6	0.05	-0.02	0.99	1.69	0.22	1.17	0.83	0.19	1.14	3.54	-0.75	0.59	0.82	-0.24	0.84
Cell division protein FtsX	Cytokinesis	ftsX	K0N3G0	0.07	-0.11	0.93	0.20	0.28	1.22	1.35	1.54	2.91	0.10	-0.24	0.85	0.94	-0.39	0.76
Sporulation initiation inhibitor protein soj	Cytokinesis	soj	K0MS45	0.46	-0.38	0.77	3.24	0.69	1.61	0.90	0.63	1.55	0.21	-0.13	0.92	1.39	-1.06	0.48
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	gpsB	K0MVN5	0.90	-0.28	0.83	0.11	0.03	1.02	0.19	0.08	1.06	4.70	1.07	2.10	0.79	-0.31	0.81
Septum site-determining protein DivIVA	Cytokinesis	divIVA	K0N4T8	0.03	-0.04	0.97	1.62	0.86	1.82	0.90	0.56	1.48	1.52	1.12	2.17	1.12	-0.91	0.53
Dumpy	Cell surface proteins/internalins	dp	K0MSV0	0.66	-0.25	0.84	2.07	-0.79	0.58	1.58	-0.94	0.52	1.37	0.87	1.82	3.31	0.54	1.46
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	glnA_2	K0MW64	0.97	0.29	1.22	2.41	-0.56	0.68	0.99	-0.31	0.81	3.02	-5.17	0.03	2.69	0.85	1.80
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	pepO_2	K0N8Q0	1.68	0.50	1.42	0.08	-0.03	0.98	1.43	0.41	1.33	2.54	-4.43	0.05	2.13	0.53	1.45
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	ssdA	K0MXE0	2.77	-0.24	0.85	4.46	2.25	4.75	3.44	2.04	4.11	2.38	-4.28	0.05	4.71	-2.49	0.18
Oligoendopeptidase F	Amino acid-related metabolism	yjbG_2	K0N6H7	0.14	-0.02	0.99	1.72	0.38	1.30	0.16	0.03	1.02	2.66	-4.17	0.06	1.97	-0.40	0.76

Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC_2	K0NAC2	0.01	0.00	1.00	0.21	-0.07	0.95	1.64	-0.48	0.72	2.16	-4.12	0.06	0.19	0.07	1.05
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	pepN	K0N2F5	2.31	0.21	1.16	2.87	-0.87	0.55	4.13	-1.13	0.46	3.91	-3.91	0.07	3.33	1.08	2.11
Oligoendopeptidase, pepF/M3 family	Amino acid-related metabolism		K0N779	0.55	0.30	1.23	2.18	1.01	2.02	0.28	0.15	1.11	1.90	-3.90	0.07	1.81	-0.72	0.61
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	pcp	K0N4Y4	2.00	-0.87	0.55	1.93	0.35	1.28	1.79	-0.33	0.80	2.43	-3.80	0.07	2.43	-1.22	0.43
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	fpaP_3	K0N682	0.26	-0.10	0.93	0.06	0.02	1.01	0.20	-0.06	0.96	2.66	-3.73	0.08	0.37	-0.12	0.92
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	pepQ	K0MTP0	0.81	0.20	1.15	0.42	-0.05	0.97	1.15	-0.19	0.88	4.40	-3.55	0.09	1.07	0.25	1.19
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	glyA	K0MV12	0.53	-0.20	0.87	3.74	1.27	2.42	3.29	1.06	2.08	3.70	-3.41	0.09	3.29	-1.47	0.36
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	yuxL	K0N5X4	0.57	0.08	1.05	2.41	0.38	1.30	2.86	0.44	1.36	3.17	-3.40	0.09	1.66	-0.31	0.81
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	pepDB	K0N678	0.78	0.26	1.20	0.06	-0.01	0.99	0.10	-0.03	0.98	3.36	-3.11	0.12	0.87	0.27	1.21
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	alsS	K0N695	2.24	-3.20	0.11	3.45	0.80	1.74	3.19	-0.65	0.64	1.54	-2.30	0.20	2.60	-4.01	0.06
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	pepV	K0N324	3.00	0.40	1.32	1.29	0.44	1.35	1.81	0.30	1.23	3.91	-2.28	0.21	0.08	-0.04	0.97
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	asnB	K0MX90	0.10	0.05	1.04	0.86	-0.32	0.80	0.89	-0.32	0.80	2.67	-2.21	0.22	1.51	0.37	1.30
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	asd	K0N1I5	0.57	0.17	1.12	2.39	0.79	1.73	1.14	0.44	1.35	2.18	-2.20	0.22	2.77	-0.62	0.65
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	pepC	K0NC50	0.17	-0.06	0.96	1.37	-0.60	0.66	1.27	-0.57	0.67	2.42	-2.12	0.23	1.08	0.54	1.45

Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	aspC	K0NAU6	0.95	-0.49	0.71	0.41	-0.11	0.93	0.34	-0.20	0.87	3.86	-2.03	0.25	0.80	-0.38	0.77
Probable dipeptidase (EC 3.4.-.-)	Amino acid-related metabolism		K0N7S0	0.78	0.18	1.13	2.52	-0.51	0.70	1.64	-0.40	0.76	0.54	-1.79	0.29	2.85	0.69	1.61
Aspartate racemase (EC 5.1.1.13)	Amino acid-related metabolism		K0N7H2	0.67	0.25	1.19	0.27	0.13	1.09	0.53	-0.20	0.87	3.20	-1.68	0.31	0.19	0.12	1.09
Probable dipeptidase (EC 3.4.-.-)	Amino acid-related metabolism		K0MXA1	0.85	2.71	6.55	0.57	1.88	3.69	1.05	3.38	10.42	0.48	-1.63	0.32	1.86	0.83	1.78
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	proC	K0N677	1.88	-0.49	0.71	1.09	0.28	1.22	0.87	0.49	1.40	2.82	-1.47	0.36	3.17	-0.77	0.59
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	pepS	K0N7D5	0.02	-0.02	0.99	1.00	0.42	1.33	0.18	0.13	1.09	0.80	-1.31	0.40	0.59	-0.43	0.74
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	patA_2	K0N7F8	0.38	0.20	1.15	0.09	0.07	1.05	0.00	0.00	1.00	0.01	-0.01	0.99	0.25	0.12	1.09
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	patB_2	K0MTW3	0.11	-0.06	0.96	1.39	0.45	1.36	0.28	0.09	1.07	1.35	0.50	1.41	1.38	-0.51	0.70
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	luxS	K0N6J0	0.26	0.45	1.37	0.03	-0.04	0.97	0.26	0.42	1.34	0.60	0.80	1.75	0.42	0.50	1.41
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	cysK	K0N8E6	0.19	0.05	1.03	4.16	1.29	2.45	2.78	0.82	1.77	3.56	1.34	2.53	3.53	-1.25	0.42
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	mtnN	K0MV90	1.82	0.53	1.44	0.62	-0.21	0.87	0.94	-0.53	0.69	1.91	1.34	2.54	3.05	0.73	1.66
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	deoD	K0N1Z0	1.11	0.38	1.30	2.37	0.81	1.75	1.62	0.77	1.71	3.48	-3.40	0.09	1.90	-0.42	0.75
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	purA	K0N1J0	0.79	0.11	1.08	2.55	-0.59	0.66	0.65	-0.17	0.89	1.46	-3.38	0.10	3.30	0.71	1.63

Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	cmk	K0N4V1	0.40	0.10	1.07	1.92	-0.40	0.76	1.22	-0.49	0.71	2.90	-2.96	0.13	1.81	0.50	1.41
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	prs1,prs	K0NAT2	0.21	-0.07	0.95	0.15	0.08	1.06	0.61	0.21	1.16	4.38	-2.81	0.14	0.36	-0.15	0.90
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	pyrG	K0MXZ1	0.24	-0.07	0.95	2.90	-0.82	0.57	1.65	-0.36	0.78	4.82	-2.35	0.20	3.17	0.75	1.68
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	apt	K0N902	0.37	-0.19	0.88	0.33	-0.13	0.91	0.60	-0.45	0.73	2.52	-1.96	0.26	0.08	-0.06	0.96
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	hpt	K0NCR2	0.10	-0.09	0.94	1.12	-0.49	0.71	0.82	-0.47	0.72	0.31	-1.06	0.48	0.57	0.39	1.31
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	guaA	K0NBJ2	1.39	0.24	1.18	2.56	-0.51	0.70	2.99	-0.70	0.61	2.59	-0.99	0.50	4.38	0.76	1.69
Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	upp	K0N4J8	0.15	0.04	1.03	2.77	-0.78	0.58	1.76	-0.48	0.72	2.63	-0.89	0.54	2.93	0.81	1.76
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	thyA	K0N522	0.11	0.04	1.03	2.96	0.77	1.71	2.02	0.71	1.63	0.36	-0.85	0.56	2.12	-0.73	0.60
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	gmk	K0N5J6	0.37	-0.22	0.86	1.64	-0.67	0.63	2.23	-1.07	0.48	1.66	-0.73	0.60	0.96	0.45	1.36
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	carB	K0N587	0.53	-0.63	0.65	1.51	0.30	1.23	1.17	0.57	1.48	1.27	-0.73	0.60	0.82	-0.93	0.52
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	pyrH	K0N5E6	0.05	-0.03	0.98	2.14	-0.43	0.74	1.27	-0.38	0.77	2.33	-0.71	0.61	0.93	0.40	1.32
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdE2	K0N5A1	2.49	-0.59	0.67	2.80	0.65	1.57	1.14	-0.28	0.82	2.57	-0.65	0.64	3.87	-1.24	0.42
Putative nrdI-like protein	Nucleic acid/nucleotide metabolism		K0N300	0.01	0.00	1.00	1.37	0.28	1.21	0.60	0.19	1.14	1.83	-0.45	0.73	1.10	-0.27	0.83

Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	xpt	K0MUR6	0.44	0.07	1.05	0.07	0.04	1.03	1.74	-0.33	0.79	1.97	-0.34	0.79	0.05	0.03	1.02
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	pyrDA, pyrD	K0N623	0.02	0.00	1.00	0.31	-0.11	0.93	0.70	-0.19	0.88	0.17	-0.06	0.96	0.37	0.11	1.08
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	dut	K0MXG3	0.58	0.14	1.10	1.19	0.29	1.23	0.47	0.15	1.11	0.24	0.10	1.07	0.80	-0.15	0.90
GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	relA	K0N8Y0	0.09	-0.08	0.94	1.22	0.67	1.59	0.13	-0.11	0.93	0.09	0.10	1.07	1.47	-0.75	0.59
Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	adk	K0N7F0	0.65	-0.13	0.91	2.08	-0.47	0.72	1.33	-0.42	0.75	0.33	0.12	1.09	2.01	0.34	1.26
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	prs1_2	K0NDQ5	0.17	-0.05	0.96	0.11	0.03	1.02	0.46	0.17	1.12	2.01	0.47	1.39	0.48	-0.08	0.94
Non-specific ribonucleoside hydrolase rihC (EC 3.2.-.-)	Nucleic acid/nucleotide metabolism	rihC	K0N803	0.07	0.09	1.06	0.46	0.47	1.38	0.39	0.43	1.35	0.54	0.61	1.53	1.56	-0.38	0.77
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	deoB	K0N1N0	2.67	0.43	1.35	2.32	0.35	1.27	2.44	0.73	1.66	1.22	0.79	1.73	0.48	0.09	1.06
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	pyrC	K0NAS6	0.01	0.02	1.01	0.09	0.19	1.14	0.87	1.07	2.10	1.16	1.04	2.05	0.08	-0.17	0.89
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC	K0N486	0.37	0.12	1.08	2.79	1.20	2.30	1.90	0.96	1.94	2.91	1.08	2.11	2.54	-1.09	0.47
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	nrdF	K0N552	0.04	0.03	1.02	0.34	0.14	1.10	1.66	-0.73	0.60	2.69	1.20	2.30	0.23	-0.11	0.93
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	guaB	K0N1G3	1.99	-0.32	0.80	1.67	-0.24	0.85	2.97	-1.10	0.47	4.04	1.24	2.36	0.38	-0.08	0.94
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	yutF	K0N383	0.30	0.10	1.07	2.04	-0.68	0.62	2.03	-0.74	0.60	3.31	1.53	2.89	3.50	0.78	1.72
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	purB	K0NA41	0.95	0.33	1.25	1.26	0.33	1.26	0.45	0.20	1.15	3.15	1.63	3.09	0.01	-0.01	1.00

Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	deoC_2, deoC	K0MSB5	2.50	0.55	1.46	1.97	0.60	1.52	2.61	0.73	1.66	4.04	1.65	3.15	0.13	-0.05	0.97
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	ndk	K0N340	0.06	-0.15	0.90	0.52	-0.60	0.66	0.11	-0.19	0.87	1.51	1.85	3.60	0.23	0.45	1.37
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	bkr4	K0N799	6.45	-5.63	0.02	1.08	0.26	1.20	4.16	-5.98	0.02	3.63	-6.32	0.01	6.11	-5.90	0.02
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	fabK	K0NA38	4.35	-4.85	0.03	0.74	0.37	1.29	3.67	-5.35	0.02	4.77	-6.27	0.01	4.58	-5.21	0.03
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	fabD	K0NBT1	6.77	-5.71	0.02	0.27	-0.07	0.95	5.68	-6.68	0.01	5.57	-5.98	0.02	6.20	-5.64	0.02
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	fabZ	K0NBS8	6.27	-5.89	0.02	2.85	0.53	1.44	6.66	-6.47	0.01	5.56	-4.88	0.03	6.16	-6.42	0.01
Acyl carrier protein (ACP)	Lipid-related metabolism	acpP_2, acpP	K0MX45	1.56	-2.37	0.19	1.25	1.33	2.51	1.99	-2.61	0.16	2.88	-4.58	0.04	2.71	-3.69	0.08
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	fabF	K0MX40	4.30	-4.15	0.06	0.47	0.27	1.21	2.02	-4.30	0.05	1.33	-4.54	0.04	5.03	-4.42	0.05
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)	Lipid-related metabolism	accC	K0N6M5	4.95	-4.56	0.04	3.74	1.54	2.91	4.08	-4.81	0.04	3.06	-4.29	0.05	5.83	-6.10	0.01
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	fabH	K0N7B0	5.00	-3.46	0.09	0.48	0.07	1.05	6.08	-4.52	0.04	5.63	-3.93	0.07	5.09	-3.53	0.09
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	fabG	K0N6N3	2.30	-3.68	0.08	1.90	1.99	3.97	2.29	-3.14	0.11	2.85	-3.44	0.09	2.88	-5.67	0.02
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	accB	K0NA35	4.03	-3.94	0.06	0.67	0.43	1.35	2.92	-3.93	0.07	4.11	-3.36	0.10	3.80	-4.37	0.05
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	sph	K0N5Q0	0.01	-0.01	0.99	1.77	0.90	1.87	2.00	1.28	2.43	2.64	-2.80	0.14	1.83	-0.91	0.53
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	accA	K0NBS6	4.14	-2.13	0.23	2.48	-0.91	0.53	2.35	-2.51	0.18	2.25	-2.09	0.23	2.78	-1.22	0.43
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	fabZ_2	K0NBT3	1.26	-2.95	0.13	0.91	1.95	3.87	1.18	-2.66	0.16	0.83	-1.70	0.31	2.71	-4.91	0.03
2-oxoisovalerate dehydrogenase subunit beta (EC 1.2.4.4)	Lipid-related metabolism	bfmBAB	K0MVK8	0.97	-0.24	0.85	3.74	-1.92	0.26	4.73	2.23	4.68	4.32	-1.51	0.35	3.31	1.68	3.21
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent	Lipid-related metabolism	gpsA	K0N3I2	0.58	-0.13	0.91	0.62	0.18	1.13	0.03	-0.01	0.99	0.98	-1.46	0.36	1.55	-0.31	0.81

glycerol-3-phosphate dehydrogenase)																		
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism	K0N6M0	K0N6M0	0.40	-0.20	0.87	0.77	-0.42	0.75	1.80	-1.36	0.39	1.25	-1.46	0.36	0.67	0.22	1.17
Uncharacterized protein yutG	Lipid-related metabolism	yutG	K0MTQ3	0.73	0.17	1.13	2.50	0.39	1.31	0.45	0.14	1.10	2.58	-1.26	0.42	0.85	-0.22	0.86
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	hmgCS1	K0N9K3	1.11	-0.18	0.88	4.51	1.16	2.23	3.53	0.80	1.74	1.73	-1.14	0.45	4.46	-1.33	0.40
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	ilvE	K0NBM4	0.69	-0.17	0.89	4.53	1.96	3.90	2.53	0.91	1.88	1.26	-0.70	0.62	4.43	-2.13	0.23
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	ispA	K0N9A2	0.71	-0.70	0.62	1.16	0.50	1.41	0.96	0.30	1.24	0.51	-0.23	0.85	1.18	-1.20	0.43
Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	plsX	K0MW37	0.54	1.22	2.32	0.45	1.01	2.02	0.24	0.60	1.51	0.01	-0.02	0.98	0.37	0.20	1.15
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	yqjQ(K0N8A1)	K0N8A1	0.76	0.50	1.41	0.06	0.11	1.08	2.15	0.94	1.92	0.01	-0.02	0.99	0.22	0.39	1.31
Uncharacterized protein	Lipid-related metabolism	YerQ	K0N7B3	2.76	-0.47	0.72	0.14	-0.05	0.97	1.82	-0.52	0.70	1.60	0.67	1.59	1.44	-0.42	0.75
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	lplJ	K0MVN0	1.83	-0.73	0.60	2.32	0.77	1.71	1.42	0.47	1.38	2.69	-4.73	0.04	3.36	-1.50	0.35
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	nadE	K0MWF6	0.79	0.14	1.10	0.01	0.00	1.00	1.56	-0.18	0.89	4.58	-3.21	0.11	0.62	0.14	1.10
Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	fhs	K0NAT0	1.69	-0.51	0.70	3.66	1.34	2.53	2.71	1.03	2.04	3.50	-3.13	0.11	3.93	-1.85	0.28
S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	metK	K0N352	0.47	-0.15	0.90	6.41	-0.89	0.54	2.85	-0.59	0.67	1.84	-2.93	0.13	2.24	0.74	1.67
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	pncB	K0N5X0	1.28	0.33	1.26	0.48	0.13	1.10	0.96	0.24	1.18	3.57	-2.78	0.15	0.56	0.20	1.15
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	garB	K0N8K3	1.14	-0.11	0.93	5.22	1.64	3.11	4.10	1.08	2.12	2.29	-2.73	0.15	5.95	-1.75	0.30
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		K0NAC0	0.53	-0.21	0.86	1.03	0.52	1.43	0.27	0.15	1.11	1.24	-1.86	0.27	1.60	-0.73	0.60
Uncharacterized protein	Cofactor-related metabolism		K0NB69	0.02	-0.01	1.00	2.44	-0.21	0.86	1.47	-0.23	0.85	2.71	-1.57	0.34	1.17	0.21	1.16
Bifunctional protein FolD	Cofactor-related metabolism	folD	K0N5K0	0.12	-0.02	0.99	2.04	0.49	1.40	1.08	-0.16	0.90	3.04	-1.54	0.34	2.33	-0.50	0.70

Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	coaD	K0N4X3	0.67	0.09	1.07	3.38	0.48	1.40	2.20	0.24	1.18	1.22	-1.45	0.37	2.31	-0.39	0.76
2-dehydropantoate 2-reductase (EC 1.1.1.169) (Ketopantoate reductase)	Cofactor-related metabolism		K0NAS0	0.30	-0.18	0.88	1.77	-1.35	0.39	2.64	1.21	2.31	1.44	-0.96	0.51	1.56	1.17	2.25
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	apbE_3	K0N6S8	1.37	0.50	1.41	1.89	1.00	2.00	1.87	1.75	3.37	0.51	-0.65	0.64	1.36	-0.50	0.71
Uncharacterized protein MJ0282	Cofactor-related metabolism		K0N1T2	0.56	0.52	1.43	0.46	-0.28	0.82	0.39	-0.25	0.84	0.87	-0.46	0.73	0.97	0.80	1.74
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	thiD_2	K0N2U9	0.43	0.09	1.07	1.93	1.16	2.24	1.53	0.52	1.43	0.46	-0.33	0.80	1.89	-1.07	0.48
FeS cluster assembly protein sufB	Cofactor-related metabolism	sufB	K0N4E5	0.41	-0.20	0.87	1.71	-0.67	0.63	1.40	-0.60	0.66	2.47	0.65	1.56	0.77	0.46	1.38
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	iscS1	K0N4U8	0.10	0.09	1.06	0.62	-0.30	0.81	1.36	-0.76	0.59	1.93	1.10	2.15	0.70	0.39	1.31
NifS/IcsS protein homolog	Cofactor-related metabolism		K0NAF3	0.08	-0.02	0.99	0.53	-0.19	0.88	1.61	-0.51	0.70	1.05	1.38	2.60	0.54	0.17	1.13
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	dnaN	K0N6S3	0.23	-0.09	0.94	0.71	-0.21	0.87	0.25	-0.10	0.93	3.48	-2.37	0.19	0.29	0.11	1.08
Single-stranded DNA-binding protein (SSB)	DNA replication-related	ssb	K0N1C2	0.30	0.12	1.09	0.39	0.22	1.16	0.06	0.04	1.03	1.86	-0.70	0.62	0.16	-0.09	0.94
DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	gyrB	K0N1B8	1.16	-0.34	0.79	0.54	-0.13	0.91	0.06	0.04	1.03	1.06	-0.47	0.72	0.98	-0.21	0.87
DNA-binding protein HU	DNA replication-related	hup	K0MVF4	0.08	-0.05	0.97	1.29	0.54	1.45	1.30	0.53	1.44	1.33	0.61	1.53	1.47	-0.59	0.66
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	gyrA	K0N6S7	0.09	-0.07	0.95	0.70	-0.41	0.75	2.19	-0.84	0.56	0.91	0.99	1.98	0.50	0.35	1.27
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	obg	K0MVD3	1.39	0.42	1.34	1.86	-0.58	0.67	1.78	-0.84	0.56	2.82	1.15	2.21	3.76	1.00	2.00
Protein RecA (Recombinase A)	DNA repair/recombination	recA_2,recA	K0N8P0	0.72	-0.41	0.76	0.19	0.16	1.12	0.47	-0.33	0.80	1.50	-3.01	0.12	1.29	-0.57	0.67
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	helD	K0N9W3	0.80	0.53	1.45	0.01	-0.01	1.00	1.20	-2.32	0.20	2.33	-2.50	0.18	1.05	0.54	1.46
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	polA	K0N9E7	0.09	-0.05	0.96	1.04	0.70	1.63	2.07	0.76	1.69	3.23	-1.70	0.31	1.03	-0.76	0.59
Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	nfo	K0NAW5	0.15	0.14	1.10	0.27	0.29	1.22	0.25	0.26	1.20	0.52	-0.69	0.62	0.25	-0.14	0.91

Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		K0N972	0.38	-0.38	0.77	0.27	0.25	1.19	0.33	0.21	1.16	0.90	-0.63	0.64	0.62	-0.63	0.64
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	uvrA	K0N3J2	0.20	0.05	1.04	2.62	-0.92	0.53	3.17	-1.25	0.42	1.96	0.79	1.73	2.67	0.97	1.96
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	ung	K0N758	0.03	0.08	1.06	0.61	0.91	1.87	0.59	0.89	1.85	0.49	0.93	1.90	0.71	-0.82	0.57
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	mnmA	K0N844	1.97	0.35	1.28	1.62	-0.51	0.70	1.49	-0.26	0.84	4.59	-4.94	0.03	2.21	0.86	1.81
tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	dus1	K0MXV9	0.24	-0.05	0.97	0.05	0.01	1.01	0.53	-0.14	0.91	2.31	-3.29	0.10	0.32	-0.06	0.96
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	yqeH	K0MW90	0.16	0.06	1.04	1.11	-0.30	0.81	1.58	-0.55	0.68	3.25	-2.95	0.13	1.28	0.36	1.28
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	yabO	K0NCR8	1.07	-0.97	0.51	0.61	0.37	1.30	1.00	-1.29	0.41	3.08	-2.40	0.19	1.49	-1.35	0.39
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	rnc	K0NB31	2.35	-0.34	0.79	3.07	0.35	1.27	0.56	-0.10	0.93	3.00	-2.05	0.24	3.27	-0.69	0.62
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshA	K0N8C7	0.44	0.05	1.04	4.49	-1.14	0.45	4.42	-0.91	0.53	5.33	-1.73	0.30	4.16	1.20	2.29
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	rnr	K0N3S4	0.07	0.03	1.02	1.95	-0.37	0.77	1.02	-0.17	0.89	5.17	-1.66	0.32	1.22	0.40	1.32
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	ybeY	K0N594	0.10	-0.02	0.98	1.55	-0.23	0.85	0.10	-0.06	0.96	1.88	-1.56	0.34	1.19	0.21	1.16
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	yqeL,rsfS	K0N5N6	1.52	0.22	1.17	3.45	-0.60	0.66	2.40	-0.63	0.65	2.67	-1.55	0.34	3.80	0.83	1.77
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	ysgA	K0N5M8	0.43	-0.75	0.59	0.75	0.63	1.55	0.20	0.20	1.15	1.77	-1.51	0.35	0.98	-1.38	0.38
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	yfmL	K0NA13	0.27	-0.09	0.94	0.16	0.07	1.05	0.64	0.40	1.32	2.94	-1.46	0.36	0.31	-0.16	0.90
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	der	K0N8E1	1.45	-0.25	0.84	0.98	-0.27	0.83	1.35	-0.39	0.76	1.04	-1.15	0.45	0.05	0.02	1.01

Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	rluB	K0N509	1.50	-0.42	0.75	0.11	0.10	1.07	1.20	-0.26	0.83	1.36	-1.10	0.47	0.74	-0.51	0.70
Queuine tRNA-ribosyltransferase (EC 2.4.2.29) (Guanine insertion enzyme) (tRNA-guanine transglycosylase)	tRNA/Ribosome assembly/processing	tgt	K0N6J4	0.05	0.10	1.07	0.34	0.46	1.38	0.35	0.45	1.37	0.30	-0.73	0.60	0.29	-0.36	0.78
Uncharacterized protein SE_0534	tRNA/Ribosome assembly/processing		K0N3F2	0.78	0.26	1.20	1.19	-0.26	0.83	2.35	-0.59	0.66	1.94	-0.45	0.73	1.80	0.53	1.44
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	yabR	K0N8A7	0.41	0.18	1.14	0.86	-0.30	0.81	0.76	-0.27	0.83	0.96	-0.38	0.77	1.66	0.48	1.40
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	queA	K0N965	0.37	-0.15	0.90	0.79	-0.31	0.81	1.26	-0.45	0.73	0.01	-0.01	0.99	0.25	0.16	1.12
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	rbfA	K0MVV7	0.06	0.02	1.01	0.19	-0.08	0.95	0.66	-0.16	0.89	0.67	0.18	1.13	0.31	0.10	1.07
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	cshB	K0N356	1.06	0.33	1.26	0.37	-0.11	0.93	0.65	-0.19	0.87	0.39	0.23	1.18	1.76	0.44	1.36
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	yacO	K0NC34	0.35	1.67	3.18	4.66	5.42	42.90	4.75	5.32	39.84	0.99	0.63	1.55	0.88	-3.75	0.07
Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	ptp3	K0NBX6	0.36	-0.15	0.90	2.39	0.87	1.83	3.16	1.06	2.08	2.66	-2.46	0.18	2.41	-1.02	0.49
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	msrA_2, msrA	K0N4W6	0.02	-0.01	1.00	1.46	0.60	1.52	0.76	0.33	1.26	0.95	-2.03	0.25	1.44	-0.61	0.66
Thioredoxin-like protein ytpP	Posttranslational modification	ytpP	K0N9F1	1.49	0.20	1.15	2.46	0.60	1.51	1.00	0.43	1.35	1.27	-1.76	0.29	1.68	-0.40	0.76
Thioredoxin	Posttranslational modification	trxA_2	K0N975	0.27	0.11	1.08	2.04	0.71	1.63	0.03	-0.02	0.99	3.20	-1.63	0.32	3.02	-0.60	0.66
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	trxB	K0N3L1	0.60	-0.20	0.87	0.09	0.02	1.02	1.27	-0.27	0.83	2.31	-1.19	0.44	0.72	-0.22	0.86
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	Posttranslational modification	citC	K0MWJ1	2.22	1.02	2.02	3.87	2.36	5.14	3.91	2.49	5.62	2.05	1.68	3.21	3.52	-1.35	0.39
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	hslU	K0N4Y1	1.98	-0.43	0.74	4.05	1.19	2.28	2.27	1.07	2.11	3.28	-2.23	0.21	4.90	-1.62	0.32
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	hslV	K0N542	2.74	-0.49	0.71	1.24	0.63	1.54	0.42	0.42	1.34	1.10	-1.57	0.34	2.05	-1.11	0.46

ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	clpX	K0MVC6	0.75	-0.19	0.88	3.17	-1.01	0.50	4.05	-1.31	0.40	2.37	-1.12	0.46	2.24	0.82	1.77
Chaperone protein DnaJ	Protein folding/turnover	dnaJ	K0N5J4	2.70	-0.64	0.64	0.10	-0.03	0.98	2.28	-0.58	0.67	0.62	-0.91	0.53	2.28	-0.61	0.66
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	clpP_2, clpP	K0N3M4	0.43	-0.17	0.89	0.74	-0.26	0.83	1.47	-0.45	0.73	1.56	-0.73	0.60	0.28	0.09	1.06
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	groS,grES	K0N700	0.16	0.16	1.12	0.14	-0.16	0.90	0.14	-0.15	0.90	0.54	-0.44	0.73	0.47	0.32	1.24
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	ftsH	K0N7I8	1.98	-0.35	0.79	1.05	-0.34	0.79	0.21	0.06	1.04	1.78	-0.31	0.81	0.00	0.00	1.00
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		K0N387	1.30	0.63	1.55	0.59	0.21	1.16	0.40	0.15	1.11	0.20	-0.10	0.93	1.19	0.42	1.34
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	tig	K0N884	0.13	0.04	1.03	2.32	-0.47	0.72	0.54	-0.16	0.89	0.06	-0.02	0.99	2.68	0.51	1.42
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	pth	K0N8B3	0.31	-0.29	0.82	0.42	0.51	1.42	0.19	-0.28	0.82	0.04	0.07	1.05	0.89	-0.80	0.57
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	dnaK	K0N5C7	0.20	-0.07	0.95	2.84	-0.77	0.59	1.28	-0.46	0.72	0.80	0.27	1.20	2.47	0.69	1.62
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	prsA	K0N5Q8	0.47	-0.14	0.91	0.46	-0.11	0.93	1.17	0.51	1.42	1.78	0.39	1.31	0.12	-0.03	0.98
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	groL,groEL	K0N7K7	1.39	-0.18	0.88	3.30	-0.85	0.55	2.70	-0.57	0.67	2.57	0.45	1.36	3.38	0.67	1.60
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	clpE	K0N644	1.95	-0.44	0.74	2.42	-0.55	0.68	1.64	-0.58	0.67	4.09	0.78	1.72	0.35	0.11	1.08
Chaperone protein ClpB	Protein folding/turnover	clpB_2	K0N887	1.99	-0.84	0.56	3.04	0.87	1.83	0.39	0.17	1.12	2.54	0.87	1.83	3.30	-1.71	0.31
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	clpC	K0N9Z7	0.19	-0.19	0.87	1.60	-1.17	0.44	2.37	-2.01	0.25	1.28	1.00	2.00	1.93	0.98	1.97
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	hslO	K0N893	0.87	0.09	1.07	0.85	-0.20	0.87	1.28	-0.40	0.76	5.78	1.22	2.32	1.15	0.29	1.23
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	htrA	K0N8D9	1.10	-0.25	0.84	3.38	1.58	2.98	0.25	0.12	1.09	2.33	1.29	2.45	3.84	-1.83	0.28
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	grpE	K0NAZ2	1.54	-0.38	0.77	2.22	-0.68	0.63	1.07	-0.44	0.74	3.95	1.55	2.92	1.16	0.30	1.23
Chaperone protein ClpB	Protein folding/turnover	clpB	K0N4Z8	1.89	-0.23	0.85	2.70	-0.71	0.61	0.82	-0.41	0.75	5.39	1.64	3.12	1.88	0.48	1.39
Uncharacterized protein	Protein folding/turnover		K0N5T8	2.73	-0.32	0.80	2.49	-1.01	0.50	1.84	-1.04	0.49	3.76	1.67	3.19	1.94	0.69	1.61
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	npr	K0MSP8	2.95	-1.12	0.46	1.06	-0.19	0.87	3.32	-1.02	0.49	3.23	-4.55	0.04	2.97	-0.92	0.53

Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	yfeX	K0N8U9	3.68	1.48	2.79	3.15	-0.85	0.56	0.42	-0.07	0.95	2.39	-3.87	0.07	4.14	2.33	5.03
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	nox_2	K0N1N9	2.70	-0.96	0.52	2.67	0.99	1.99	0.29	0.12	1.09	1.98	-3.60	0.08	3.29	-1.95	0.26
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	dkgB	K0N347	1.69	-0.54	0.69	4.82	1.96	3.90	3.63	1.48	2.79	4.10	-3.54	0.09	4.02	-2.50	0.18
Penicillin acylase (EC 3.5.1.11)	Cell defense/detoxification		K0N2B8	0.82	0.44	1.36	2.88	1.14	2.20	2.52	1.07	2.09	3.60	-3.42	0.09	1.49	-0.70	0.62
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	11E,P100	K0N513	0.05	0.02	1.02	2.10	0.92	1.89	1.13	0.41	1.33	1.66	-2.63	0.16	1.78	-0.90	0.54
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	tpx	K0MTJ5	2.03	-0.90	0.54	2.65	0.84	1.79	0.83	0.21	1.16	3.04	-2.58	0.17	3.12	-1.73	0.30
Lactaldehyde dehydrogenase (EC 1.2.1.21) (EC 1.2.1.22)	Cell defense/detoxification	aldA	K0NCB9	2.70	-1.71	0.31	3.91	1.97	3.91	1.23	-0.34	0.79	1.54	-1.40	0.38	3.84	-3.68	0.08
Glutathione peroxidase	Cell defense/detoxification	gpo	K0N6T6	1.22	-0.37	0.77	3.87	2.00	4.00	3.54	1.54	2.90	2.56	-1.26	0.42	4.60	-2.37	0.19
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	maa	K0N8I9	0.59	-1.04	0.49	0.14	-0.36	0.78	0.35	0.56	1.47	0.61	-0.92	0.53	0.34	-0.68	0.63
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	mco	K0N7A4	2.22	0.36	1.28	1.14	-0.20	0.87	1.04	0.59	1.50	0.47	0.21	1.16	3.56	0.55	1.47
Uncharacterized protein ACIAD3023	Cell defense/detoxification		K0N2T5	0.02	-0.01	0.99	4.28	3.44	10.85	3.48	2.92	7.58	2.35	0.98	1.97	5.19	-3.45	0.09
CutC-like protein M6_Spy0363	Cell defense/detoxification		K0N3H0	0.61	0.23	1.18	1.12	0.38	1.30	0.48	0.18	1.13	2.62	1.19	2.27	0.58	-0.14	0.90
Uncharacterized protein Lin2081	Cell defense/detoxification		K0N4U3	1.31	-0.43	0.74	2.25	0.75	1.68	1.99	-0.70	0.62	3.26	1.37	2.58	3.89	-1.18	0.44
Uncharacterized protein ynbB	Cell defense/detoxification	ynbB	K0N9B7	1.61	0.41	1.32	2.67	-0.85	0.56	1.88	-0.74	0.60	3.75	1.71	3.28	3.40	1.25	2.38
Tautomerase (EC 5.3.2.-)	General prediction only		K0MVQ1	0.43	-2.16	0.22	1.15	-0.89	0.54	0.54	-1.82	0.28	3.78	-5.54	0.02	0.23	-1.27	0.41

UPF0337 protein yhjA	General prediction only	yhjA	K0N7S1	1.79	-1.32	0.40	0.29	-0.27	0.83	0.26	-0.24	0.85	3.50	-3.75	0.07	2.14	-1.04	0.49
Phosphatase YidA (EC 3.1.3.-)	General prediction only	yidA	K0NDD5	0.46	-0.06	0.96	4.43	1.39	2.62	4.52	1.53	2.88	4.12	-3.68	0.08	4.16	-1.45	0.37
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	ydgI_2	K0N508	0.22	-0.12	0.92	3.47	1.29	2.44	3.54	1.49	2.81	1.48	-3.05	0.12	2.52	-1.41	0.38
UPF0337 protein lp_1708	General prediction only		K0N2J8	0.35	0.35	1.27	1.47	1.18	2.26	1.75	1.48	2.79	1.91	-2.99	0.13	1.90	-0.83	0.56
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	ywpJ	K0N9U2	0.03	-0.01	0.99	0.89	0.23	1.17	0.99	0.39	1.31	1.06	-2.60	0.16	0.81	-0.24	0.85
Autoinducer-2 (AI-2) kinase	General prediction only		K0NB06	4.80	1.87	3.66	2.98	-0.95	0.52	0.81	0.47	1.39	2.78	-2.46	0.18	5.06	2.82	7.04
Predicted hydrolase of HD superfamily	General prediction only		K0N6Z0	0.43	0.31	1.24	0.61	0.38	1.30	0.52	-0.37	0.78	2.23	-2.45	0.18	0.18	-0.07	0.95
Putative tRNA-binding protein ytpR	General prediction only	ytpR	K0NB80	0.01	-0.01	1.00	1.12	-0.61	0.66	1.59	-0.83	0.56	1.72	-2.35	0.20	2.15	0.60	1.52
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	yhfP	K0MTE1	0.18	-0.10	0.93	1.91	1.16	2.23	2.48	1.59	3.00	3.29	-1.86	0.28	1.94	-1.26	0.42
Virulence factor mviM	General prediction only	mviM	K0N4B2	0.96	-0.45	0.73	1.10	0.47	1.39	0.12	0.08	1.06	2.62	-1.86	0.28	2.90	-0.92	0.53
UPF0659 protein YMR090W	General prediction only	ylbE	K0N671	0.38	0.13	1.09	0.12	-0.05	0.96	0.16	0.06	1.04	0.46	-1.75	0.30	0.45	0.18	1.13
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	mhqA_3	K0N5N7	1.19	-0.23	0.85	3.36	1.72	3.29	2.88	1.36	2.58	2.95	-1.71	0.31	3.90	-1.95	0.26
Uncharacterized protein YxeH	General prediction only	yxeH	K0N1Y7	1.21	-0.89	0.54	1.29	0.52	1.44	0.68	0.18	1.13	2.60	-1.24	0.42	1.65	-1.42	0.37
Uncharacterized protein ylxR	General prediction only	ylxR	K0NAZ6	0.32	0.07	1.05	0.66	-0.21	0.86	0.32	-0.11	0.93	0.66	-1.24	0.42	0.83	0.28	1.21
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	glyr1	K0N992	0.40	0.18	1.13	3.05	1.42	2.68	2.18	0.80	1.74	1.69	-1.08	0.47	2.43	-1.24	0.42
Uncharacterized protein	General prediction only		K0N6M8	2.10	-0.16	0.90	0.64	0.35	1.28	0.01	0.00	1.00	1.39	-0.95	0.52	0.96	-0.51	0.70
FMN-binding domain protein	General prediction only		K0NC29	0.85	0.53	1.45	2.11	1.00	2.00	2.63	1.64	3.13	1.61	-0.88	0.54	1.00	-0.47	0.72
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		K0N5D9	0.15	-0.07	0.95	0.41	0.14	1.10	1.49	-0.29	0.82	0.60	-0.72	0.61	0.41	-0.21	0.87
Acetyltransferase	General prediction only		K0N2Z8	0.62	0.18	1.13	0.21	0.13	1.09	0.40	-0.16	0.90	0.59	-0.68	0.62	0.07	0.05	1.03
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	yhaA	K0N9E4	0.84	-0.60	0.66	0.37	0.16	1.11	0.68	-0.86	0.55	0.43	-0.66	0.63	0.98	-0.76	0.59
Predicted hydrolase of the HAD superfamily	General prediction only	mtlD	K0N9D4	0.61	0.14	1.10	3.09	0.94	1.92	3.87	1.38	2.60	0.83	-0.60	0.66	2.70	-0.80	0.58
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	ycnE	K0N7R3	0.79	0.30	1.23	1.25	0.59	1.51	0.34	0.29	1.22	0.59	-0.59	0.66	0.77	-0.29	0.82

Uncharacterized protein	General prediction only		K0NAY8	1.51	-0.27	0.83	1.93	0.77	1.71	1.56	1.05	2.06	0.62	-0.37	0.77	2.45	-1.04	0.48
Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	Steap4	K0MS41	0.89	-0.38	0.77	1.23	0.84	1.79	0.31	0.15	1.11	0.38	0.13	1.09	1.69	-1.21	0.43
Histidinol-phosphatase	General prediction only		K0N4F8	0.34	0.17	1.13	1.93	1.85	3.61	1.39	1.48	2.79	0.11	0.18	1.13	1.84	-1.68	0.31
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	ykwC	K0N7M3	0.15	0.09	1.06	0.69	0.41	1.33	0.02	0.01	1.01	0.29	0.25	1.19	0.58	-0.32	0.80
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	mhqD	K0NB71	0.28	0.09	1.07	2.39	0.88	1.84	0.18	0.23	1.17	0.65	0.30	1.23	2.17	-0.79	0.58
Nucleoid-associated protein BN194_23980	General prediction only		K0NA95	0.19	0.09	1.06	0.60	-0.15	0.90	1.00	-0.27	0.83	1.78	0.31	1.24	0.61	0.24	1.18
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	HBN1	K0N597	1.58	0.75	1.68	1.14	-0.55	0.69	0.98	-0.53	0.69	0.85	0.45	1.37	4.09	1.30	2.45
Uncharacterized protein ycaC	General prediction only	ycaC	K0N948	3.67	-1.04	0.49	4.13	1.44	2.71	1.72	0.32	1.25	2.50	0.57	1.49	6.84	-2.48	0.18
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		K0NAA2	0.55	-0.23	0.86	3.73	2.15	4.43	1.79	0.68	1.60	1.69	0.79	1.73	4.81	-2.37	0.19
Uncharacterized protein yghZ	General prediction only	yghZ	K0N7U8	0.35	0.18	1.13	3.14	1.94	3.83	2.95	1.94	3.83	2.85	1.73	3.31	3.82	-1.76	0.29
Uncharacterized protein	Unknown/uncharacterized		K0N2Y6	1.08	-0.31	0.81	0.39	0.10	1.07	0.14	0.06	1.04	4.69	-3.45	0.09	2.12	-0.41	0.75
Uncharacterized protein	Unknown/uncharacterized		K0N4V4	0.11	0.03	1.02	0.93	0.29	1.22	1.32	0.33	1.26	1.30	-2.99	0.13	0.95	-0.26	0.83
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		K0N4Y3	0.04	0.02	1.01	2.39	-0.87	0.55	2.16	-0.75	0.59	3.52	-2.84	0.14	2.40	0.89	1.85
Uncharacterized protein	Unknown/uncharacterized		K0N1N3	0.08	0.05	1.04	4.73	2.51	5.70	4.00	1.77	3.41	1.96	-2.81	0.14	3.66	-2.46	0.18
Uncharacterized protein	Unknown/uncharacterized		K0N6Y5	0.31	-0.14	0.91	0.70	-0.23	0.85	1.82	-0.51	0.70	2.77	-2.54	0.17	0.19	0.09	1.06
Uncharacterized protein	Unknown/uncharacterized		K0N764	0.40	-0.06	0.96	1.57	0.22	1.17	0.61	-0.12	0.92	2.15	-2.35	0.20	1.42	-0.29	0.82
Uncharacterized protein	Unknown/uncharacterized		K0N555	0.60	0.40	1.32	1.53	-0.40	0.76	0.74	-0.24	0.85	2.45	-2.30	0.20	1.25	0.80	1.74
UPF0356 protein BN194_15030	Unknown/uncharacterized		K0N856	0.02	0.00	1.00	2.38	-0.60	0.66	0.73	-0.30	0.81	1.66	-1.86	0.28	2.23	0.59	1.51
Uncharacterized protein	Unknown/uncharacterized		K0N4M6	0.07	-0.05	0.97	2.28	0.42	1.34	2.34	0.59	1.50	2.29	-1.74	0.30	1.02	-0.47	0.72
Uncharacterized protein	Unknown/uncharacterized		K0N2T7	0.80	-0.19	0.88	2.26	-0.77	0.59	1.65	-0.55	0.68	4.08	-1.35	0.39	1.63	0.59	1.50
Protein QmcA	Unknown/uncharacterized	qmcA	K0NA10	0.52	-0.44	0.74	0.39	0.24	1.18	2.13	1.20	2.29	1.43	-1.25	0.42	0.71	-0.68	0.62
Uncharacterized protein	Unknown/uncharacterized		K0N932	2.77	-1.72	0.30	0.94	-0.31	0.81	2.16	-1.10	0.47	2.02	-0.96	0.51	2.80	-1.41	0.38

UPF0291 protein BN194_17750	Unknown/uncharacterized		K0N5P0	0.25	0.11	1.08	1.22	-1.16	0.45	0.33	0.16	1.12	1.42	-0.94	0.52	1.30	1.26	2.40
Uncharacterized protein	Unknown/uncharacterized		K0NAX5	0.31	0.47	1.39	0.39	-0.60	0.66	1.18	0.76	1.69	0.95	-0.82	0.57	0.59	1.08	2.11
UPF0210 protein BN194_09830	Unknown/uncharacterized		K0N6U0	1.37	0.31	1.24	2.11	0.55	1.47	2.03	0.68	1.60	2.28	-0.69	0.62	0.92	-0.24	0.84
Uncharacterized protein	Unknown/uncharacterized		K0N7T4	0.66	-0.16	0.89	1.06	0.19	1.14	0.29	-0.08	0.94	0.33	-0.60	0.66	1.52	-0.36	0.78
PspC domain-containing protein	Unknown/uncharacterized	ythC	K0N3H5	6.26	-2.18	0.22	3.35	0.37	1.29	3.80	-1.41	0.38	3.25	-0.51	0.70	6.11	-2.55	0.17
Uncharacterized protein	Unknown/uncharacterized		K0N3D6	1.22	0.39	1.31	2.47	-0.67	0.63	1.36	-0.35	0.78	1.29	-0.37	0.77	3.03	1.06	2.09
Uncharacterized protein	Unknown/uncharacterized		K0N5V7	0.68	0.17	1.12	1.03	-0.15	0.90	0.68	0.61	1.53	1.56	-0.30	0.81	1.52	0.32	1.25
Uncharacterized protein	Unknown/uncharacterized		K0N9Y6	0.79	0.33	1.25	3.71	1.79	3.46	1.43	1.20	2.30	0.10	-0.17	0.89	3.12	-1.46	0.36
DegV domain-containing protein lin2658	Unknown/uncharacterized		K0N8L5	0.48	0.10	1.07	0.09	0.04	1.03	1.05	-0.21	0.86	0.93	-0.15	0.90	0.17	0.07	1.05
Uncharacterized protein ykuJ	Unknown/uncharacterized	ykuJ	K0N348	0.74	0.31	1.24	0.33	0.21	1.16	0.94	0.45	1.36	0.23	-0.13	0.92	0.22	0.10	1.07
Uncharacterized protein	Unknown/uncharacterized		K0N5A4	2.06	-0.48	0.72	0.75	-0.09	0.94	3.73	1.96	3.89	0.06	-0.10	0.93	1.75	-0.39	0.76
Nucleic acid-binding protein	Unknown/uncharacterized		K0N9D5	0.47	-0.73	0.60	0.51	0.48	1.39	0.26	0.30	1.23	0.00	0.00	1.00	1.07	-1.21	0.43
Uncharacterized protein	Unknown/uncharacterized		K0N7D4	0.24	0.33	1.26	1.25	1.41	2.65	1.78	2.03	4.08	0.00	0.00	1.00	1.72	-1.08	0.47
Uncharacterized protein yueI	Unknown/uncharacterized	yueI	K0NAC7	0.79	0.54	1.45	1.14	1.00	2.00	1.14	0.98	1.98	0.08	0.19	1.14	0.51	-0.46	0.73
Uncharacterized protein SAR1202	Unknown/uncharacterized		K0N5I6	0.14	-0.04	0.97	0.54	-0.12	0.92	1.86	-0.60	0.66	0.29	0.26	1.19	0.61	0.08	1.06
Uncharacterized protein	Unknown/uncharacterized		K0MVS9	0.46	-0.10	0.93	1.16	0.23	1.17	0.79	0.20	1.15	2.35	0.30	1.23	1.19	-0.33	0.79
Uncharacterized protein	Unknown/uncharacterized		K0N9Q9	0.89	-0.75	0.59	0.88	0.93	1.90	1.33	1.77	3.42	0.23	0.35	1.28	1.91	-1.68	0.31
Uncharacterized protein	Unknown/uncharacterized		K0N715	0.85	-0.24	0.85	3.35	1.70	3.26	3.32	1.31	2.47	1.14	0.37	1.29	4.16	-1.95	0.26
DegV domain-containing protein CA_C1624	Unknown/uncharacterized		K0NAD8	0.47	-0.73	0.60	0.78	1.32	2.50	0.25	-0.42	0.75	0.14	0.43	1.35	2.02	-2.05	0.24
Uncharacterized protein YqhY	Unknown/uncharacterized	yqhY	K0N9A7	0.64	-0.23	0.85	0.15	0.08	1.06	0.69	-0.19	0.87	2.63	0.54	1.45	0.53	-0.32	0.80
Uncharacterized protein	Unknown/uncharacterized		K0MTK3	0.04	0.01	1.01	1.98	0.85	1.81	3.43	1.86	3.63	1.98	0.57	1.48	2.30	-0.84	0.56
Protein LemA	Unknown/uncharacterized	lemA	K0N8J7	4.18	-0.71	0.61	1.26	-0.31	0.81	0.54	-0.25	0.84	1.19	0.63	1.54	1.63	-0.40	0.76

Uncharacterized protein	Unknown/uncharacterized		K0N5I7	3.49	1.05	2.07	0.28	-0.10	0.93	1.62	0.94	1.92	2.04	0.81	1.75	3.14	1.15	2.22
Uncharacterized protein	Unknown/uncharacterized		K0MXC2	0.27	-0.08	0.95	1.39	0.33	1.26	0.81	0.18	1.13	2.29	0.85	1.81	1.61	-0.41	0.75
Uncharacterized protein	Unknown/uncharacterized		K0N910	0.27	-0.09	0.94	0.72	0.15	1.11	0.54	0.10	1.07	2.72	0.96	1.94	0.75	-0.24	0.85
Uncharacterized protein ypuA	Unknown/uncharacterized	ypuA	K0N8I3	0.01	0.01	1.00	2.51	0.91	1.88	2.64	1.14	2.21	2.73	0.98	1.98	2.88	-0.91	0.53
UPF0297 protein BN194_08510	Unknown/uncharacterized		K0N358	0.60	-0.22	0.86	1.53	-0.38	0.77	1.34	-0.35	0.78	0.92	1.03	2.04	0.38	0.16	1.12
Uncharacterized protein	Unknown/uncharacterized		K0N984	0.53	-0.28	0.83	2.32	0.42	1.34	2.63	0.73	1.66	2.55	1.04	2.05	1.41	-0.69	0.62
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		K0NBV1	0.11	-0.06	0.96	1.17	0.55	1.46	0.07	0.02	1.01	3.02	1.17	2.25	1.05	-0.60	0.66
UPF0342 protein yheA	Unknown/uncharacterized	yheA	K0N9F7	1.77	1.09	2.12	0.07	0.07	1.05	0.28	0.36	1.29	1.72	1.20	2.30	1.27	1.01	2.02
UPF0145 protein BN194_07140	Unknown/uncharacterized		K0MT82	1.72	-0.66	0.63	1.28	0.26	1.19	0.02	-0.01	0.99	3.96	1.24	2.37	2.27	-0.92	0.53
Uncharacterized protein	Unknown/uncharacterized		K0N8V3	0.46	0.24	1.18	2.20	1.14	2.21	2.54	1.50	2.83	1.73	1.26	2.40	3.99	-0.91	0.53
Uncharacterized protein	Unknown/uncharacterized		K0N8E8	0.01	0.00	1.00	3.86	1.07	2.11	4.37	1.49	2.81	3.49	1.30	2.46	2.70	-1.08	0.47
GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		K0N5C6	0.47	-1.21	0.43	0.03	0.06	1.05	0.41	0.58	1.50	1.75	1.85	3.60	0.51	-1.27	0.41
Uncharacterized protein	Unknown/uncharacterized		K0NAC8	1.74	0.37	1.29	0.78	0.16	1.12	1.74	0.42	1.34	4.26	1.88	3.69	2.84	0.21	1.16
UPF0154 protein BN194_17740	Unknown/uncharacterized		K0MVY5	0.04	0.03	1.02	0.62	-0.29	0.82	0.81	0.83	1.78	3.97	3.36	10.27	0.75	0.32	1.25
>tr|K0NBL8|K0NBL8_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_21520 PE=3 SV=1	Unknown/uncharacterized	K0NBL8	K0NBL8	1.08	-0.21	0.87	1.94	-0.74	0.60	1.33	-0.43	0.74	3.09	-1.52	0.35	1.63	0.53	1.45
>tr|K0N788|K0N788_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_22500 PE=4 SV=1	Unknown/uncharacterized	K0N788	K0N788	3.68	-4.89	0.03	1.45	1.01	2.01	4.21	-5.82	0.02	2.73	-3.44	0.09	4.74	-5.89	0.02
>tr|K0N2Q1|K0N2Q1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_06460 PE=4 SV=1;>tr|K0MXJ1|K0MXJ1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_24990 PE=4 SV=1	Unknown/uncharacterized	K0N2Q1	K0N2Q1;K0MXJ1	1.61	0.41	1.33	1.43	0.61	1.53	3.83	1.24	2.36	0.29	0.07	1.05	0.43	-0.20	0.87

>tr|K0N1K5|K0N1K5_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_01360 PE=4 SV=1	Unknown/uncharacterized	K0N1K5	K0N1K5	0.30	0.77	1.70	0.64	0.91	1.88	1.11	1.54	2.91	0.09	0.16	1.12	0.06	-0.14	0.91
>tr|K0N4Z7|K0N4Z7_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02080 PE=4 SV=1	Unknown/uncharacterized	K0N4Z7	K0N4Z7	0.42	-0.19	0.87	0.87	-0.19	0.88	0.61	0.72	1.64	1.43	2.12	4.35	0.01	-0.01	1.00
>tr|K0N7I1|K0N7I1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02220 PE=4 SV=1	Unknown/uncharacterized	K0N7I1	K0N7I1	1.01	0.68	1.60	5.46	4.62	24.63	2.27	0.96	1.95	0.77	1.32	2.49	3.75	-3.95	0.06
>tr|K0N8W1|K0N8W1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07270 PE=4 SV=1	Unknown/uncharacterized	K0N8W1	K0N8W1	0.28	-0.25	0.84	5.03	5.41	42.40	0.50	1.82	3.53	2.01	0.62	1.54	4.00	-5.65	0.02
>tr|K0N2W3|K0N2W3_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07360 PE=4 SV=1	Unknown/uncharacterized	K0N2W3	K0N2W3	0.29	-0.08	0.94	3.57	1.41	2.65	4.17	1.82	3.52	1.30	-0.53	0.69	4.29	-1.49	0.36
>tr|K0NB98|K0NB98_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_19420 PE=4 SV=1	Unknown/uncharacterized	K0NB98	K0NB98	0.61	-0.58	0.67	0.90	-0.89	0.54	0.04	-0.05	0.97	2.60	-3.81	0.07	0.76	0.31	1.24
>tr|K0N6D0|K0N6D0_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_20650 PE=4 SV=1	Unknown/uncharacterized	K0N6D0	K0N6D0	1.32	1.60	3.02	0.04	0.05	1.04	0.63	-0.61	0.65	1.72	1.73	3.32	1.65	1.54	2.91
PTS system IIB component, L-Asc family	Phosphotransferase systems		K0N861	0.10	-0.71	0.61	0.83	3.07	8.41	0.11	-0.76	0.59	0.74	-2.80	0.14	0.95	-3.78	0.07
Cellobiose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	celA_5	K0N945	0.23	-0.24	0.85	0.26	0.33	1.26	0.11	0.07	1.05	1.70	-2.31	0.20	0.39	-0.57	0.67
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE_3	K0N5N9	0.37	0.21	1.16	2.84	-1.25	0.42	2.84	-1.31	0.40	3.40	-1.73	0.30	2.80	1.46	2.75
PTS system IIB component, Gat family	Phosphotransferase systems		K0N6A5	2.57	-1.07	0.48	3.42	-1.54	0.34	0.07	0.03	1.02	3.87	-1.64	0.32	1.27	0.47	1.39
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	ptsH	K0N9I2	0.26	0.25	1.19	0.45	-0.38	0.77	0.34	0.27	1.21	1.86	-1.26	0.42	0.57	0.63	1.55
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	gmuB	K0MXC7	0.00	0.00	1.00	0.92	-0.28	0.82	0.50	-0.18	0.88	0.18	-0.17	0.89	0.80	0.28	1.22
Mannose permease IID component	Phosphotransferase systems	manZ_9	K0N954	0.66	0.26	1.20	1.15	0.57	1.49	2.52	1.50	2.82	0.21	-0.12	0.92	0.83	-0.31	0.81

Mannose permease IID component	Phosphotransferase systems	manZ	K0MSE1	0.06	0.17	1.12	0.91	0.93	1.91	1.39	1.49	2.81	0.02	-0.05	0.97	0.35	-0.77	0.59
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	manX_5	K0NDL4	2.87	-0.46	0.73	1.72	0.35	1.27	3.14	0.85	1.80	0.68	0.15	1.11	3.20	-0.81	0.57
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	fruA_4	K0MY77	3.34	1.43	2.69	1.84	0.86	1.82	4.73	1.94	3.84	1.10	0.22	1.16	1.21	0.57	1.48
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	levE	K0N7U7	1.05	-0.34	0.79	0.21	0.09	1.06	0.86	0.27	1.21	1.04	0.35	1.27	1.87	-0.43	0.74
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	mtlF	K0N8N0	1.78	0.71	1.63	1.84	1.03	2.04	2.50	1.13	2.18	1.08	0.42	1.33	0.61	-0.32	0.80
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	hprK	K0N6Y3	0.27	-0.11	0.92	1.45	0.50	1.42	0.02	-0.02	0.99	2.87	1.11	2.16	1.80	-0.62	0.65
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		K0N1P6	1.19	0.60	1.51	0.38	-0.16	0.89	1.89	0.24	1.18	2.54	1.30	2.46	1.25	0.76	1.69
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	bglP	K0MT60	0.01	0.01	1.01	5.05	-1.12	0.46	1.06	-0.26	0.83	5.19	2.32	5.00	2.18	1.12	2.18
>tr|K0NAP8|K0NAP8_LACCA ParC protein OS=Lactobacillus casei W56 GN=parC PE=4 SV=1	Phosphotransferase systems	K0NAP8	K0NAP8	0.48	-2.66	0.16	1.08	-5.37	0.02	0.86	-3.23	0.11	0.38	-2.42	0.19	0.34	2.71	6.56
>tr|K0N5T2|K0N5T2_LACCA Phosphoenolpyruvate-protein phosphotransferase OS=Lactobacillus casei W56 GN=ptsI PE=3 SV=1	Phosphotransferase systems	ptsI	K0N5T2	0.60	0.13	1.09	1.11	-0.18	0.88	1.49	0.27	1.20	3.92	-3.08	0.12	1.47	0.31	1.24
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	ykpA	K0N8V6	1.19	0.29	1.22	1.04	-0.25	0.84	1.52	-0.42	0.75	2.37	-2.66	0.16	1.72	0.53	1.45
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	potA	K0MU90	1.56	-0.24	0.85	0.12	-0.03	0.98	2.07	0.58	1.49	3.15	-1.66	0.32	1.61	-0.21	0.86
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_3	K0MWS9	0.36	0.20	1.15	0.61	0.34	1.27	0.43	0.33	1.26	1.20	-0.81	0.57	0.36	-0.14	0.90
ABC-type uncharacterized transport system, ATPase component	ABC-type transporter systems		K0N6C9	0.83	0.33	1.26	0.16	0.08	1.06	1.55	0.78	1.72	2.33	-0.55	0.68	0.42	0.25	1.19
Oligopeptide-binding protein oppA	ABC-type transporter systems	oppA	K0N983	0.24	0.07	1.05	0.05	0.02	1.01	1.61	0.51	1.42	1.50	-0.35	0.78	0.36	0.06	1.04

Glycerol-3-phosphate ABC transporter substrate-binding protein	ABC-type transporter systems		K0N3T6	0.63	-0.19	0.88	1.38	0.33	1.25	2.66	0.84	1.80	0.02	0.01	1.00	1.48	-0.51	0.70
ABC-type phosphate/phosphonate transport system,periplasmic component	ABC-type transporter systems		K0NAI1	1.63	-0.51	0.70	0.20	0.05	1.04	2.31	0.75	1.69	0.80	0.12	1.09	1.62	-0.56	0.68
ABC transporter substrate-binding protein	ABC-type transporter systems		K0N2V5	0.35	-0.20	0.87	0.98	-0.56	0.68	1.27	-0.68	0.63	0.19	0.13	1.09	0.86	0.36	1.28
Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	bceA_2	K0N9X1	0.57	0.70	1.62	0.73	0.87	1.83	1.70	2.08	4.24	0.09	0.19	1.14	1.49	-0.17	0.89
Maltose ABC transporter, periplasmic maltose-binding protein	ABC-type transporter systems		K0N3U4	1.08	-0.41	0.75	3.24	1.77	3.41	2.86	1.70	3.26	1.12	0.25	1.19	3.33	-2.18	0.22
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	glnQ_4	K0N971	0.47	0.16	1.11	2.25	-0.57	0.67	0.56	-0.18	0.88	1.39	0.42	1.34	2.70	0.72	1.65
D-ribose-binding protein	ABC-type transporter systems	rbsB	K0MSF6	1.16	-0.41	0.75	0.38	-0.08	0.94	1.41	0.47	1.38	1.99	0.47	1.39	0.82	-0.33	0.80
ABC transporter, permease protein	ABC-type transporter systems		K0N8H4	1.46	-0.28	0.82	0.13	-0.09	0.94	2.43	0.65	1.57	3.70	0.50	1.42	0.32	-0.20	0.87
ABC transporter substrate-binding protein	ABC-type transporter systems		K0N2Z3	2.73	-0.19	0.87	1.92	-0.17	0.89	2.23	0.57	1.48	4.27	0.63	1.54	0.28	-0.02	0.99
Lipoprotein	ABC-type transporter systems	metQ_2	K0MV23	2.67	-0.39	0.76	3.29	-0.86	0.55	0.02	-0.01	0.99	4.29	0.96	1.94	2.57	0.47	1.38
Glutamine-binding periplasmic protein	ABC-type transporter systems	glnH_2	K0N8I1	0.33	0.23	1.17	1.64	-0.78	0.58	0.03	0.03	1.02	1.50	1.29	2.45	2.12	1.01	2.01
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	oppD	K0NB35	0.08	0.01	1.01	3.46	-0.62	0.65	0.84	-0.19	0.88	3.74	1.47	2.77	3.19	0.63	1.55
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	oppF	K0N5I3	0.37	-0.69	0.62	0.58	-0.20	0.87	0.71	0.23	1.17	3.25	1.84	3.58	0.25	-0.50	0.71
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	msmK	K0N747	0.95	1.23	2.34	0.93	-0.72	0.61	1.40	-1.03	0.49	3.42	3.09	8.49	1.52	1.94	3.85
Cadmium efflux system accessory protein	Other transporter proteins	cadC	K0MWU0	0.25	-0.28	0.82	2.00	2.04	4.11	1.32	1.41	2.66	0.71	0.53	1.44	2.17	-2.32	0.20
Probable flavodoxin-1	Membrane bioenergetics	ykuN_2	K0NA19	0.25	0.08	1.06	0.27	-0.17	0.89	0.21	-0.13	0.91	1.21	-1.36	0.39	0.50	0.24	1.18

N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	nagA	K0MWF9	0.16	-0.10	0.93	0.14	-0.04	0.97	0.16	-0.03	0.98	3.65	-5.48	0.02	0.07	-0.05	0.96
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	treA	K0N662	1.08	0.34	1.27	3.04	-1.43	0.37	3.18	-1.82	0.28	2.90	-4.99	0.03	3.67	1.78	3.43
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		K0N1L0	0.85	0.67	1.59	0.59	-0.48	0.72	0.75	-0.65	0.64	2.30	-4.66	0.04	4.52	1.15	2.22
Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	pox5	K0NBB6	2.64	-0.73	0.60	5.39	2.65	6.28	5.46	2.74	6.67	4.43	-4.53	0.04	4.97	-3.38	0.10
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	glgD	K0MWU4	0.90	-0.37	0.77	1.48	0.54	1.46	2.29	0.85	1.80	4.71	-4.17	0.06	2.17	-0.91	0.53
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	Carbohydrate-related metabolism		K0NCZ6	0.34	-0.07	0.95	2.21	0.47	1.39	0.43	0.07	1.05	3.65	-4.13	0.06	2.53	-0.55	0.68
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	agaS	K0MSD9	0.14	-0.07	0.95	1.51	0.34	1.27	0.34	0.09	1.06	2.20	-3.98	0.06	1.15	-0.41	0.75
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	pmi	K0N7U2	0.75	0.41	1.32	0.43	0.22	1.17	0.89	0.40	1.32	2.65	-3.50	0.09	0.47	0.18	1.14
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	lacC	K0N8Y4	0.12	-0.04	0.98	2.70	-0.80	0.57	3.03	-0.72	0.61	2.61	-3.23	0.11	2.37	0.77	1.70
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	pflB	K0N8I5	1.91	0.84	1.79	5.85	2.88	7.37	6.00	3.96	15.58	1.62	-2.97	0.13	3.31	-2.04	0.24
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	mtlD_3mtlD	K0N9C8	1.86	0.58	1.50	1.41	0.58	1.50	1.28	0.72	1.65	2.93	-2.76	0.15	0.00	0.00	1.00
Protein lacX, plasmid	Carbohydrate-related metabolism	lacX	K0NCY0	0.21	0.06	1.04	2.85	0.78	1.72	2.62	1.07	2.10	4.22	-2.70	0.15	3.32	-0.72	0.61
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	glgC	K0N6T3	1.86	-0.24	0.85	1.23	0.31	1.24	4.00	0.94	1.92	2.21	-2.54	0.17	1.93	-0.55	0.68
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	ldh	K0N7J5	0.30	0.10	1.07	1.07	-0.29	0.82	0.70	-0.24	0.85	2.64	-2.39	0.19	2.37	0.40	1.31
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2,lacD	K0N6A8	0.36	-0.10	0.94	2.54	-0.58	0.67	1.72	-0.52	0.70	5.48	-2.19	0.22	1.71	0.48	1.40

Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	aldB	K0MWH5	0.48	-0.27	0.83	0.65	0.36	1.28	0.43	-0.29	0.82	1.80	-2.19	0.22	1.29	-0.62	0.65
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	manD	K0N1P4	0.39	0.12	1.09	1.19	0.18	1.14	0.26	-0.06	0.96	3.48	-2.09	0.24	0.17	-0.06	0.96
Uncharacterized protein YwcC	Carbohydrate-related metabolism	ywcC	K0N6V0	0.06	0.03	1.02	2.44	0.73	1.66	2.52	0.66	1.58	4.12	-2.08	0.24	1.83	-0.70	0.62
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	galK	K0MTA3	0.33	-0.29	0.82	1.98	1.51	2.85	2.18	1.71	3.28	0.72	-1.96	0.26	3.09	-1.79	0.29
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	glpK	K0N694	2.41	-2.62	0.16	4.37	2.02	4.05	0.62	-0.29	0.82	4.20	-1.79	0.29	3.34	-4.64	0.04
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	agl	K0N8T1	0.01	0.00	1.00	3.93	1.34	2.53	3.49	1.44	2.71	2.82	-1.70	0.31	3.30	-1.34	0.40
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	lacB	K0MTB7	0.05	-0.01	0.99	1.16	-0.48	0.72	2.25	-0.68	0.63	2.21	-1.40	0.38	1.16	0.47	1.39
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	ldh1,ldh	K0N8S5	0.84	-0.29	0.82	3.41	2.64	6.23	3.36	2.57	5.93	1.64	-1.35	0.39	3.94	-2.93	0.13
Uncharacterized oxidoreductase YrbE (EC 1.-.-.-)	Carbohydrate-related metabolism	yrbE	K0N524	1.57	-1.67	0.31	4.08	4.16	17.82	2.21	1.87	3.65	1.87	-1.31	0.40	3.64	-5.82	0.02
Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	ADH2	K0N307	4.40	4.47	22.16	4.66	5.07	33.54	4.49	4.75	26.82	0.66	-1.30	0.41	3.16	-0.60	0.66
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	lacD2_2,lacD	K0N7P0	0.15	0.05	1.03	0.04	-0.01	0.99	0.19	0.08	1.06	2.95	-0.99	0.50	0.15	0.06	1.04
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	fruK_2	K0N8P7	2.10	1.33	2.52	0.25	-0.14	0.91	0.85	0.47	1.39	1.74	-0.98	0.51	3.15	1.47	2.78
Inosose dehydratase (EC 4.2.1.44) (2-keto-myo-inositol dehydratase)	Carbohydrate-related metabolism	iolE	K0MS68	0.45	-0.49	0.71	4.32	1.65	3.13	1.26	-0.74	0.60	1.57	-0.91	0.53	1.97	-2.14	0.23
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	lacA	K0N2T4	0.52	0.18	1.13	1.75	-0.37	0.77	1.68	-0.35	0.78	1.92	-0.90	0.54	1.84	0.55	1.47

Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	act	K0MVI3	1.38	-0.61	0.66	0.19	-0.23	0.85	0.62	0.67	1.59	0.11	0.15	1.11	0.31	-0.38	0.77
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	nagB	K0MYW0	2.96	0.37	1.29	1.98	-0.65	0.64	1.17	-0.35	0.78	1.34	0.31	1.24	2.69	1.02	2.02
Inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase (EC 1.1.1.18) (EC 1.1.1.369) (Myo-inositol 2-dehydrogenase/D-chiro-inositol 3-dehydrogenase)	Carbohydrate-related metabolism	iolG	K0N7J1	0.02	-0.03	0.98	3.14	3.23	9.41	0.98	0.72	1.65	0.51	0.82	1.77	3.17	-3.26	0.10
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	iolS	K0NB94	0.02	-0.01	0.99	4.42	1.46	2.75	3.65	1.39	2.63	2.09	0.88	1.83	3.36	-1.47	0.36
Probable L-ascorbate-6-phosphate lactonase ulaG (EC 3.1.1.-)	Carbohydrate-related metabolism	ulaG	K0MYF8	0.25	0.53	1.45	3.60	1.44	2.72	2.91	1.77	3.41	1.18	1.04	2.05	0.47	-0.91	0.53
3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase (THcHDO hydrolase) (EC 3.7.1.22)	Carbohydrate-related metabolism	iolD	K0N1T3	0.08	0.18	1.13	2.73	3.92	15.13	1.55	1.86	3.63	0.88	1.05	2.06	2.57	-3.74	0.07
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	pta	K0MU95	0.01	0.00	1.00	4.30	1.54	2.91	3.67	1.78	3.44	3.66	1.50	2.83	3.85	-1.54	0.34
5-dehydro-2-deoxygluconokinase (EC 2.7.1.92) (2-deoxy-5-keto-D-gluconate kinase)	Carbohydrate-related metabolism	iolC	K0N1H4	0.17	0.22	1.16	4.35	3.66	12.65	2.16	1.07	2.10	1.58	1.54	2.90	2.79	-3.44	0.09
>tr|K0N518|K0N518_LACCA IolA protein OS=Lactobacillus casei W56 GN=iolA PE=3 SV=1	Carbohydrate-related metabolism	iolA	K0N518	0.90	0.80	1.75	3.43	4.03	16.31	2.04	1.71	3.27	0.11	0.15	1.11	3.84	-3.22	0.11
>tr|K0N2V4|K0N2V4_LACCA GlpO protein OS=Lactobacillus casei W56 GN=glpO PE=4 SV=1	Carbohydrate-related metabolism	glpO	K0N2V4	1.81	-2.15	0.23	4.68	2.47	5.53	0.58	0.18	1.14	4.08	-1.78	0.29	3.02	-4.61	0.04
>tr|K0N8X1|K0N8X1_LACCA Galactose-1-phosphate uridylyltransferase OS=Lactobacillus casei W56 GN=galT PE=3 SV=1	Carbohydrate-related metabolism	K0N8X1	K0N8X1	0.44	0.10	1.07	4.02	1.64	3.12	4.00	1.97	3.91	1.77	-0.44	0.74	5.03	-1.55	0.34
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	pdhD	K0N4P1	4.72	-2.00	0.25	4.92	2.56	5.90	7.45	2.54	5.82	3.26	-4.47	0.05	5.47	-4.56	0.04
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	yqeC	K0N532	2.35	-0.83	0.56	1.95	-0.61	0.66	0.14	0.05	1.04	4.81	-4.35	0.05	0.86	-0.22	0.86

Aldose 1-epimerase (EC 5.1.3.3)	Central glycolytic/intermediary pathways		K0MTA8	0.42	0.08	1.06	4.54	2.61	6.09	4.08	2.54	5.80	1.36	-4.09	0.06	4.40	-2.53	0.17
Aldose 1-epimerase	Central glycolytic/intermediary pathways		K0NAP4	1.58	-0.51	0.70	1.68	0.56	1.47	0.82	0.28	1.22	3.94	-3.84	0.07	4.63	-1.07	0.48
Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	pyk	K0N8B6	0.35	0.06	1.04	3.61	-0.71	0.61	2.90	-0.47	0.72	4.96	-3.48	0.09	3.10	0.77	1.71
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	zwf	K0N966	0.11	0.09	1.07	0.78	0.37	1.30	0.22	-0.12	0.92	3.36	-2.76	0.15	0.38	-0.28	0.82
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	tpiA	K0N736	2.32	0.64	1.55	0.80	-0.20	0.87	0.69	0.16	1.12	4.19	-2.67	0.16	2.63	0.84	1.79
Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	fba_2	K0N2C9	1.02	0.29	1.22	2.37	-0.67	0.63	2.28	-0.66	0.63	3.08	-2.56	0.17	3.51	0.96	1.94
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	pgcA	K0N9K8	0.53	-0.12	0.92	2.79	0.63	1.55	2.37	0.53	1.44	4.59	-2.18	0.22	3.34	-0.75	0.59
Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	gntK	K0MS76	1.39	-0.38	0.77	0.21	-0.09	0.94	0.55	0.22	1.16	1.99	-1.69	0.31	0.64	-0.29	0.82
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	pfkA	K0NAK6	0.15	-0.06	0.96	2.32	-0.80	0.57	3.16	-0.81	0.57	3.31	-1.27	0.42	1.90	0.75	1.68
Pyruvate, phosphate dikinase (EC 2.7.9.1)	Central glycolytic/intermediary pathways	ppdK	K0NAC6	0.84	-1.00	0.50	1.86	2.23	4.71	2.89	4.21	18.46	0.26	-1.14	0.45	4.04	-3.23	0.11
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	pdhA	K0N860	3.26	-1.84	0.28	4.14	1.94	3.84	3.80	1.93	3.82	0.41	-0.52	0.70	4.59	-3.78	0.07
Uncharacterized protein	Central glycolytic/intermediary pathways		K0N8A3	0.00	0.00	1.00	2.63	1.74	3.34	2.47	1.67	3.18	0.84	-0.49	0.71	4.68	-1.74	0.30
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	gnd	K0N5N2	0.05	0.02	1.01	2.47	0.89	1.85	1.90	0.69	1.61	0.62	0.30	1.23	3.50	-0.87	0.55
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	fbp	K0N6C3	1.20	-0.27	0.83	4.88	2.90	7.47	5.65	3.22	9.29	0.24	0.31	1.24	5.02	-3.17	0.11

Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	rbsK	K0N1R2	0.16	-0.08	0.95	0.05	-0.03	0.98	0.29	0.11	1.08	1.13	0.38	1.30	0.10	-0.05	0.97
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	pdhB	K0MVA7	4.48	-1.56	0.34	4.97	1.82	3.54	4.34	2.04	4.12	1.39	0.49	1.40	5.66	-3.38	0.10
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	pdhC	K0N4W5	3.47	-1.93	0.26	4.66	2.29	4.90	4.85	2.27	4.84	1.33	0.51	1.42	4.74	-4.22	0.05
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	dhaM	K0N2C2	0.91	0.33	1.25	4.00	1.73	3.33	3.40	1.72	3.30	1.45	0.62	1.53	3.14	-1.41	0.38
Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	rpiA_2, ripA	K0N8W9	0.68	1.41	2.66	0.32	0.88	1.85	2.20	3.06	8.37	0.67	1.19	2.28	0.16	0.53	1.44
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	dhaK_2	K0N5Q3	0.60	0.27	1.21	3.27	2.01	4.02	2.92	1.83	3.56	2.39	1.40	2.63	3.63	-1.74	0.30
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	glcK	K0NB57	0.92	-0.29	0.82	0.85	-0.20	0.87	0.02	0.01	1.01	3.24	1.41	2.65	0.36	-0.09	0.94
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	gpmA2,gpmA	K0MX58	0.23	0.06	1.04	2.74	-0.13	0.91	0.12	0.04	1.03	3.85	1.46	2.75	0.89	0.19	1.14
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	pgk	K0N9R1	0.86	0.46	1.37	0.91	-0.27	0.83	0.64	-0.28	0.82	2.84	1.47	2.78	1.62	0.73	1.66
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	rpe	K0N5T1	0.42	0.13	1.09	1.44	0.30	1.23	0.11	0.05	1.03	2.63	1.63	3.10	0.85	-0.17	0.89
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	eno	K0MU67	0.99	0.12	1.09	2.92	-0.51	0.70	1.47	-0.34	0.79	4.57	1.65	3.13	3.77	0.63	1.55
>tr|K0N3R3|K0N3R3_LACCA Gap protein OS=Lactobacillus casei W56 GN=gap PE=3 SV=1	Central glycolytic/intermediary pathways	gap	K0N3R3;K0N4X1	0.34	0.16	1.12	1.58	-0.53	0.69	0.80	-0.31	0.81	3.19	-2.80	0.14	1.63	0.69	1.61
>tr|K0N1M9|K0N1M9_LACCA Probable phosphoketolase OS=Lactobacillus casei W56 GN=xpkA PE=3 SV=1	Central glycolytic/intermediary pathways	xpkA	K0N1M9;K0N8X7	2.86	-0.69	0.62	1.23	-0.26	0.84	1.19	-0.22	0.86	5.16	-4.23	0.05	2.78	-0.43	0.74

>tr|K0N7I6|K0N7I6_LACCA Glucose-6-phosphate isomerase OS=Lactobacillus casei W56 GN=pgi PE=3 SV=1	Central glycolytic/intermediary pathways	pgi	K0N7I6;K0N4A6	0.06	0.04	1.03	1.91	0.55	1.46	1.72	0.52	1.44	2.31	-5.92	0.02	0.97	-0.51	0.70
>tr|K0N7B1|K0N7B1_LACCA Acetate kinase OS=Lactobacillus casei W56 GN=ackA PE=3 SV=1	Central glycolytic/intermediary pathways	ackA	K0N7B1;K0N6W4	0.32	0.16	1.12	3.62	2.46	5.50	3.70	2.68	6.41	2.49	-2.58	0.17	6.10	-2.30	0.20
Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		K0N684	0.56	-0.12	0.92	1.25	0.18	1.13	1.07	0.20	1.15	3.39	-2.95	0.13	1.75	-0.30	0.81
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	citF	K0N607	3.10	2.12	4.35	4.22	4.25	19.04	5.26	4.83	28.37	0.72	-2.37	0.19	2.76	-2.13	0.23
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	pycB	K0MWI8	3.92	2.45	5.48	6.31	5.13	35.03	6.43	5.55	46.70	0.61	-0.87	0.55	4.09	-2.68	0.16
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	citD	K0N9Q5	0.82	1.19	2.29	1.94	3.00	7.97	2.18	3.55	11.75	0.19	-0.81	0.57	4.99	-1.80	0.29
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	citE	K0NBF4	1.09	1.31	2.48	2.47	3.49	11.26	2.65	3.93	15.24	0.23	-0.70	0.61	4.91	-2.19	0.22
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	pyc	K0NAI2	1.57	0.24	1.18	2.69	0.94	1.92	2.12	0.56	1.47	0.56	-0.31	0.81	2.34	-0.70	0.61
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	citX	K0N6A3	1.31	1.47	2.78	2.58	2.73	6.62	2.85	3.18	9.08	0.63	0.95	1.93	1.55	-1.25	0.42
Biotin carboxyl carrier protein	Tricarboxylic acid pathway	bcc	K0NBF7	2.14	1.00	1.99	2.81	3.27	9.67	2.40	3.22	9.31	4.03	1.72	3.29	2.08	-2.28	0.21
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	rpoZ	K0N5T7	0.45	-0.21	0.87	0.13	0.08	1.06	0.66	-0.31	0.81	2.96	-3.26	0.10	0.99	-0.29	0.82
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	rpoA	K0N7E5	0.10	-0.04	0.97	2.83	-0.40	0.76	1.67	-0.34	0.79	2.51	-0.72	0.61	0.97	0.36	1.28
RNA polymerase sigma factor SigA	RNA polymerase	rpoD,sigA	K0NAV6	0.32	-0.39	0.76	0.42	-0.51	0.70	0.43	-0.51	0.70	0.41	-0.71	0.61	0.17	0.12	1.09
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	rpoE	K0N7L4	1.11	0.22	1.17	0.78	-0.27	0.83	0.80	-0.27	0.83	1.59	-0.42	0.75	1.42	0.49	1.41
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	rpoC	K0NAN3	0.49	-0.08	0.94	3.10	-0.59	0.66	2.99	-0.60	0.66	0.17	0.04	1.03	3.43	0.51	1.42

DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	rpoB	K0MXV4	0.02	0.01	1.00	4.89	-0.64	0.64	2.70	-0.44	0.74	1.54	0.40	1.32	2.92	0.65	1.56
Transcriptional regulator, TetR family	Transcriptional regulation		K0MUM1	2.84	-0.41	0.75	2.68	-0.56	0.68	2.88	-0.69	0.62	2.70	-3.52	0.09	1.05	0.15	1.11
Transcriptional regulator	Transcriptional regulation		K0N551	1.90	-0.59	0.66	2.46	0.88	1.84	0.21	0.14	1.10	1.63	-2.33	0.20	4.20	-1.47	0.36
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	phoU	K0MTZ9	1.83	-0.70	0.62	2.63	0.97	1.95	0.16	0.09	1.07	2.35	-2.26	0.21	4.04	-1.67	0.31
Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	rp2	K0N598	0.68	0.29	1.22	2.08	0.95	1.93	2.00	1.00	2.00	2.68	-2.16	0.22	2.63	-0.66	0.63
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	rex_2,rex	K0NBZ5	0.70	-1.64	0.32	1.30	0.81	1.75	0.81	0.62	1.53	1.97	-1.31	0.40	1.11	-2.45	0.18
HTH-type transcriptional repressor yvoA	Transcriptional regulation	yvoA_2	K0N9L8	0.04	-0.04	0.97	1.50	1.20	2.30	0.30	-0.23	0.85	1.15	-0.91	0.53	1.82	-1.24	0.42
Transcriptional regulator, xre family	Transcriptional regulation		K0N6Y7	0.00	0.00	1.00	1.52	0.61	1.53	1.11	0.52	1.44	2.12	-0.88	0.54	0.97	-0.61	0.66
Glucitol operon repressor	Transcriptional regulation	srlR	K0MYG3	0.38	-0.89	0.54	1.74	0.45	1.37	1.55	0.43	1.35	2.37	-0.72	0.61	0.62	-1.34	0.40
Probable catabolite control protein A	Transcriptional regulation	ccpA	K0N323	0.23	0.07	1.05	0.66	0.17	1.12	1.45	0.30	1.23	1.21	-0.69	0.62	0.42	-0.10	0.93
Transcriptional regulator	Transcriptional regulation		K0N6I4	0.44	-0.25	0.84	2.48	-0.28	0.82	0.61	0.25	1.19	0.99	-0.66	0.63	0.05	0.04	1.02
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	ohrR	K0N3J7	1.50	-0.61	0.66	0.02	-0.01	1.00	0.40	-0.33	0.79	0.28	-0.14	0.91	1.54	-0.60	0.66
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		K0N3Z3	0.38	0.21	1.16	1.40	-0.71	0.61	0.92	-0.55	0.68	0.14	-0.08	0.95	2.07	0.93	1.90
Transcriptional regulator lytR	Transcriptional regulation	lytR_3	K0N6U3	0.59	-0.49	0.71	0.23	0.07	1.05	2.64	1.21	2.32	1.13	0.32	1.25	0.71	-0.56	0.68
MerR family transcriptional regulator	Transcriptional regulation		K0N833	1.28	-0.73	0.60	5.24	-7.06	0.01	5.41	-7.33	0.01	1.06	0.48	1.39	4.75	6.33	80.64
Transcriptional regulator, XRE family	Transcriptional regulation		K0NDP4	0.52	-0.33	0.79	0.02	-0.01	0.99	0.28	-0.14	0.91	2.54	0.85	1.81	0.41	-0.32	0.80
Pur operon repressor	Transcriptional regulation	purR_2	K0N7M9	0.03	0.04	1.03	0.48	-0.70	0.61	0.57	-0.81	0.57	1.03	1.32	2.49	0.75	0.74	1.67
Uncharacterized protein	Transcriptional regulation		K0N6Q3	0.33	-1.09	0.47	0.92	0.24	1.18	0.62	-0.29	0.82	1.85	1.45	2.73	0.42	-1.33	0.40
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	nrnA	K0N309	0.00	0.00	1.00	0.01	0.00	1.00	0.35	0.08	1.06	2.62	-3.77	0.07	0.01	0.00	1.00

Uncharacterized protein	RNA degradation		K0MVC2	0.58	1.09	2.13	0.43	0.84	1.79	0.38	0.77	1.71	0.20	-0.44	0.74	1.01	0.25	1.19
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	rnjA	K0NAH6	0.03	-0.01	0.99	0.39	0.06	1.04	0.56	0.16	1.12	0.84	0.23	1.17	0.19	-0.08	0.95
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	rny	K0N3E5	0.61	-0.90	0.54	0.70	0.33	1.25	3.47	0.92	1.89	2.69	1.78	3.44	0.82	-1.23	0.43
Cold shock protein 1	Transcription-associated proteins	csp	K0MT67	1.26	1.49	2.81	0.03	-0.05	0.97	0.66	0.72	1.65	0.79	-2.07	0.24	1.88	1.54	2.90
Cold shock protein CspA	Transcription-associated proteins	cspA	K0NAH0	0.26	-0.50	0.71	0.02	0.01	1.00	0.43	0.17	1.13	2.58	-1.35	0.39	0.26	-0.50	0.71
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	nusB	K0NB49	0.50	-0.50	0.71	1.26	-0.20	0.87	0.15	0.06	1.04	1.14	-1.08	0.47	0.28	-0.30	0.81
Cold shock-like protein CspLA	Transcription-associated proteins	cspLA	K0N438	0.50	0.82	1.77	0.12	0.17	1.12	0.27	0.27	1.20	0.74	-0.64	0.64	0.40	0.66	1.57
Transcription termination/antitermination protein NusG	Transcription-associated proteins	nusG	K0N730	0.77	0.27	1.20	1.04	-0.63	0.65	0.95	-0.62	0.65	1.66	0.55	1.46	1.53	0.90	1.86
Transcription termination/antitermination protein NusA	Transcription-associated proteins	nusA	K0N927	1.64	0.11	1.08	2.35	-0.50	0.71	1.67	-0.38	0.77	5.98	0.65	1.57	2.58	0.62	1.53
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	greA	K0NB62	0.63	0.12	1.09	1.60	-0.36	0.78	0.08	-0.03	0.98	3.39	0.85	1.80	2.26	0.48	1.40
50S ribosomal protein L33	Ribosomal proteins	rpmG	K0N697	1.01	-0.37	0.78	2.44	-0.91	0.53	0.90	-0.46	0.73	1.74	-5.11	0.03	1.23	0.54	1.46
50S ribosomal protein L16	Ribosomal proteins	rplP	K0N863	0.61	0.28	1.21	1.69	-0.76	0.59	1.76	-0.92	0.53	4.07	-3.95	0.06	3.74	1.04	2.06
30S ribosomal protein S14 type Z	Ribosomal proteins	rpsZ,rpsN	K0MXS9	0.00	0.00	1.00	0.98	-0.63	0.65	1.31	-1.06	0.48	3.38	-3.90	0.07	0.98	0.62	1.54
50S ribosomal protein L29	Ribosomal proteins	rpmC	K0MXT6	0.29	0.03	1.02	2.83	-0.50	0.71	2.83	-0.51	0.70	5.78	-3.79	0.07	2.84	0.53	1.45
50S ribosomal protein L20	Ribosomal proteins	rplT	K0N5Y4	0.19	-0.07	0.96	2.38	-0.81	0.57	1.86	-0.55	0.68	4.41	-3.65	0.08	3.32	0.74	1.67
50S ribosomal protein L24	Ribosomal proteins	rplX	K0N7F9	0.05	-0.03	0.98	0.91	-0.35	0.78	0.93	-0.40	0.76	4.13	-3.36	0.10	1.28	0.32	1.25
50S ribosomal protein L2	Ribosomal proteins	rplB	K0MXU1	0.56	-0.17	0.89	2.99	-0.73	0.60	2.76	-0.65	0.64	3.28	-2.89	0.14	2.06	0.57	1.48
50S ribosomal protein L31 type B	Ribosomal proteins	rpmE2	K0NCV4	0.10	-0.07	0.95	0.57	-0.23	0.85	1.48	-0.51	0.70	4.14	-2.70	0.15	0.23	0.16	1.12
50S ribosomal protein L32	Ribosomal proteins	rpmF	K0N4T0	0.41	-0.83	0.56	1.01	-1.95	0.26	0.70	-1.33	0.40	1.57	-2.51	0.18	0.70	1.12	2.17

50S ribosomal protein L6	Ribosomal proteins	rplF	K0NCK5	0.31	0.07	1.05	3.52	-0.89	0.54	3.02	-0.76	0.59	5.46	-2.43	0.19	3.13	0.96	1.95
30S ribosomal protein S15	Ribosomal proteins	rpsO	K0N4Q6	0.46	-0.21	0.87	2.07	-0.94	0.52	0.99	-0.50	0.71	3.47	-2.40	0.19	2.97	0.74	1.67
30S ribosomal protein S20	Ribosomal proteins	rpsT	K0N4X9	0.71	-0.33	0.80	2.10	-0.81	0.57	1.05	-0.62	0.65	4.20	-2.37	0.19	0.93	0.48	1.39
30S ribosomal protein S14	Ribosomal proteins	rpsN	K0N3D1	0.54	-0.35	0.79	0.42	0.48	1.39	0.53	0.38	1.30	2.86	-2.32	0.20	0.95	-0.82	0.56
50S ribosomal protein L27	Ribosomal proteins	rpmA	K0NB51	0.03	-0.05	0.97	0.54	-0.35	0.78	0.79	-0.55	0.68	2.95	-2.27	0.21	0.30	0.30	1.23
30S ribosomal protein S7	Ribosomal proteins	rpsG	K0NAM9	0.36	-0.06	0.96	2.26	-0.55	0.68	2.12	-0.60	0.66	4.69	-2.14	0.23	1.81	0.49	1.41
30S ribosomal protein S6	Ribosomal proteins	rpsF	K0N0Z1	0.30	0.09	1.07	2.02	-0.57	0.67	1.34	-0.38	0.77	3.79	-2.09	0.23	2.74	0.66	1.58
50S ribosomal protein L1	Ribosomal proteins	rplA	K0N7M7	0.80	-0.13	0.92	3.09	-0.84	0.56	2.26	-0.64	0.64	4.60	-2.01	0.25	3.55	0.71	1.64
30S ribosomal protein S3	Ribosomal proteins	rpsC	K0N7G5	0.29	0.11	1.08	1.44	-0.62	0.65	1.56	-0.85	0.56	2.75	-1.98	0.25	1.63	0.73	1.66
50S ribosomal protein L4	Ribosomal proteins	rplD	K0N7H0	0.13	-0.04	0.97	3.36	-0.86	0.55	2.34	-0.80	0.58	3.68	-1.97	0.25	3.12	0.82	1.76
30S ribosomal protein S12	Ribosomal proteins	rpsL	K0MXV0	0.75	-0.14	0.91	2.41	-0.79	0.58	1.76	-0.62	0.65	3.34	-1.94	0.26	2.46	0.65	1.57
50S ribosomal protein L19	Ribosomal proteins	rplS	K0NB12	0.75	0.15	1.11	2.58	-0.61	0.65	2.04	-0.68	0.63	4.58	-1.91	0.27	3.52	0.77	1.70
30S ribosomal protein S17	Ribosomal proteins	rpsQ	K0NAL6	0.25	0.21	1.16	2.61	-0.85	0.55	3.16	-0.80	0.57	3.79	-1.88	0.27	1.46	1.06	2.09
50S ribosomal protein L35	Ribosomal proteins	rpmI	K0N5P1	1.17	-0.47	0.72	1.99	-0.85	0.56	2.40	-0.70	0.62	2.60	-1.82	0.28	0.77	0.38	1.30
30S ribosomal protein S2	Ribosomal proteins	rpsB	K0N936	0.59	0.13	1.09	2.13	-0.50	0.71	2.73	-0.55	0.68	3.83	-1.75	0.30	2.43	0.62	1.54
50S ribosomal protein L21	Ribosomal proteins	rplU	K0MW61	0.04	-0.09	0.94	0.75	-1.04	0.49	0.81	-0.95	0.52	0.80	-1.75	0.30	0.53	0.94	1.92
50S ribosomal protein L30	Ribosomal proteins	rpmD	K0MXS6	1.91	-0.23	0.85	3.76	-0.86	0.55	3.25	-0.88	0.54	3.24	-1.66	0.32	3.15	0.63	1.55
30S ribosomal protein S19	Ribosomal proteins	rpsS	K0NAM1	0.38	-0.12	0.92	2.29	-0.70	0.61	1.87	-0.92	0.53	3.10	-1.28	0.41	3.00	0.59	1.50
50S ribosomal protein L17	Ribosomal proteins	rplQ	K0N841	0.06	-0.10	0.93	1.50	-1.09	0.47	1.15	-1.00	0.50	1.26	-1.17	0.44	0.91	0.99	1.98
30S ribosomal protein S4	Ribosomal proteins	rpsD	K0MV63	0.10	-0.02	0.98	3.73	-0.75	0.59	3.14	-0.66	0.63	3.42	-1.14	0.45	2.75	0.73	1.66
50S ribosomal protein L14	Ribosomal proteins	rplN	K0NCL3	0.25	0.05	1.04	2.35	-0.63	0.64	2.72	-0.66	0.63	4.18	-1.14	0.45	2.58	0.68	1.61
50S ribosomal protein L23	Ribosomal proteins	rplW	K0N869	0.22	-0.11	0.92	2.40	-0.86	0.55	2.00	-0.79	0.58	2.59	-1.12	0.46	2.11	0.74	1.68

50S ribosomal protein L5	Ribosomal proteins	rplE	K0N859	0.04	-0.01	1.00	3.36	-0.81	0.57	2.85	-0.75	0.59	4.42	-1.12	0.46	3.42	0.80	1.74
30S ribosomal protein S11	Ribosomal proteins	rpsK	K0NCJ0	0.49	-0.28	0.82	1.95	-0.94	0.52	1.75	-0.99	0.50	2.23	-1.11	0.46	1.95	0.65	1.57
50S ribosomal protein L9	Ribosomal proteins	rplI	K0N4K3	1.11	-0.26	0.84	0.46	0.16	1.11	0.09	-0.04	0.97	2.56	-1.08	0.47	1.09	-0.41	0.75
50S ribosomal protein L3	Ribosomal proteins	rplC	K0NCN1	0.38	-0.07	0.95	2.58	-0.69	0.62	2.36	-0.66	0.63	2.40	-1.03	0.49	2.30	0.62	1.53
30S ribosomal protein S5	Ribosomal proteins	rpsE	K0N853	0.47	-0.17	0.89	2.57	-0.81	0.57	2.21	-0.89	0.54	2.51	-1.03	0.49	2.37	0.64	1.56
30S ribosomal protein S21	Ribosomal proteins	rpsU	K0N5E5	0.04	-0.02	0.99	2.95	-0.96	0.51	1.39	-0.52	0.70	2.26	-0.98	0.51	2.39	0.94	1.92
30S ribosomal protein S16	Ribosomal proteins	rpsP	K0N5H1	0.24	0.26	1.20	0.43	-0.39	0.76	0.48	-0.44	0.74	1.04	-0.88	0.54	0.90	0.65	1.57
30S ribosomal protein S18	Ribosomal proteins	rpsR	K0N6T2	0.05	-0.09	0.94	0.77	-1.20	0.44	0.58	-1.05	0.48	0.70	-0.86	0.55	0.76	1.11	2.16
50S ribosomal protein L13	Ribosomal proteins	rplM	K0N828	0.02	0.01	1.00	2.71	-0.80	0.58	2.71	-0.86	0.55	3.51	-0.80	0.58	2.83	0.80	1.74
50S ribosomal protein L18	Ribosomal proteins	rplR	K0N7F4	0.29	0.12	1.08	1.66	-0.85	0.55	1.59	-0.72	0.61	1.71	-0.77	0.59	2.15	0.97	1.96
30S ribosomal protein S13	Ribosomal proteins	rpsM	K0NAK3	0.38	-0.20	0.87	1.79	-0.85	0.55	1.81	-0.85	0.56	0.92	-0.50	0.71	2.80	0.66	1.58
50S ribosomal protein L22	Ribosomal proteins	rplV	K0NCM1	0.16	0.06	1.04	3.35	-0.68	0.62	2.25	-0.65	0.64	1.89	-0.44	0.74	2.54	0.74	1.67
50S ribosomal protein L10	Ribosomal proteins	rplJ	K0MXD8	1.06	-0.11	0.92	3.66	-0.85	0.56	3.12	-0.84	0.56	1.56	-0.31	0.81	4.15	0.73	1.66
30S ribosomal protein S8	Ribosomal proteins	rpsH	K0NAL1	0.06	-0.03	0.98	1.96	-0.95	0.52	2.06	-0.82	0.57	0.61	-0.21	0.86	2.28	0.92	1.90
30S ribosomal protein S9	Ribosomal proteins	rpsI	K0MXR0	0.50	-0.14	0.91	2.41	-0.94	0.52	1.08	-0.58	0.67	0.55	-0.16	0.90	2.45	0.80	1.74
50S ribosomal protein L15	Ribosomal proteins	rplO	K0NAK7	0.12	-0.06	0.96	2.22	-0.69	0.62	1.69	-0.53	0.69	0.52	-0.14	0.91	1.80	0.63	1.55
30S ribosomal protein S10	Ribosomal proteins	rpsJ	K0NAM5	0.22	-0.04	0.97	2.52	-0.72	0.61	2.31	-0.72	0.61	0.27	-0.09	0.94	2.63	0.68	1.60
50S ribosomal protein L11	Ribosomal proteins	rplK	K0N724	0.55	-0.14	0.91	2.51	-0.96	0.51	1.96	-0.73	0.60	2.00	0.47	1.39	2.55	0.83	1.77
30S ribosomal protein S1 homolog	Ribosomal proteins	ypfD	K0NAL9	0.28	-0.15	0.90	1.47	-0.36	0.78	0.87	-0.33	0.79	2.41	0.61	1.53	0.41	0.21	1.16
50S ribosomal protein L7/L12	Ribosomal proteins	rplL	K0NA98	4.79	0.72	1.65	1.73	-0.58	0.67	0.47	-0.12	0.92	4.32	1.01	2.01	2.97	1.30	2.46
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	glyS	K0N5D3	0.52	0.10	1.07	2.42	-0.59	0.67	1.86	-0.56	0.68	3.16	-4.37	0.05	2.45	0.68	1.61
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	aspS	K0N5F3	0.08	0.03	1.02	1.91	-0.74	0.60	2.02	-0.70	0.62	4.00	-3.71	0.08	1.83	0.77	1.71

Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	ileS	K0N4L9	0.80	0.34	1.26	0.91	-0.39	0.76	0.90	-0.38	0.77	1.72	-3.46	0.09	1.59	0.73	1.65
Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	leuS	K0N3A9	1.02	0.27	1.21	0.36	-0.06	0.96	0.49	-0.06	0.96	1.37	-3.38	0.10	1.22	0.33	1.26
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	pheT	K0N5M4	0.10	-0.04	0.98	0.88	-0.24	0.84	0.23	0.07	1.05	3.80	-2.89	0.13	1.01	0.21	1.16
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	pheS	K0NB64	0.50	-0.14	0.91	1.59	-0.36	0.78	0.02	-0.01	0.99	4.50	-2.22	0.21	0.61	0.22	1.16
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	cysS	K0NAB2	0.38	0.16	1.12	1.31	0.23	1.18	0.42	0.19	1.14	2.35	-2.06	0.24	0.14	-0.07	0.95
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	gatA	K0N3Z6	0.04	0.01	1.01	0.04	0.01	1.01	0.34	-0.07	0.96	3.61	-1.84	0.28	0.01	0.00	1.00
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	trpS	K0N7S4	0.33	-0.09	0.94	0.87	-0.25	0.84	0.35	-0.14	0.91	1.29	-1.77	0.29	0.44	0.16	1.12
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatB	K0NA01	0.04	-0.01	0.99	0.39	0.13	1.10	0.20	0.06	1.04	4.54	-1.75	0.30	0.38	-0.14	0.90
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	serS	K0N9N4	1.70	0.44	1.35	1.54	-0.35	0.79	0.04	-0.01	0.99	3.54	-1.65	0.32	3.30	0.78	1.72
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	thrS	K0N5P5	0.05	0.00	1.00	4.79	-0.52	0.70	2.51	-0.31	0.81	5.05	-1.57	0.34	6.25	0.52	1.43
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	proS	K0N5E2	1.12	0.19	1.14	2.20	-0.54	0.69	1.30	-0.29	0.82	3.12	-1.48	0.36	3.48	0.73	1.66
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	alaS	K0N6K2	0.63	-0.18	0.88	1.58	-0.45	0.73	0.98	-0.32	0.80	1.75	-1.05	0.48	0.70	0.28	1.21
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	gatC	K0N436	0.70	0.12	1.09	0.07	0.02	1.01	0.88	0.43	1.35	2.21	-0.52	0.70	0.51	0.10	1.07
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	asnS	K0N569	1.47	0.66	1.58	0.86	-0.39	0.76	0.71	-0.43	0.74	0.26	0.24	1.18	3.12	1.06	2.08
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	gltX	K0NC38	0.09	0.03	1.02	2.13	-0.65	0.64	1.01	-0.32	0.80	0.61	0.26	1.19	2.47	0.67	1.60
Protein hit	tRNA aminoacyl synthesis	hit	K0MWA8	1.74	0.74	1.67	2.22	0.97	1.96	1.68	1.00	2.00	2.36	1.07	2.10	0.84	-0.23	0.85

Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	valS	K0N4J6	0.09	0.01	1.01	0.62	-0.26	0.83	0.21	-0.08	0.94	3.79	1.24	2.36	0.63	0.27	1.21
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	argS	K0NB86	0.03	0.01	1.01	2.16	-0.69	0.62	1.23	-0.41	0.75	3.19	1.34	2.53	2.14	0.70	1.62
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	lysS	K0NAN7	0.64	0.29	1.22	0.75	-0.27	0.83	0.33	-0.16	0.90	2.58	1.52	2.87	1.27	0.56	1.47
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	hisS	K0N5A0	0.49	0.15	1.11	2.42	-0.84	0.56	1.78	-0.59	0.67	3.54	1.58	2.98	3.28	1.00	2.00
>tr|K0N6A9|K0N6A9_LACCA Tyrosine--tRNA ligase OS=Lactobacillus casei W56 GN=tyrS PE=4 SV=1	tRNA aminoacyl synthesis	tyrS	K0N6A9	0.12	0.05	1.04	1.69	-0.65	0.64	0.34	-0.20	0.87	2.53	-2.52	0.17	1.80	0.70	1.63
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	metG	K0NAU5	1.15	-0.41	0.75	1.83	-0.28	0.82	1.86	-0.31	0.81	4.15	1.60	3.04	0.32	-0.12	0.92
Translation initiation factor IF-1	Protein translation (initiation)	infA	K0N847	0.40	0.20	1.15	1.41	-0.52	0.69	0.11	-0.07	0.95	3.39	-2.82	0.14	1.36	0.73	1.66
Translation initiation factor IF-3	Protein translation (initiation)	infC	K0NB73	0.68	-0.22	0.86	2.38	-0.88	0.54	2.33	-0.96	0.51	3.22	-1.67	0.31	2.30	0.66	1.58
Translation initiation factor IF-2	Protein translation (initiation)	infB	K0N5K7	0.53	-0.14	0.91	1.93	-0.68	0.62	1.52	-0.56	0.68	1.73	0.58	1.50	2.04	0.55	1.46
Elongation factor P	Protein translation (elongation)	efp_2	K0N712	0.07	-0.07	0.95	1.86	1.01	2.01	1.69	0.87	1.83	0.14	-0.10	0.93	1.28	-1.08	0.47
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	tuf	K0N4R1	0.77	0.15	1.11	2.34	-0.31	0.80	1.68	-0.25	0.84	2.09	0.20	1.15	2.19	0.46	1.38
Elongation factor P	Protein translation (elongation)	efp	K0MW57	1.22	0.39	1.31	0.39	-0.11	0.93	0.23	-0.10	0.93	2.88	1.01	2.02	1.84	0.50	1.41
Elongation factor G (EF-G)	Protein translation (elongation)	fusA	K0NCN8	2.11	0.22	1.16	4.70	-0.81	0.57	3.34	-0.80	0.57	3.73	1.13	2.18	4.91	1.03	2.04
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	typA	K0N4W9	0.11	0.04	1.03	3.76	-0.87	0.55	3.56	-0.96	0.52	3.02	1.17	2.26	2.88	0.91	1.88
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	tsf	K0NB01	0.05	0.01	1.01	1.44	-0.34	0.79	0.70	-0.23	0.85	3.77	1.38	2.60	1.72	0.35	1.27
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	map	K0N7E0	0.04	-0.02	0.99	0.42	-0.13	0.91	0.15	-0.06	0.96	3.43	-2.49	0.18	0.49	0.11	1.08

Ribosome-binding ATPase YchF	Protein translation (peptide release)	engD,ychF	K0N7F7	0.09	-0.01	0.99	2.56	-0.42	0.75	1.99	-0.42	0.75	4.06	-1.13	0.46	2.72	0.40	1.32
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	def	K0N4N6	0.05	0.02	1.02	1.86	-0.29	0.82	0.13	-0.04	0.97	3.26	-1.11	0.46	0.98	0.32	1.24
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	frr	K0N5M3	2.83	-0.57	0.67	0.36	0.09	1.07	0.08	0.04	1.03	3.66	0.83	1.78	2.70	-0.67	0.63
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	prfB	K0N6W9	0.61	-0.17	0.89	1.76	-0.69	0.62	1.94	-0.67	0.63	2.89	1.13	2.19	1.65	0.52	1.43
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	prfA	K0N4C6	0.25	-0.12	0.92	0.59	-0.16	0.89	0.16	-0.09	0.94	3.50	1.45	2.74	0.09	0.04	1.03

Annexure 4: Master table CFE containing –log p values, t test difference and fold change of all conditions of Experiment P2

Protein names	Function	Gene	Protein IDs	Tween 80 Vs control			Citrate Vs control			Tween 80 Vs citrate		
				-log t test p value	t-test Difference	Fold change	-log t test p value	t-test Difference	Fold change	-log t test p value	t-test Difference	Fold change
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	late peptidoglycan biosynthesis	ddl	K0MRY4	1.72	-0.50	0.71	1.78	-0.38	0.77	0.42	-0.12	0.92
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	late peptidoglycan biosynthesis	dacA	K0MS53	0.94	2.01	4.03	0.70	1.54	2.91	2.23	0.47	1.38
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	late peptidoglycan biosynthesis	murE	K0N1S5	0.94	0.26	1.20	2.63	1.34	2.53	2.46	-1.08	0.47
UDP-glucose 4-epimerase (EC 5.1.3.2)	teichoic acid decoration	galE	K0N2R3	0.47	0.23	1.18	1.44	0.73	1.66	1.57	-0.50	0.71
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	teichoic acid D-alanylation	dltA	K0MTN0	0.89	0.97	1.96	1.19	1.17	2.25	0.27	-0.20	0.87
Phosphoglucosamine mutase (EC 5.4.2.10)	early peptidoglycan biosynthesis	glmM	K0N3Y7	1.74	0.96	1.95	1.73	0.72	1.65	0.44	0.24	1.18
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	early peptidoglycan biosynthesis	glmS	K0N3V9	0.14	0.06	1.04	2.60	0.85	1.80	2.62	-0.79	0.58
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	late peptidoglycan biosynthesis	murD	K0NAG5	0.05	-0.15	0.90	2.05	1.46	2.75	0.69	-1.61	0.33
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	teichoic acid decoration	rmlB	K0MWS0	0.68	1.24	2.36	0.84	1.49	2.82	0.75	-0.25	0.84
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	teichoic acid decoration		K0N6R1	0.24	0.15	1.11	0.17	0.11	1.08	0.10	0.04	1.03
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	exopolysaccharide biosynthesis	rmlB_2	K0NBN4	0.19	-0.07	0.95	1.24	-0.22	0.86	0.48	0.14	1.10
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	exopolysaccharide biosynthesis	BN194_21350	K0N6Q5	0.82	-0.75	0.59	0.71	-0.57	0.67	0.22	-0.18	0.88
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	early peptidoglycan biosynthesis	murA2, murA	K0NAR9	0.83	0.85	1.80	0.57	0.60	1.52	1.29	0.25	1.19
Bifunctional protein GlmU	early peptidoglycan biosynthesis	glmU	K0MY10	1.17	0.84	1.78	2.62	1.83	3.55	2.07	-0.99	0.50

>tr|K0N9X8|K0N9X8_LACCA SpsK protein OS=Lactobacillus casei W56 GN=spsK PE=4 SV=1;>tr|K0N6D6|K0N6D6_LACCA SpsK_2 protein OS=Lactobacillus casei W56 GN=spsK_2 PE=4 SV=1	Cell wall biogenesis	spsK	K0N9X8;K0N6D6	1.35	0.96	1.94	0.71	0.55	1.46	1.01	0.41	1.33
>tr|K0N699|K0N699_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA PE=3 SV=1;>tr|K0MWW4|K0MWW4_LACCA Glucose-1-phosphate thymidylyltransferase OS=Lactobacillus casei W56 GN=rmlA_2 PE=3 SV=1	Cell wall biogenesis	rmlA	K0N699;K0MWW4	1.75	-0.93	0.53	0.29	-0.19	0.88	1.64	-0.74	0.60
Regulatory protein vanR	cell wall alteration signalling	vanR	K0N7G4	0.16	-0.18	0.88	0.89	0.80	1.75	2.83	-0.99	0.50
Sensor protein CiaH (EC 2.7.13.3)	unknown signal transduction	ciaH	K0N319	1.40	3.30	9.82	0.37	-0.61	0.65	1.53	3.91	15.04
UPF0478 protein SAOUHSC_01855	chemotaxis?		K0N365	1.26	-0.48	0.72	0.23	-0.10	0.93	2.30	-0.38	0.77
Uncharacterized transcriptional regulatory protein yclJ	unknown signal transduction	yclJ	K0MUE5	0.15	-0.19	0.88	1.04	0.81	1.75	1.24	-1.00	0.50
Universal stress protein	stress regulation?		K0NAC5	0.69	0.46	1.38	2.18	1.51	2.85	2.86	-1.05	0.48
Response regulator ArlR	oxidative stress sensing?	arlR	K0N5X3	1.02	2.19	4.55	0.76	1.79	3.45	0.26	0.40	1.32
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	ATP synthesis, H+ extrusion	atpA	K0N4K1	2.16	-0.36	0.78	2.86	-0.98	0.51	2.42	0.62	1.54
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	ATP synthesis, H+ extrusion	atpG	K0N4D3	0.95	1.85	3.61	0.02	0.06	1.04	3.65	1.80	3.47
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	ATP synthesis, H+ extrusion	atpD	K0NAB3	1.58	-0.37	0.77	2.44	-0.92	0.53	1.82	0.55	1.46
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	ATP synthesis	ppaC	K0N4Z4	1.48	-0.45	0.73	0.54	-0.29	0.82	0.31	-0.15	0.90
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	electron transport		K0N9E0	0.31	0.25	1.19	0.46	0.34	1.27	0.78	-0.10	0.94
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	electron transport	yjlD	K0NAA7	0.04	0.08	1.06	0.48	0.76	1.69	0.96	-0.68	0.62
Polyphosphate kinase (EC 2.7.4.1) (ATP-polyphosphate phosphotransferase) (Polyphosphoric acid kinase)	polyphopshate conversion to/from ATP	ppk	K0ND10	0.35	-0.39	0.77	0.94	1.00	2.00	1.55	-1.39	0.38
UPF0092 membrane protein yrbF	protein secretion: Sec system (insertion)	yrbF	K0MTL6	1.40	-0.65	0.64	0.90	-0.99	0.50	0.27	0.35	1.27
Protein translocase subunit SecA	protein secretion: Sec system (trafficking)	secA	K0N9J2	2.52	0.81	1.75	1.96	0.80	1.74	0.02	0.01	1.01
Signal recognition particle protein (Fifty-four homolog)	protein secretion; SRP pathway (trafficking)	ffh	K0NB27	1.72	-0.96	0.51	0.15	0.13	1.10	1.87	-1.09	0.47
Signal recognition particle receptor FtsY (SRP receptor)	protein secretion; SRP pathway (trafficking)	ftsY	K0N5R8	0.39	-1.28	0.41	0.53	-0.36	0.78	0.27	-0.92	0.53

Stage 0 sporulation protein J	cell division (chromosomal segegration)	spo0J	K0N1F9	0.86	-0.30	0.81	1.04	0.53	1.44	1.46	-0.83	0.56
Cell division ATP-binding protein FtsE	cell division; divisome complex	ftsE	K0MTZ2	0.07	-0.07	0.95	0.23	0.21	1.16	0.70	-0.28	0.82
MreB-like protein	cell division; cell shape directing complex	mbl	K0N4K5	1.80	-1.19	0.44	1.47	-0.70	0.62	1.06	-0.49	0.71
Rod shape-determining protein MreB	cell division; cell shape directing complex	mreB	K0N4R7	1.57	1.19	2.27	2.00	1.72	3.29	1.66	-0.53	0.69
Cell division protein FtsA	cell division; divisome complex	ftsA	K0N4T3	0.12	-0.15	0.90	0.42	0.57	1.48	0.95	-0.72	0.61
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	L-threonine biosynthesis; L-lysine biosynthesis; L-methionine biosynthesis	asd	K0N1I5	0.01	-0.01	0.99	0.59	0.42	1.34	0.92	-0.43	0.74
Aspartate racemase (EC 5.1.1.13)	metabolism of aspartate		K0N7H2	2.27	1.46	2.76	0.55	0.70	1.62	0.71	0.76	1.70
Oligoendopeptidase F homolog (EC 3.4.24.-)	peptidase for amino acid acquistion	yjbG	K0N560	0.03	-0.05	0.96	0.47	-0.61	0.65	2.62	0.56	1.47
Aminopeptidase N (EC 3.4.11.2)	peptidase for amino acid acquistion	pepN	K0N2F5	1.11	1.49	2.81	0.36	0.51	1.42	2.06	0.98	1.97
Cysteine synthase (EC 2.5.1.47)	L-cysteine biosynthesis	cysK	K0N8E6	1.96	-1.82	0.28	2.56	-1.39	0.38	0.54	-0.43	0.74
Oligoendopeptidase F	peptidase for amino acid acquistion	yjbG_2	K0N6H7	1.59	-0.40	0.76	1.06	-0.32	0.80	0.28	-0.08	0.95
Xaa-Pro dipeptidase (EC 3.4.13.9)	peptidase for amino acid acquistion	pepQ	K0MTP0	0.81	1.60	3.04	0.55	1.14	2.21	1.88	0.46	1.37
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	peptidase for amino acid acquistion	pepV	K0N324	0.51	0.13	1.10	1.58	0.33	1.25	0.68	-0.19	0.88
Oligoendopeptidase, pepF/M3 family	peptidase for amino acid acquistion		K0N779	0.39	-0.17	0.89	1.25	-0.40	0.76	0.90	0.23	1.17
Probable dipeptidase (EC 3.4.-.-)	peptidase for amino acid acquistion		K0N7S0	1.57	0.40	1.32	0.85	-0.17	0.89	2.83	0.57	1.48
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	glycine biosynthesis; folate biosynthesis; one carbon pool by folate	glyA	K0MV12	0.79	1.39	2.62	1.22	2.09	4.25	1.82	-0.70	0.62
Glycine cleavage system H protein	glycine cleavage system	gcvH	K0N4K8	0.36	0.55	1.46	0.40	0.60	1.51	0.17	-0.05	0.97
Neutral endopeptidase (EC 3.4.24.-)	peptidase for amino acid acquistion	pepO_2	K0N8Q0	0.63	-0.34	0.79	1.55	-0.67	0.63	1.02	0.32	1.25
Aspartate aminotransferase (EC 2.6.1.1)	L-aspartate biosynthesis; L-	aspC	K0NAU6	2.91	0.74	1.67	1.81	0.26	1.20	2.68	0.48	1.39

	phenylalanine/ L-tyrosine biosynthesis											
Glutamine synthetase (EC 6.3.1.2)	L-glutamine biosynthesis	glnA_2	K0MW64	2.23	1.23	2.35	1.34	0.66	1.58	3.13	0.57	1.48
Uncharacterized peptidase yuxL (EC 3.4.21.-)	peptidase for amino acid acquistion?	yuxL	K0N5X4	0.57	0.43	1.35	0.17	0.12	1.09	0.62	0.30	1.23
Probable dipeptidase B (EC 3.4.-.-)	peptidase for amino acid acquistion	pepDB	K0N678	0.19	-0.44	0.74	0.35	-0.22	0.86	0.09	-0.22	0.86
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	peptidase for amino acid acquistion	fpaP_3	K0N682	0.10	-0.11	0.93	2.28	1.43	2.70	1.59	-1.55	0.34
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	L-aspartate biosynthesis	asnB	K0MX90	0.98	-0.50	0.70	0.89	-0.50	0.71	0.01	0.00	1.00
Probable dipeptidase (EC 3.4.-.-)	peptidase for amino acid aquistion		K0MXA1	0.81	0.83	1.78	1.31	1.29	2.45	1.33	-0.46	0.73
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	succinate/GABA/aldehyde metabolism?	ssdA	K0MXE0	2.31	-0.66	0.63	0.41	-0.08	0.95	2.60	-0.58	0.67
Aminopeptidase C (EC 3.4.22.40)	peptidase for amino acid acquistion	pepC	K0NC50	0.64	-0.95	0.52	2.58	-1.26	0.42	0.18	0.31	1.24
Aminopeptidase C (EC 3.4.22.40)	peptidase for amino acid acquistion	pepC_2	K0NAC2	1.36	-0.31	0.81	2.13	-0.45	0.73	0.52	0.15	1.11
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	(deoxy)ribose 1-phosphate biosynthesis	deoC	K0N486	0.75	0.95	1.93	1.47	1.75	3.37	1.30	-0.81	0.57
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	adenosine/adenine/AMP biosynthesis	purA	K0N1J0	0.28	0.70	1.63	0.38	0.90	1.86	0.35	-0.19	0.87
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	guanosine/guanine/GMP biosynthesis	guaB	K0N1G3	0.45	-0.26	0.84	1.43	-0.80	0.57	1.77	0.54	1.46
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	(deoxy)ribose 1-phosphate biosynthesis	deoC_2,deoC	K0MSB5	0.44	0.93	1.90	0.60	1.18	2.26	0.43	-0.25	0.84
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	(deoxy)ribose 1-phosphate biosynthesis	deoB	K0N1N0	1.10	2.39	5.23	1.06	2.27	4.83	0.21	0.11	1.08
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	purine nucleoside interconversion/salvage	deoD	K0N1Z0	0.42	0.54	1.46	1.10	1.20	2.30	1.43	-0.66	0.63
Nucleoside diphosphate kinase (EC 2.7.4.6)	(deoxy)nucleotide biosynthesis except ATP	ndk	K0N340	0.33	0.43	1.35	0.19	-0.38	0.77	0.56	0.82	1.76
Uncharacterized hydrolase yutF (EC 3.-.-.-)	nucleoside salvage	yutF	K0N383	0.77	0.33	1.26	0.54	-0.13	0.91	1.15	0.46	1.38
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	GMP biosynthesis	xpt	K0MUR6	1.90	1.13	2.19	0.09	0.33	1.26	0.25	0.80	1.74
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	purine biosynthesis	purB	K0NA41	0.30	0.33	1.25	0.01	-0.01	0.99	0.75	0.34	1.26

Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	pyrimidine nucleoside salvage	upp	K0N4J8	3.17	1.08	2.11	2.43	0.46	1.38	2.56	0.62	1.54
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	deoxynucleotide biosynthesis for DNA	nrdE2	K0N5A1	0.70	0.89	1.85	1.38	1.73	3.32	2.68	-0.84	0.56
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	deoxynucleotide biosynthesis for DNA	nrdF	K0N552	2.57	-0.99	0.50	3.06	-0.92	0.53	0.19	-0.07	0.95
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	GMP/AMP biosynthesis	apt	K0N902	0.41	-0.56	0.68	0.07	0.11	1.08	0.79	-0.67	0.63
Uridylate kinase (EC 2.7.4.22)	uracil/uridine/UMP/UTP biosynthesis	pyrH	K0N5E6	1.60	1.73	3.31	1.52	1.69	3.23	0.04	0.04	1.03
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	UMP/uridine/uracil biosynthesis	pyrDA, pyrD	K0N623	0.02	0.05	1.03	1.10	0.85	1.80	0.44	-0.80	0.57
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	guanosine/guanine/GMP biosynthesis	guaA	K0NBJ2	2.22	0.72	1.64	0.69	0.21	1.15	4.49	0.51	1.42
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	DNA synthesis (keeps dUTP levels low)	dut	K0MXG3	0.98	1.47	2.77	0.85	1.24	2.37	0.52	0.22	1.17
Adenylate kinase (EC 2.7.4.3)	ADP biosynthesis; energy homeostasis	adk	K0N7F0	0.35	0.29	1.23	0.03	-0.04	0.97	0.32	0.33	1.26
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	CTP biosynthesis; nucleoside interconversion	pyrG	K0MXZ1	2.54	0.56	1.48	0.07	-0.03	0.98	2.32	0.59	1.50
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	purine biosynthesis	prs1,prs	K0NAT2	0.37	-0.12	0.92	0.16	0.07	1.05	0.60	-0.19	0.87
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	purine biosynthesis	prs1_2	K0NDQ5	0.71	0.76	1.69	1.66	1.73	3.31	2.78	-0.97	0.51
Oleate hydratase (EC 4.2.1.53)	fatty acid degradation or detoxification?	sph	K0N5Q0	0.77	1.91	3.75	0.23	0.68	1.60	1.91	1.23	2.35
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	phospholipid biosynthesis	gpsA	K0N3I2	0.82	0.96	1.95	1.57	1.84	3.57	3.10	-0.87	0.55
Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex (EC 2.3.1.168)	BCFA primer synthesis	bfmBB	K0N8M3	0.81	0.84	1.79	1.12	1.03	2.04	0.27	-0.19	0.88
2-oxoisovalerate dehydrogenase subunit beta (EC 1.2.4.4)	BCFA primer synthesis	bfmBAB	K0MVK8	3.01	1.31	2.48	4.13	1.36	2.56	0.13	-0.05	0.97
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	BCFA primer synthesis	bfmBC	K0N582	1.20	1.34	2.54	2.21	1.83	3.56	0.46	-0.49	0.71
Probable butyrate kinase (BK) (EC 2.7.2.7) (Branched-chain carboxylic acid kinase)	end-product formation	buk	K0N529	1.25	1.70	3.25	1.00	1.35	2.55	1.19	0.35	1.27
Phosphate butyryltransferase (EC 2.3.1.19)	end-product formation	ptb	K0NAS3	0.90	1.43	2.70	1.06	1.67	3.19	0.77	-0.24	0.85
Hydroxymethylglutaryl-CoA synthase	mevalonate pathway for isoprenoid backbones	hmgCS1	K0N9K3	2.06	1.32	2.50	2.02	1.14	2.20	0.48	0.19	1.14

Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	L-leucine/L-isoleucine /L-valine metabolism	ilvE	K0NBM4	0.44	-0.45	0.73	0.65	0.60	1.52	2.43	-1.06	0.48
Probable fatty acid methyltransferase (EC 2.1.1.-)	cyclopropane fatty acid synthesis		K0N6M0	0.26	0.50	1.41	1.10	1.80	3.49	3.27	-1.30	0.40
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	fatty acid biosynthesis	fabZ	K0NBS8	2.84	-3.47	0.09	4.22	3.59	12.06	4.11	-7.06	0.01
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	fatty acid biosynthesis	accB	K0NA35	1.05	-2.16	0.22	0.57	1.14	2.20	3.04	-3.29	0.10
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	fatty acid biosynthesis	fabF	K0MX40	3.17	-4.46	0.05	3.13	2.04	4.12	3.89	-6.51	0.01
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	fatty acid biosynthesis	bkr4	K0N799	0.44	-0.71	0.61	4.25	3.59	12.04	2.54	-4.30	0.05
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	fatty acid biosynthesis	fabG	K0N6N3	2.14	-3.36	0.10	0.15	0.19	1.14	2.27	-3.55	0.09
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	fatty acid biosynthesis	fabD	K0NBT1	0.90	-1.97	0.25	1.76	3.78	13.74	4.13	-5.75	0.02
Probable nitronate monooxygenase (EC 1.13.12.16)	fatty acid biosynthesis	fabK	K0NA38	3.63	-4.30	0.05	1.12	1.08	2.11	4.04	-5.38	0.02
Acyl carrier protein (ACP)	fatty acid biosynthesis	acpP_2 , acpP	K0MX45	0.97	-2.59	0.17	1.03	2.65	6.26	4.03	-5.23	0.03
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	fatty acid biosynthesis	fabH	K0N7B0	0.03	0.02	1.02	1.98	2.99	7.94	2.08	-2.97	0.13
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	fatty acid biosynthesis	fabZ_2	K0NBT3	2.84	-2.43	0.19	3.26	2.88	7.34	4.91	-5.30	0.03
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)	fatty acid biosynthesis	accC	K0N6M5	2.15	-1.73	0.30	3.22	3.00	8.01	5.08	-4.73	0.04
Uncharacterized protein MJ0282	vitamin B6 metabolism?		K0N1T2	1.57	2.42	5.35	0.03	0.17	1.13	0.66	2.25	4.75
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	thiamine biosynthesis	thiD_2	K0N2U9	0.06	-0.04	0.97	1.12	0.50	1.42	2.41	-0.54	0.69
Probable tRNA sulfurtransferase (EC 2.8.1.4) (Sulfur carrier protein ThiS sulfurtransferase) (Thiamine biosynthesis protein ThiI) (tRNA 4-thiouridine synthase)	tRNA modification; thiamine biosynthesis	thiI	K0N7Z7	0.27	-1.33	0.40	0.12	0.46	1.37	0.54	-1.79	0.29
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	tRNA modification; iron-cluster assembly; thiamine biosynthesis	iscS1	K0N4U8	0.94	0.59	1.50	1.71	1.10	2.14	1.92	-0.51	0.70
2-dehydropantoate 2-reductase (EC 1.1.1.169) (Ketopantoate reductase)	pantothenate/CoA biosynthesis		K0NAS0	3.72	1.58	2.98	5.12	1.07	2.10	1.82	0.51	1.42
Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	one carbon pool by folate	fhs	K0NAT0	0.16	0.29	1.23	0.73	1.11	2.16	2.70	-0.82	0.57
Lipoate--protein ligase (EC 2.7.7.63)	lipoate metabolism	lplJ	K0MVN0	0.20	0.26	1.20	1.29	1.40	2.63	3.74	-1.13	0.46
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	NAD(P)H biosynthesis	nadE	K0MWF6	1.04	0.35	1.27	0.00	0.00	1.00	1.99	0.35	1.27
Glutathione amide reductase (EC 1.8.1.16)	glutathione biosynthesis	garB	K0N8K3	0.38	0.13	1.09	1.92	0.70	1.62	2.47	-0.57	0.67

DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication elongation	dnaN	K0N6S3	1.64	1.60	3.03	2.40	2.63	6.21	3.28	-1.04	0.49
DNA gyrase subunit A (EC 5.99.1.3)	DNA topological change	gyrA	K0N6S7	0.04	0.33	1.26	0.00	0.04	1.03	1.17	0.29	1.22
Single-stranded DNA-binding protein (SSB)	DNA replication initiation; DNA repair (homologous recombination)	ssb	K0N1C2	0.62	1.00	2.00	0.75	1.15	2.21	0.19	-0.14	0.90
Replicative DNA helicase (EC 3.6.4.12)	DNA replication initiation	dnaC	K0MRW2	2.82	-1.12	0.46	2.66	-0.92	0.53	1.48	-0.20	0.87
DNA-binding protein HU	DNA topology change	hup	K0MVF4	1.45	1.25	2.38	1.56	1.39	2.61	0.39	-0.13	0.91
DNA polymerase I (EC 2.7.7.7)	DNA repair (multiple roles)	polA	K0N9E7	0.29	0.57	1.49	0.33	0.63	1.54	0.06	-0.05	0.96
DNA helicase (EC 3.6.4.12)	nucleotide excision, mismatch repair	helD	K0N9W3	3.09	1.70	3.24	2.65	1.47	2.77	0.51	0.22	1.17
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA modification	queA	K0N965	0.50	-1.10	0.47	0.48	-0.24	0.85	0.38	-0.86	0.55
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	ribosome processing (LSU); RNA chaperone	cshB	K0N356	0.13	-0.24	0.84	1.38	-0.52	0.70	0.14	0.27	1.21
Uncharacterized protein SE_0534	ribosome-associated (stabilisation); attenuates translation		K0N3F2	0.41	0.26	1.20	0.76	0.47	1.38	0.69	-0.21	0.87
Ribonuclease R (RNase R) (EC 3.1.13.1)	ribosomal RNA processing	rnr	K0N3S4	1.45	0.81	1.75	1.13	0.59	1.51	0.98	0.22	1.16
Ribosomal RNA small subunit methyltransferase H (EC 2.1.1.199) (16S rRNA m(4)C1402 methyltransferase) (rRNA (cytosine-N(4)-)-methyltransferase RsmH)	ribosomal RNA processing (SSU)	rsmH	K0N814	0.33	-0.37	0.77	0.36	0.23	1.17	0.60	-0.60	0.66
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	ribosomal RNA processing (SSU/LSU)	rnc	K0NB31	1.51	-1.35	0.39	0.53	0.51	1.42	4.93	-1.86	0.28
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	ribosomal RNA processing (LSU)	ysgA	K0N5M8	0.51	-0.72	0.61	0.00	0.00	1.00	0.53	-0.73	0.60
Ribosomal silencing factor RsfS	unknown ribosome-associated function	yqeL,rsfS	K0N5N6	3.09	1.62	3.07	0.02	-0.07	0.95	0.81	1.69	3.23
tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA modification	dus1	K0MXV9	0.24	0.20	1.15	0.72	0.53	1.45	1.23	-0.33	0.79
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	ribosome processing (LSU); RNA chaperone	cshA	K0N8C7	1.20	0.80	1.74	0.90	0.41	1.33	0.76	0.39	1.31
Thioredoxin reductase (EC 1.8.1.9)	thioredoxin reduction	trxB	K0N3L1	1.60	-0.83	0.56	1.14	-0.68	0.63	0.33	-0.16	0.90
[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)	activates citrate lyase via acetylation	citC	K0MWJ1	1.52	-1.87	0.27	0.32	-0.37	0.77	1.72	-1.49	0.36
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	protein folding		K0N387	0.20	-0.16	0.90	0.24	-0.16	0.90	0.00	0.00	1.00
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	recycling defective proteins; virulence	clpP_2, clpP	K0N3M4	2.67	-0.90	0.54	2.22	-0.67	0.63	0.75	-0.23	0.85

Trigger factor (TF) (EC 5.2.1.8) (PPIase)	nascent protein folding	tig	K0N884	1.92	1.02	2.02	1.44	0.67	1.59	0.97	0.35	1.28
Chaperone protein ClpB	recycling defective proteins	clpB	K0N4Z8	0.86	1.57	2.97	0.53	1.04	2.06	1.26	0.53	1.44
ATP-dependent protease ATPase subunit HslU	recycling defective proteins	hslU	K0N4Y1	0.40	-0.18	0.88	0.31	0.26	1.20	0.60	-0.45	0.73
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	nascent protein folding; protein rescue	dnaK	K0N5C7	0.44	-0.22	0.86	0.76	-0.33	0.79	0.33	0.11	1.08
Foldase protein PrsA (EC 5.2.1.8)	protein secretion: exported protein folding	prsA	K0N5Q8	3.29	-0.54	0.69	2.76	0.78	1.72	3.59	-1.32	0.40
ATP-dependent Clp protease ATP-binding subunit ClpE	recycling defective proteins	clpE	K0N644	1.18	-0.67	0.63	0.86	0.65	1.57	1.88	-1.32	0.40
Uncharacterized protein	recycling defective proteins		K0N5T8	0.32	0.40	1.32	1.88	2.00	4.00	2.65	-1.60	0.33
Probable ATP-dependent Clp protease ATP-binding subunit	recycling defective proteins	clpC	K0N9Z7	0.44	1.02	2.03	0.43	1.01	2.02	0.01	0.01	1.00
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	nascent protein folding	groL,groEL	K0N7K7	2.12	2.08	4.23	2.60	1.94	3.84	0.14	0.14	1.10
10 kDa chaperonin (GroES protein) (Protein Cpn10)	nascent protein folding	groS,grES	K0N700	1.59	-1.50	0.35	2.56	-1.26	0.42	0.23	-0.24	0.85
Chaperone protein ClpB	recycling defective proteins	clpB_2	K0N887	0.54	-0.44	0.74	0.47	0.39	1.31	4.36	-0.83	0.56
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	membrane protein assemby/recycling	ftsH	K0N7I8	1.07	0.31	1.24	1.38	0.40	1.32	0.94	-0.09	0.94
Probable reductase (EC 1.1.-.-)	methylglyoxal removal via acetol	11E,P100	K0N513	0.36	0.75	1.68	0.67	1.27	2.42	2.88	-0.52	0.70
NADH oxidase (EC 1.6.99.3)	thiol group reduction (similar to glutathione)	nox_2	K0N1N9	0.06	0.03	1.02	4.24	2.00	4.00	3.11	-1.97	0.26
NADH peroxidase (EC 1.11.1.1)	oxidative stress management	npr	K0MSP8	0.47	0.33	1.25	0.89	0.61	1.52	1.20	-0.28	0.82
Penicillin acylase (EC 3.5.1.11)	detoxification (penicillin, bile salts?)		K0N2B8	0.77	1.37	2.59	1.51	2.59	6.04	2.08	-1.22	0.43
Uncharacterized protein ACIAD3023	hydroperoxide removal		K0N2T5	1.55	1.08	2.11	1.60	1.89	3.71	0.85	-0.81	0.57
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	oxidative stress management	yfeX	K0N8U9	1.30	1.04	2.06	2.58	1.73	3.32	0.94	-0.69	0.62
Probable thiol peroxidase (EC 1.11.1.-)	antioxidant using thioredoxin	tpx	K0MTJ5	0.25	0.67	1.59	0.30	0.78	1.71	0.31	-0.11	0.93
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	methylglyoxal removal via acetol	dkgB	K0N347	3.28	-1.34	0.40	1.45	-0.44	0.74	3.91	-0.89	0.54
Glutathione peroxidase	H2O2/hydroperoxide removal	gpo	K0N6T6	0.69	-0.33	0.80	0.75	0.36	1.28	2.27	-0.68	0.62

CutC-like protein M6_Spy0363	copper homeostasis		K0N3H0	0.85	0.23	1.17	0.17	0.07	1.05	0.45	0.16	1.11
Uncharacterized protein ynbB	aluminium tolerance?	ynbB	K0N9B7	0.88	-0.59	0.67	2.00	-1.31	0.40	1.58	0.72	1.65
Lactaldehyde dehydrogenase (EC 1.2.1.21) (EC 1.2.1.22)	detoxification of aldehydes	aldA	K0NCB9	0.76	0.76	1.69	1.05	0.94	1.91	0.38	-0.18	0.88
Uncharacterized protein ybfG	unknown function	ybfG	K0N4B3	3.53	1.37	2.58	3.68	1.29	2.44	0.26	0.08	1.06
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	unknown function	ykwC	K0N7M3	0.73	-1.46	0.36	0.68	0.55	1.47	1.11	-2.01	0.25
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	unknown function		K0N5D9	0.82	-1.00	0.50	0.41	-0.39	0.76	0.68	-0.61	0.66
Uncharacterized protein yieF	unknown function	yieF_2	K0MT25	2.80	-2.93	0.13	0.58	0.52	1.43	4.56	-3.45	0.09
Uncharacterized protein ywnB	unknown function	ywnB	K0N6C4	1.35	-1.76	0.30	2.14	-1.44	0.37	0.23	-0.32	0.80
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	unknown function	yhfP	K0MTE1	0.25	-0.27	0.83	0.21	0.15	1.11	0.55	-0.43	0.74
Acetyltransferase	unknown function		K0N2Z8	0.16	-0.16	0.89	0.07	-0.08	0.95	0.35	-0.09	0.94
Predicted hydrolase of HD superfamily	unknown function		K0N6Z0	0.05	-0.02	0.99	0.99	-0.19	0.88	0.39	0.16	1.12
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	unknown function	ywpJ	K0N9U2	1.62	-1.74	0.30	0.93	-0.94	0.52	0.88	-0.80	0.57
Putative monooxygenase ycnE (EC 1.-.-.-)	unknown function	ycnE	K0N7R3	0.61	-0.41	0.75	0.03	-0.03	0.98	1.10	-0.38	0.77
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	unknown function	yqjQ	K0N8A1	0.34	-0.46	0.73	0.25	0.34	1.27	0.87	-0.80	0.58
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	unknown function	ydgI_2	K0N508	0.47	-0.35	0.79	1.85	1.43	2.69	3.74	-1.77	0.29
Putative nitroreductase HBN1 (EC 1.-.-.-)	unknown function	HBN1	K0N597	0.50	0.37	1.29	0.17	-0.13	0.92	1.38	0.50	1.41
Uncharacterized protein	unknown function		K0NAY8	0.23	0.13	1.09	1.32	0.64	1.55	1.58	-0.51	0.70
Uncharacterized protein ylxR	unknown function	ylxR	K0NAZ6	0.43	-0.06	0.96	0.47	-1.11	0.46	0.44	1.05	2.07
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	unknown function	mhqA_3	K0N5N7	0.69	0.36	1.29	0.66	0.30	1.23	0.10	0.06	1.04
Putative tRNA-binding protein ytpR	unknown function (tRNA-associated?)	ytpR	K0NB80	1.39	0.83	1.78	1.66	1.37	2.58	0.89	-0.53	0.69
6-aminohexanoate-cyclic-dimer hydrolase	unknown function		K0NAA2	0.17	-0.04	0.97	1.25	0.32	1.25	1.71	-0.36	0.78
FMN-binding domain protein	conjugation?		K0NC29	1.29	-0.79	0.58	0.40	0.41	1.33	1.69	-1.20	0.44
Uncharacterized protein ywfO	unknown function	ywfO	K0MXZ5	0.54	-0.58	0.67	0.69	-1.57	0.34	0.46	0.99	1.99
Uncharacterized protein yxkA	unknown function	yxkA	K0NAV1	0.65	-1.04	0.49	0.88	0.52	1.43	1.07	-1.55	0.34
Uncharacterized protein yghZ	unknown function	yghZ	K0N7U8	0.90	0.54	1.45	1.96	1.28	2.43	2.28	-0.75	0.60
Phosphatase YidA (EC 3.1.3.-)	unknown function	yidA	K0NDD5	1.34	0.50	1.41	3.86	2.54	5.82	4.44	-2.04	0.24
Uncharacterized protein ycaC	unknown function	ycaC	K0N948	0.08	-0.04	0.97	2.21	0.83	1.78	2.24	-0.87	0.55

Putative oxidoreductase GLYR1 (EC 1.-.-.-)	unknown function	glyr1	K0N992	1.21	-0.92	0.53	0.14	-0.12	0.92	1.46	-0.80	0.58
Uncharacterized protein	unknown function		K0N1N3	0.60	0.47	1.38	1.13	0.85	1.80	0.77	-0.38	0.77
Uncharacterized protein	unknown function		K0N2T7	0.46	-0.61	0.65	0.70	0.59	1.51	1.27	-1.21	0.43
UPF0145 protein BN194_07140	unknown function		K0MT82	0.71	-1.42	0.37	0.25	0.28	1.22	0.98	-1.70	0.31
Uncharacterized protein	unknown function		K0N2Y6	0.08	-0.13	0.91	3.45	1.70	3.24	1.50	-1.83	0.28
Uncharacterized protein	unknown function		K0MTK3	3.05	1.56	2.95	4.52	3.12	8.69	2.66	-1.56	0.34
UPF0297 protein BN194_08510	unknown function		K0N358	0.10	-0.15	0.90	0.72	0.85	1.81	1.83	-1.00	0.50
UPF0473 protein BN194_08530	unknown function		K0N6K6	5.03	-0.79	0.58	0.40	-0.23	0.85	1.09	-0.56	0.68
UPF0210 protein BN194_09830	unknown function		K0N6U0	0.34	0.42	1.34	0.55	0.62	1.54	0.59	-0.20	0.87
PspC domain-containing protein	unknown function	ythC	K0N3H5	1.39	-0.87	0.55	0.62	0.26	1.20	1.79	-1.13	0.46
Uncharacterized protein	unknown function		K0N9Y6	1.35	-1.16	0.45	0.62	-0.55	0.68	1.93	-0.60	0.66
DegV domain-containing protein CA_C1624	unknown function		K0NAD8	0.58	-0.42	0.75	2.31	1.14	2.20	2.07	-1.56	0.34
Uncharacterized protein	unknown function		K0N4M6	1.96	-0.95	0.52	1.26	-0.48	0.72	1.25	-0.47	0.72
UPF0356 protein BN194_15030	unknown function		K0N856	1.79	1.24	2.35	0.18	0.14	1.10	3.15	1.10	2.14
Uncharacterized protein	uncharacterised protein		K0N8E8	0.18	-0.11	0.93	0.48	0.22	1.17	1.03	-0.33	0.79
DegV domain-containing protein lin2658	unknown function		K0N8L5	0.18	0.18	1.13	0.83	0.74	1.67	1.50	-0.56	0.68
GTP cyclohydrolase 1 type 2 homolog	unknown function		K0N5C6	0.73	-1.42	0.37	0.58	-0.21	0.87	0.61	-1.21	0.43
Uncharacterized protein	unknown function		K0N5I7	0.36	0.35	1.28	1.23	1.21	2.32	1.39	-0.86	0.55
UPF0154 protein BN194_17740	unknown function		K0MVY5	0.04	0.02	1.02	0.59	-0.23	0.86	0.60	0.25	1.19
Uncharacterized protein SAR1202	unknown function		K0N5I6	1.18	-0.58	0.67	1.63	0.84	1.79	3.84	-1.42	0.37
Uncharacterized protein YqhY	unknown function	yqhY	K0N9A7	0.15	-0.38	0.77	3.05	2.25	4.77	1.28	-2.63	0.16
UPF0342 protein yheA	unknown function	yheA	K0N9F7	1.25	0.55	1.46	1.42	1.92	3.79	1.01	-1.37	0.39
Uncharacterized protein	unknown function		K0N6Y5	0.22	-0.39	0.76	0.73	1.07	2.10	3.39	-1.46	0.36
Uncharacterized protein	unknown function		K0N715	0.50	0.74	1.67	1.82	2.64	6.22	4.34	-1.90	0.27
Uncharacterized protein	unknown function		K0NAC8	1.11	1.18	2.27	0.76	0.83	1.78	2.25	0.35	1.28
Uncharacterized protein	unknown function		K0MXR4	0.19	-0.46	0.73	0.29	0.40	1.32	0.48	-0.86	0.55
CBS domain-containing protein	unknown function		K0N7J7	1.74	-0.64	0.64	0.02	-0.02	0.99	0.87	-0.63	0.65
Uncharacterized protein	unknown function		K0N8V3	0.07	0.08	1.06	0.41	0.43	1.35	0.82	-0.35	0.79

Uncharacterized protein	unknown function		K0N932	1.11	-2.06	0.24	0.40	0.09	1.06	1.16	-2.15	0.23
Uncharacterized protein	unknown function	K0N788	K0N788	0.62	-0.97	0.51	2.32	2.48	5.59	2.40	-3.45	0.09
Uncharacterized protein	unknown function	K0N2W3	K0N2W3	0.51	0.29	1.22	1.93	0.72	1.65	0.99	-0.43	0.74
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	glucose/mannose uptake	levE	K0N7U7	0.90	0.49	1.40	1.91	1.28	2.42	1.53	-0.79	0.58
Mannose permease IID component	glucose/mannose uptake	manZ	K0MSE1	0.14	0.25	1.19	0.18	0.32	1.25	0.09	-0.07	0.95
Putative PTS system mannose-specific EIIAB component	glucose/mannose uptake		K0N1P6	2.26	1.56	2.96	2.46	1.15	2.22	0.58	0.41	1.33
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	beta-glucoside uptake	bglP	K0MT60	0.05	-0.03	0.98	0.12	0.06	1.04	0.32	-0.09	0.94
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	PTS general components	hprK	K0N6Y3	0.04	-0.04	0.97	0.30	0.23	1.17	1.03	-0.27	0.83
Phosphocarrier protein HPr (EC 2.7.11.-)	PTS general components	ptsH	K0N9I2	0.89	1.38	2.61	0.68	0.66	1.58	0.41	0.73	1.66
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	fructose uptake	fruA_4	K0MY77	0.05	-0.09	0.94	0.41	0.57	1.49	1.15	-0.66	0.63
Mannose permease IID component	glucose/mannose uptake	manZ_9	K0N954	3.49	-0.90	0.54	1.81	-0.37	0.77	2.27	-0.52	0.70
Sorbose permease IIC component	glucose/mannose uptake	sorA_4	K0N8G4	0.06	0.15	1.11	1.59	1.29	2.44	0.62	-1.14	0.45
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	glucose/mannose uptake	manX_5	K0NDL4	0.76	-0.40	0.76	1.77	0.67	1.59	2.33	-1.06	0.48
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	mannitol uptake	mtlF	K0N8N0	0.48	0.32	1.25	0.65	0.40	1.32	0.33	-0.08	0.95
Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Phosphotransferase system, enzyme I)	ptsI	K0N5T2	0.69	0.14	1.10	1.51	-0.27	0.83	2.25	0.41	1.33	
D-ribose-binding protein	D-ribose uptake	rbsB	K0MSF6	0.11	-0.10	0.93	0.12	-0.12	0.92	0.05	0.02	1.02
Nod factor export ATP-binding protein I (EC 3.6.3.-)	unknown transport	nodI	K0N2J7	1.13	-0.68	0.62	0.65	-0.43	0.74	1.36	-0.26	0.84
Uncharacterized ABC transporter ATP-binding protein YkpA	unknown transport	ykpA	K0N8V6	0.74	0.98	1.97	0.39	0.56	1.47	2.44	0.42	1.34
ABC-type uncharacterized transport system, ATPase component	unknown transport		K0N6C9	0.08	0.23	1.17	2.06	0.46	1.38	0.08	-0.23	0.85
Multiple sugar-binding transport ATP-binding protein MsmK	maltose/maltodextrin uptake	msmK	K0N747	0.01	0.01	1.01	0.25	-0.17	0.89	0.54	0.18	1.13
Maltose ABC transporter, periplasmic maltose-binding protein	maltose/maltodextrin uptake		K0N3U4	1.77	-0.64	0.64	0.96	-0.34	0.79	1.03	-0.30	0.81
Glycerol-3-phosphate ABC transporter substrate-binding protein	sugar/glycerol uptake		K0N3T6	2.06	-0.45	0.73	1.96	0.48	1.40	4.07	-0.93	0.52
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	polyamine uptake?	potA	K0MU90	1.42	0.92	1.89	2.20	0.84	1.79	0.09	0.07	1.05

Lipoprotein	methionine uptake	metQ_2	K0MV23	2.62	-2.31	0.20	0.27	-0.18	0.88	3.33	-2.13	0.23
Oligopeptide-binding protein oppA	oligopeptide uptake	oppA	K0N983	0.08	-0.10	0.93	0.35	-0.17	0.89	0.05	0.07	1.05
Oligopeptide transport ATP-binding protein OppD	oligopeptide uptake	oppD	K0NB35	0.31	0.12	1.09	0.29	-0.14	0.91	0.73	0.26	1.20
Oligopeptide-binding protein oppA	oligopeptide uptake	oppA_2	K0MWL6	0.65	-1.00	0.50	0.29	-0.54	0.69	0.70	-0.46	0.73
Glutamine transport ATP-binding protein GlnQ	polar amino acid uptake	glnQ_3	K0MWS9	1.14	-0.83	0.56	1.46	-0.41	0.75	0.51	-0.42	0.75
ABC-type phosphate/phosphonate transport system,periplasmic component	phosphonate uptake		K0NAI1	2.50	1.50	2.82	2.90	1.55	2.92	0.12	-0.05	0.97
ABC transporter, permease protein	sugar/glycerol-3-phosphate uptake?		K0N8H4	0.01	-0.01	0.99	0.03	0.03	1.02	0.18	-0.05	0.97
Glutamine transport ATP-binding protein GlnQ	polar amino acid uptake	glnQ_4	K0N971	0.12	0.04	1.03	0.42	0.13	1.09	0.41	-0.09	0.94
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	fermentation; end-product formation		K0N1L0	1.03	0.28	1.22	2.42	-0.24	0.85	1.76	0.52	1.44
Acetate kinase (EC 2.7.2.1) (Acetokinase)	fermentation; end-product formation	ackA	K0N7B1	0.56	-1.03	0.49	1.27	1.73	3.31	2.17	-2.75	0.15
Mannose-6-phosphate isomerase (EC 5.3.1.8)	mannose catabolism	pmi	K0N7U2	1.17	1.41	2.66	1.02	1.23	2.34	0.94	0.18	1.14
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	N-acetylated sugar catabolism	agaS	K0MSD9	1.94	-0.72	0.61	1.82	-0.85	0.56	0.38	0.13	1.10
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	N-acetylglucosamine catabolism	manD	K0N1P4	1.40	-1.30	0.40	0.28	0.26	1.19	2.51	-1.56	0.34
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	trehalose catabolism	treA	K0N662	0.14	-0.11	0.93	0.63	-0.44	0.74	1.02	0.33	1.26
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	fermentation; end-product formation	ldh1,ldh	K0N8S5	0.78	0.97	1.97	1.00	1.26	2.40	0.65	-0.29	0.82
6-phospho-beta-galactosidase (EC 3.2.1.85) (Beta-D-phosphogalactoside galactohydrolase) (P-beta-Gal)	lactose catabolism	lacG	K0N8W7	0.04	0.06	1.04	0.07	0.07	1.05	0.01	-0.01	0.99
Galactokinase (EC 2.7.1.6) (Galactose kinase)	galactose catabolism	galK	K0MTA3	0.09	0.07	1.05	0.31	-0.16	0.89	0.35	0.23	1.17
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	galactose/tagatose catabolism	lacD2,lacD	K0N6A8	3.13	1.86	3.63	2.79	1.65	3.14	1.10	0.21	1.16
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	lactose catabolism	lacB	K0MTB7	0.78	0.78	1.72	1.11	0.74	1.67	0.04	0.04	1.03
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	lactose catabolism	lacA	K0N2T4	1.27	1.18	2.26	0.85	0.62	1.54	0.88	0.56	1.47
Aldehyde-alcohol dehydrogenase	fermentation; end-product formation	ADH2	K0N307	0.29	0.13	1.09	3.44	2.22	4.66	4.60	-2.09	0.23
Uncharacterized protein YwcC	pentose phosphate pathway	ywcC	K0N6V0	0.65	0.23	1.17	1.06	0.31	1.24	0.35	-0.08	0.94
Intracellular maltogenic amylase (EC 3.2.1.-)	maltodextrin catabolism	bbmA	K0N3T4	2.08	1.85	3.61	1.35	1.04	2.05	1.98	0.82	1.76

Uncharacterized glycosyl hydrolase yvdK (EC 3.2.1.-)	maltose catabolism	yvdK	K0N3S7	0.11	0.12	1.09	0.93	-0.81	0.57	3.02	0.93	1.91
Phosphate acetyltransferase (EC 2.3.1.8)	fermentation, end-product formation	pta	K0MU95	2.81	0.57	1.48	3.77	1.66	3.16	3.10	-1.09	0.47
Formate acetyltransferase (EC 2.3.1.54)	fermentation, end-product formation	pflB	K0N8I5	1.82	0.47	1.38	3.63	1.85	3.61	3.26	-1.39	0.38
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	fermentation; end-product formation	act	K0MVI3	0.20	-0.09	0.94	1.06	0.93	1.90	1.26	-1.02	0.49
Pyruvate oxidase (EC 1.2.3.3)	fermentation; end-product metabolism	pox5	K0NBB6	0.05	-0.05	0.97	1.80	1.16	2.23	3.95	-1.20	0.43
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	N-acetylglucosamine catabolism	nagA	K0MWF9	0.91	0.41	1.33	0.89	0.32	1.25	0.22	0.09	1.06
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	fermentation; end-product formation	aldB	K0MWH5	0.07	-0.22	0.86	0.77	0.75	1.68	0.43	-0.97	0.51
Glycogen phosphorylase (EC 2.4.1.1)	starch/glycogen hydrolysis	glgP	K0NBM1	0.22	-0.37	0.78	1.44	1.17	2.26	1.36	-1.54	0.34
Glycogen synthase (EC 2.4.1.21) (Starch [bacterial glycogen] synthase)	starch/glycogen synthesis	glgA	K0N9Z2	0.36	0.36	1.28	2.72	3.03	8.19	4.22	-2.67	0.16
Glucose-1-phosphate adenylyltransferase, GlgD subunit	starch/glycogen synthesis	glgD	K0MWU4	1.30	-1.06	0.48	0.80	0.57	1.48	2.89	-1.62	0.32
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	starch/glycogen synthesis	glgC	K0N6T3	1.92	1.67	3.18	3.24	3.72	13.22	4.00	-2.05	0.24
1,4-alpha-glucan branching enzyme (EC 2.4.1.18)	starch/glycogen hydrolysis/synthesis	glgB	K0N6B8	0.28	-0.27	0.83	1.12	0.97	1.96	2.98	-1.25	0.42
NADH-dependent butanol dehydrogenase A (EC 1.1.1.-)	fermentation; end-product metabolism	bdhA	K0MX50	0.39	0.55	1.46	0.58	0.75	1.68	0.56	-0.20	0.87
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	fermentation; end-product formation	ldh	K0N7J5	1.89	0.61	1.53	0.94	0.22	1.17	1.21	0.39	1.31
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	galactose/tagatose catabolism	lacD2_2,lacD	K0N7P0	3.67	-0.68	0.63	3.07	-0.85	0.56	1.02	0.17	1.13
Protein lacX, plasmid	lactose catabolism	lacX	K0NCY0	1.26	-0.49	0.71	1.04	-0.41	0.75	0.21	-0.08	0.95
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	fermentation; end-product formation		K0NCZ6	0.38	-0.05	0.97	0.28	-0.04	0.98	0.07	-0.01	0.99
Alpha-glucosidase (EC 3.2.1.20)	degradation of dextrin/maltotriose	agl	K0N8T1	0.71	0.92	1.89	1.13	1.43	2.69	2.98	-0.50	0.71
Protein IolS (EC 1.1.1.-)	myo-inositol catabolism	iolS	K0NB94	0.53	1.05	2.07	1.12	2.06	4.18	3.17	-1.01	0.50
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	mannitol catabolism	mtlD_3 mtlD	K0N9C8	0.99	-0.23	0.85	1.86	-0.46	0.73	1.01	0.23	1.17
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	N-acetylglucosamine catabolism	nagB	K0MYW0	1.64	0.47	1.39	1.83	-0.46	0.73	3.33	0.93	1.91

Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (EC 2.7.7.12) (UDP-glucose--hexose-1-phosphate uridylyltransferase)	Carbohydrate-related metabolism	galT	K0N8X1	0.88	-0.24	0.84	0.42	0.17	1.12	1.60	-0.41	0.75
Probable phosphoketolase (EC 4.1.2.-)	pentose phosphate pathway; D-xylulose catabolism	xpkA	K0N1M9	2.19	-0.41	0.75	0.65	-0.11	0.93	2.76	-0.30	0.81
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	glycolysis	dhaK_2	K0N5Q3	0.33	0.63	1.55	1.19	1.84	3.58	1.75	-1.21	0.43
Fructose-bisphosphate aldolase (EC 4.1.2.13)	glycolysis	fba_2	K0N2C9	3.09	0.84	1.78	0.47	-0.10	0.94	3.41	0.93	1.91
Aldose 1-epimerase (EC 5.1.3.3)	galactose/tagatose catabolism		K0MTA8	0.67	0.28	1.21	3.38	0.69	1.62	1.00	-0.41	0.75
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	pentose phosphate pathway	zwf	K0N966	1.69	1.21	2.31	1.41	0.99	1.98	0.52	0.22	1.17
Phosphoglucomutase (EC 5.4.2.2)	glycolysis	pgcA	K0N9K8	0.55	0.19	1.14	1.07	0.31	1.24	0.54	-0.11	0.92
Phosphoglycerate kinase (EC 2.7.2.3)	glycolysis	pgk	K0N9R1	1.15	-0.24	0.85	1.79	-0.32	0.80	0.31	0.08	1.06
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	glycolysis	tpiA	K0N736	0.16	0.15	1.11	1.04	0.46	1.37	0.47	-0.31	0.81
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	glycolysis	eno	K0MU67	1.68	-0.44	0.74	1.83	-0.50	0.71	0.46	0.06	1.05
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	glycolysis	pdhA	K0N860	1.61	-0.63	0.64	3.40	1.27	2.41	3.26	-1.90	0.27
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	glycolysis	pdhB	K0MVA7	1.66	-0.20	0.87	4.42	1.41	2.66	4.92	-1.61	0.33
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	glycolysis	pdhC	K0N4W5	2.14	-0.35	0.78	3.90	1.58	3.00	4.59	-1.93	0.26
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	glycolysis	pdhD	K0N4P1	0.11	-0.06	0.96	2.59	1.74	3.34	2.58	-1.80	0.29
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	glycolysis	pfkA	K0NAK6	0.78	0.34	1.26	1.17	-0.45	0.73	3.12	0.79	1.73
Pyruvate kinase (EC 2.7.1.40)	glycolysis	pyk	K0N8B6	1.69	0.77	1.71	0.23	0.12	1.09	2.87	0.65	1.57
Aldose 1-epimerase	glycolysis		K0NAP4	0.15	0.18	1.13	1.87	1.83	3.56	4.51	-1.65	0.32
Glucokinase (EC 2.7.1.2)	glycolysis	glcK	K0NB57	1.98	0.49	1.41	1.01	0.24	1.18	1.88	0.25	1.19
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	pentose phosphate pathway	gnd	K0N5N2	1.19	-0.45	0.73	0.11	-0.04	0.97	1.23	-0.41	0.75
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	glycolysis	fbp	K0N6C3	0.04	-0.06	0.96	0.51	0.32	1.24	0.34	-0.38	0.77
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	glycolysis	gpmA2 ,gpmA	K0MX58	0.25	-0.22	0.86	0.28	-0.20	0.87	0.03	-0.02	0.99
Pyruvate, phosphate dikinase (EC 2.7.9.1)	glycolysis	ppdK	K0NAC6	3.30	1.04	2.05	0.02	-0.01	1.00	4.28	1.04	2.06

Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	pentose phosphate pathway	rpiA_2, ripA	K0N8W9	0.94	0.24	1.18	3.51	1.03	2.04	2.75	-0.79	0.58
Glyceraldehyde-3-phosphate dehydrogenase		gap	K0N3R3	0.64	0.22	1.17	0.55	0.12	1.08	0.28	0.11	1.08
Glucose-6-phosphate isomerase		pgi	K0N7I6;K0N4A6	0.10	0.05	1.03	0.50	0.17	1.13	0.30	-0.12	0.92
Pyruvate carboxylase (EC 6.4.1.1)	TCA cycle	pyc	K0NAI2	0.30	0.22	1.17	0.04	-0.03	0.98	0.59	0.26	1.19
Pyruvate carboxylase subunit B (EC 6.4.1.1)	citrate utilization	pycB	K0MWI8	2.08	2.08	4.22	3.71	5.54	46.58	5.08	-3.46	0.09
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	citrate utilization	citX	K0N6A3	0.80	-1.13	0.46	0.72	0.25	1.19	0.97	-1.37	0.39
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	citrate utilization	citF	K0N607	0.81	0.20	1.15	4.91	2.52	5.72	5.17	-2.32	0.20
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	citrate utilization	citE	K0NBF4	1.62	-1.03	0.49	1.88	0.95	1.94	3.06	-1.99	0.25
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	citrate utilization	citD	K0N9Q5	1.37	-1.01	0.50	2.60	1.47	2.77	3.06	-2.47	0.18
RNA polymerase sigma factor SigA	RNA polymerase	rpoD,sigA	K0NAV6	0.52	0.35	1.27	0.00	-0.01	1.00	0.36	0.35	1.28
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	rpoA	K0N7E5	0.57	0.25	1.19	0.60	-0.22	0.86	1.71	0.47	1.38
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	rpoC	K0NAN3	0.57	0.13	1.09	0.96	-0.21	0.87	2.68	0.33	1.26
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	rpoB	K0MXV4	1.47	0.35	1.28	1.10	-0.21	0.86	2.99	0.57	1.48
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	rpoE	K0N7L4	2.93	0.84	1.79	1.15	0.18	1.14	2.97	0.66	1.58
Probable catabolite control protein A	regulation of catabolic enzyme coding genes	ccpA	K0N323	1.02	0.54	1.46	2.68	0.87	1.82	0.65	-0.32	0.80
Phosphate-specific transport system accessory protein PhoU	regulation of phosphate uptake genes	phoU	K0MTZ9	0.94	-1.19	0.44	1.78	1.83	3.55	2.79	-3.01	0.12
Probable transcriptional regulatory protein BN194_11600	regulatory role (unknown)		K0N3Z3	0.19	0.34	1.26	0.02	0.03	1.02	0.26	0.31	1.24
Transcriptional regulator	unknown regulation		K0N551	0.19	0.29	1.22	1.83	2.37	5.17	3.48	-2.08	0.24
Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	regulatory role (gluconeogenesis?)	rp2	K0N598	0.49	1.47	2.76	1.02	2.85	7.19	2.23	-1.38	0.38
HTH-type transcriptional repressor yvoA	regulatory role unknown	yvoA_2	K0N9L8	0.16	-0.28	0.83	0.50	0.84	1.79	0.77	-1.12	0.46
Uncharacterized transcriptional regulator in ATPase CF(0) region	regulatory role unknown		K0N6F6	0.34	-0.49	0.71	0.74	-0.78	0.58	0.25	0.28	1.22

Transcriptional regulator, xre family	regulatory role unknown		K0N6Y7	1.46	1.00	2.00	2.35	1.50	2.83	1.13	-0.50	0.71
Redox-sensing transcriptional repressor Rex	regulates genes assoc. fermentation; NADH:NAD sensor	rex_2,rex	K0NBZ5	0.69	0.34	1.26	1.21	0.53	1.45	0.58	-0.19	0.87
MerR family transcriptional regulator	regulation of drug resistance transporter		K0N833	1.04	-1.16	0.45	5.05	6.09	68.26	3.94	-7.25	0.01
Pur operon repressor	regulation of purine biosynthesis genes	purR_2	K0N7M9	1.04	0.79	1.73	0.03	-0.05	0.97	0.68	0.84	1.79
Glucitol operon repressor	regulatory role (carbohydrate-related?)	srlR	K0MYG3	0.68	-3.05	0.12	0.65	-0.72	0.61	0.52	-2.33	0.20
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation (nanoRNA)	nrnA	K0N309	0.85	0.28	1.22	0.95	0.32	1.24	0.27	-0.03	0.98
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation (RNA degradosome)	rnjA	K0NAH6	0.40	1.02	2.03	0.26	0.70	1.63	1.27	0.32	1.25
Cold shock protein 1	RNA chaperone	csp	K0MT67	0.14	0.53	1.44	0.69	-0.70	0.62	0.38	1.23	2.34
Cold shock-like protein CspLA	RNA chaperone	cspLA	K0N438	0.24	0.66	1.58	0.04	0.08	1.06	0.22	0.58	1.49
Transcription termination/antitermination protein NusA	transcription elongation	nusA	K0N927	2.18	0.67	1.59	3.98	1.37	2.58	2.39	-0.70	0.61
30S ribosomal protein S6	30S (SSU) ribosome	rpsF	K0N0Z1	0.57	0.47	1.38	0.17	0.15	1.11	0.58	0.32	1.25
30S ribosomal protein S18	30S (SSU) ribosome	rpsR	K0N6T2	0.59	1.52	2.87	0.02	-0.05	0.96	0.70	1.57	2.97
50S ribosomal protein L9	50S (LSU) ribosome	rplI	K0N4K3	1.04	1.86	3.64	1.25	2.22	4.67	1.69	-0.36	0.78
30S ribosomal protein S4	30S (SSU) ribosome	rpsD	K0MV63	1.04	0.41	1.33	1.23	-0.31	0.81	1.61	0.72	1.64
30S ribosomal protein S20	30S (SSU) ribosome	rpsT	K0N4X9	1.14	1.08	2.12	0.23	0.21	1.15	0.83	0.88	1.84
30S ribosomal protein S15	30S (SSU) ribosome	rpsO	K0N4Q6	0.03	-0.04	0.97	2.30	-1.43	0.37	1.58	1.39	2.62
30S ribosomal protein S1 homolog	30S (SSU) ribosome	ypfD	K0NAL9	0.95	0.44	1.36	0.23	-0.13	0.92	1.59	0.57	1.48
30S ribosomal protein S2	30S (SSU) ribosome	rpsB	K0N936	0.90	0.21	1.16	1.96	-0.39	0.76	2.97	0.60	1.52
50S ribosomal protein L19	50S (LSU) ribosome	rplS	K0NB12	0.49	0.57	1.48	0.73	-0.79	0.58	3.86	1.36	2.57
30S ribosomal protein S16	30S (SSU) ribosome	rpsP	K0N5H1	0.10	-0.10	0.93	0.26	-0.09	0.94	0.01	-0.01	0.99
50S ribosomal protein L21	50S (LSU) ribosome	rplU	K0MW61	0.44	0.96	1.95	0.13	-0.32	0.80	0.66	1.28	2.43
50S ribosomal protein L20	50S (LSU) ribosome	rplT	K0N5Y4	0.61	1.79	3.45	0.22	0.74	1.67	2.31	1.05	2.07
50S ribosomal protein L7/L12	50S (LSU) ribosome	rplL	K0NA98	2.80	1.01	2.02	2.59	1.06	2.09	0.09	-0.05	0.96
50S ribosomal protein L10	50S (LSU) ribosome	rplJ	K0MXD8	3.75	0.73	1.66	3.26	0.53	1.44	1.56	0.21	1.15
50S ribosomal protein L1	50S (LSU) ribosome	rplA	K0N7M7	1.90	0.47	1.38	1.43	-0.31	0.80	3.62	0.78	1.72

50S ribosomal protein L11	50S (LSU) ribosome	rplK	K0N724	4.51	1.58	2.99	2.16	0.61	1.53	2.97	0.96	1.95
30S ribosomal protein S9	30S (SSU) ribosome	rpsI	K0MXR0	0.51	1.88	3.67	0.30	1.19	2.28	1.65	0.69	1.61
50S ribosomal protein L13	50S (LSU) ribosome	rplM	K0N828	0.39	0.08	1.06	1.22	-0.34	0.79	1.32	0.42	1.33
50S ribosomal protein L17	50S (LSU) ribosome	rplQ	K0N841	1.14	3.32	9.96	0.72	2.08	4.24	1.53	1.23	2.35
30S ribosomal protein S11	30S (SSU) ribosome	rpsK	K0NCJ0	2.61	2.47	5.53	1.09	0.81	1.76	3.39	1.65	3.14
30S ribosomal protein S13	30S (SSU) ribosome	rpsM	K0NAK3	1.77	1.35	2.55	0.11	-0.12	0.92	1.38	1.47	2.78
50S ribosomal protein L15	50S (LSU) ribosome	rplO	K0NAK7	1.16	0.51	1.42	0.17	-0.11	0.93	2.05	0.62	1.53
50S ribosomal protein L30	50S (LSU) ribosome	rpmD	K0MXS6	0.50	-2.03	0.24	1.47	-3.83	0.07	0.45	1.80	3.49
30S ribosomal protein S5	30S (SSU) ribosome	rpsE	K0N853	0.34	1.36	2.57	0.25	1.05	2.06	0.92	0.31	1.24
50S ribosomal protein L18	50S (LSU) ribosome	rplR	K0N7F4	1.39	3.44	10.84	1.13	2.80	6.95	1.53	0.64	1.56
50S ribosomal protein L6	50S (LSU) ribosome	rplF	K0NCK5	0.56	0.41	1.33	0.90	-0.40	0.76	1.31	0.81	1.76
30S ribosomal protein S8	30S (SSU) ribosome	rpsH	K0NAL1	1.13	-0.26	0.84	2.03	-0.75	0.60	1.19	0.49	1.40
30S ribosomal protein S14 type Z	30S (SSU) ribosome	rpsZ,rpsN	K0MXS9	0.11	-0.17	0.89	1.23	-0.61	0.65	0.34	0.44	1.36
50S ribosomal protein L5	50S (LSU) ribosome	rplE	K0N859	0.01	0.01	1.01	2.11	-0.68	0.62	2.48	0.69	1.62
50S ribosomal protein L24	50S (LSU) ribosome	rplX	K0N7F9	0.62	1.26	2.39	0.35	0.76	1.70	0.83	0.49	1.41
50S ribosomal protein L14	50S (LSU) ribosome	rplN	K0NCL3	0.66	0.27	1.20	1.48	-0.44	0.74	1.72	0.70	1.63
50S ribosomal protein L29	50S (LSU) ribosome	rpmC	K0MXT6	0.67	2.24	4.72	0.40	1.43	2.69	2.66	0.81	1.76
50S ribosomal protein L16	50S (LSU) ribosome	rplP	K0N863	1.85	2.00	3.99	0.56	0.68	1.60	1.50	1.32	2.49
30S ribosomal protein S3	30S (SSU) ribosome	rpsC	K0N7G5	1.14	2.11	4.32	0.03	-0.04	0.98	1.31	2.15	4.43
50S ribosomal protein L22	50S (LSU) ribosome	rplV	K0NCM1	1.69	1.16	2.24	0.56	0.34	1.27	1.87	0.82	1.77
30S ribosomal protein S19	30S (SSU) ribosome	rpsS	K0NAM1	0.62	1.66	3.16	0.30	0.89	1.86	1.49	0.76	1.70
50S ribosomal protein L2	50S (LSU) ribosome	rplB	K0MXU1	1.90	0.33	1.25	1.65	-0.32	0.80	3.54	0.65	1.56
50S ribosomal protein L23	50S (LSU) ribosome	rplW	K0N869	1.05	0.40	1.32	0.78	-0.23	0.85	2.29	0.63	1.55
50S ribosomal protein L4	50S (LSU) ribosome	rplD	K0N7H0	0.99	0.47	1.39	0.52	-0.26	0.83	3.08	0.74	1.67
50S ribosomal protein L3	50S (LSU) ribosome	rplC	K0NCN1	1.04	0.34	1.26	1.63	-0.54	0.69	2.56	0.88	1.84
30S ribosomal protein S10	30S (SSU) ribosome	rpsJ	K0NAM5	0.78	-0.35	0.79	1.90	-0.90	0.54	1.72	0.55	1.47
30S ribosomal protein S7	30S (SSU) ribosome	rpsG	K0NAM9	1.23	-0.24	0.85	2.84	-0.76	0.59	2.40	0.52	1.43
30S ribosomal protein S12	30S (SSU) ribosome	rpsL	K0MXV0	1.16	0.18	1.13	2.84	-1.10	0.47	3.01	1.28	2.42

50S ribosomal protein L31 type B	50S (LSU) ribosome	rpmE2	K0NCV4	0.80	0.47	1.39	0.92	-0.40	0.76	1.53	0.87	1.83
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	protein synthesis; tRNA charging	alaS	K0N6K2	1.16	0.64	1.55	2.36	1.47	2.77	2.71	-0.83	0.56
Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	protein synthesis; tRNA charging	leuS	K0N3A9	0.57	0.42	1.34	2.30	1.71	3.26	2.72	-1.29	0.41
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	protein synthesis; tRNA charging	gatC	K0N436	0.18	-0.54	0.69	0.58	0.68	1.60	0.52	-1.22	0.43
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	protein synthesis; tRNA charging	gatA	K0N3Z6	0.22	-0.06	0.96	0.91	0.16	1.12	1.27	-0.22	0.86
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	protein synthesis; tRNA charging	gatB	K0NA01	1.19	0.54	1.46	1.72	0.74	1.67	0.65	-0.20	0.87
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	protein synthesis; tRNA charging	valS	K0N4J6	1.02	-0.54	0.69	1.38	0.80	1.74	3.45	-1.34	0.39
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	protein synthesis; tRNA charging	ileS	K0N4L9	0.22	-0.07	0.95	2.71	-0.65	0.64	2.59	0.59	1.50
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	protein synthesis; tRNA charging	asnS	K0N569	0.80	0.23	1.17	0.55	0.21	1.15	0.04	0.02	1.02
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	protein synthesis; tRNA charging	glyS	K0N5D3	0.24	0.15	1.11	1.33	-0.61	0.65	2.27	0.76	1.70
Aspartate--tRNA ligase (EC 6.1.1.12)	protein synthesis; tRNA charging	aspS	K0N5F3	0.49	1.01	2.01	0.77	1.50	2.82	2.06	-0.49	0.71
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	protein synthesis; tRNA charging	hisS	K0N5A0	0.47	0.35	1.28	1.40	0.93	1.90	1.88	-0.57	0.67
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	protein synthesis; tRNA charging	proS	K0N5E2	0.09	-0.05	0.97	0.81	-0.31	0.81	0.96	0.26	1.20
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	protein synthesis; tRNA charging	pheT	K0N5M4	2.01	0.59	1.51	2.52	0.79	1.73	1.29	-0.20	0.87
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	protein synthesis; tRNA charging	thrS	K0N5P5	1.60	0.93	1.91	1.62	0.92	1.89	0.04	0.01	1.01
Protein hit	protein synthesis; tRNA charging	hit	K0MWA8	1.54	-1.02	0.49	3.80	1.57	2.96	2.94	-2.59	0.17
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	protein synthesis; tRNA charging	argS	K0NB86	0.71	0.30	1.23	1.99	0.89	1.86	4.41	-0.59	0.66
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	protein synthesis; tRNA charging	serS	K0N9N4	0.27	0.21	1.16	0.01	0.01	1.01	0.39	0.20	1.15
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	protein synthesis; tRNA charging	cysS	K0NAB2	0.37	-0.56	0.68	0.14	0.23	1.17	0.86	-0.79	0.58
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	protein synthesis; tRNA charging	gltX	K0NC38	0.38	0.43	1.34	0.03	0.04	1.03	1.85	0.39	1.31
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	protein synthesis; tRNA charging	lysS	K0NAN7	0.16	0.32	1.25	0.16	0.32	1.25	0.00	0.00	1.00
Methionine--tRNA ligase (EC 6.1.1.10)	protein synthesis; tRNA charging	metG	K0NAU5	0.31	-0.18	0.88	2.36	1.56	2.95	3.52	-1.74	0.30

Tryptophan--tRNA ligase (EC 6.1.1.2)	protein synthesis; tRNA charging	trpS	K0N7S4	0.37	-0.69	0.62	0.24	-0.41	0.75	0.26	-0.28	0.82
Translation initiation factor IF-2	protein synthesis; translation initiation	infB	K0N5K7	2.23	1.15	2.22	1.84	0.77	1.71	1.22	0.38	1.30
Translation initiation factor IF-3	protein synthesis; translation initiation	infC	K0NB73	1.49	-0.61	0.65	1.79	-0.86	0.55	1.03	0.25	1.19
Translation initiation factor IF-1	protein synthesis; translation initiation	infA	K0N847	1.02	1.98	3.95	1.07	2.08	4.24	0.35	-0.10	0.93
GTP-binding protein TypA/BipA homolog	protein synthesis; ribosome function	typA	K0N4W9	1.65	1.50	2.83	1.97	1.86	3.63	1.57	-0.36	0.78
Elongation factor Tu (EF-Tu)	protein synthesis; translation elongation	tuf	K0N4R1	1.90	0.69	1.61	0.07	0.02	1.01	1.88	0.68	1.60
Elongation factor Ts (EF-Ts)	protein synthesis; translation elongation	tsf	K0NB01	1.23	1.15	2.21	0.99	0.83	1.78	0.47	0.31	1.24
Elongation factor G (EF-G)	protein synthesis; translation elongation	fusA	K0NCN8	1.66	1.17	2.25	0.30	0.19	1.14	1.65	0.98	1.97
Peptide chain release factor 1 (RF-1)	protein synthesis; translation release	prfA	K0N4C6	0.89	1.18	2.27	0.97	1.30	2.46	0.31	-0.11	0.92
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	protein synthesis; translation release	frr	K0N5M3	2.60	0.89	1.86	3.76	1.55	2.93	2.65	-0.66	0.63
Peptide chain release factor 3 (RF-3)	protein synthesis; translation release	prfC	K0N9I7	0.83	-0.55	0.68	0.37	0.30	1.23	0.98	-0.85	0.56

Annexure 05 : CFE proteins not detected in one or more growth conditions for cells cultured in media containing Tween 80 or Citrate or the Control media (experiment P2)

Orange shaded cells = proteins uniquely found in Cit; Green shaded cells = identifying families of similar proteins that are detected in the control; N = not detected; Y = detected; L = low level of expression

Protein name	**Gene Locus**	**Gene/protein symbol**	**Functional Class**	**Class Code**	**Function**	**Detected in CFE:**		
						Control	Tween 80	Citrate
UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2	BN194_26780	MurA2	Cell wall biogenesis	1.1	early peptidoglycan biosynthesis	N	Y	Y

UDP-N-acetylmuramoylalanine--D-glutamate ligase	BN194_14720	MurD	Cell wall biogenesis	1.1	late peptidoglycan biosynthesis	N	Y	Y
UDP-N-acetylmuramoyl-L-alanyl-D-glutamate-2,6-diaminopimelate ligase	BN194_02160	MurE	Cell wall biogenesis	1.1	late peptidoglycan biosynthesis	N	Y	Y
UDP-glucose 4-epimerase	BN194_21400	GalE2	Cell wall biogenesis	1.1	teichoic acid decoration	N	Y	Y
divergent methyl-accepting chemotaxis-like domain, DUF948 superfamily, UPF0478 protein SAOUHSC_01855, transmembrane protein	BN194_08710	YtxG	Signal transduction	1.3	chemotaxis? General stress?	N	N	Y
polyphosphate kinase	BN194_27270	Ppk	Membrane bioenergetics	1.4	polyphopshate conversion to/from ATP	N	Y	Y
quinone-oxidoreductase	BN194_18780	YogA	Membrane bioenergetics	1.4	electron transport	N	Y	Y
signal recognition particle protein	BN194_17820	Ffh	Protein export	1.6	protein secretion; SRP pathway (trafficking)	N	Y	Y
rod shape-determining protein MreB	BN194_14550	MreB	Cytokinesis	1.7	cell division; cell shape directing complex	N	Y	Y
aspartate racemase	N194_02170		Amino acid-related metabolism	2.2	metabolism of aspartate	N	Y	Y
aspartate-semialdehyde dehydrogenase	BN194_01060	Asd	Amino acid-related metabolism	2.2	L-threonine biosynthesis; L-lysine biosynthesis; L-methionine biosynthesis	N	Y	Y
oligoendopeptidase F	BN194_02530	YjbG	Amino acid-related metabolism	2.2	peptidase for amino acid acquistion	N	Y	Y
Proline iminopeptidase	BN194_21160	FpaP3	Amino acid-related metabolism	2.2	peptidase for amino acid acquistion	N	Y	Y
cysteinyl aminopeptidase, peptidase C1 family	BN194_24670	PepC	Amino acid-related metabolism	2.2	peptidase for amino acid acquistion	N	N	Y
adenine phosphoribosyltransferase	BN194_17380	Apt	Nucleic acid/nucleotide metabolism	2.3	GMP/AMP biosynthesis	N	Y	Y
adenylate kinase	BN194_26010	Adk	Nucleic acid/nucleotide metabolism	2.3	ADP biosynthesis; energy homeostasis	N	Y	Y
deoxyribose-phosphate aldolase	BN194_00080	DeoC[1]	Nucleic acid/nucleotide metabolism	2.3	(deoxy)ribose 1-phosphate biosynthesis	N	Y	Y
deoxyribose-phosphate aldolase	BN194_02790	DeoC[1]	Nucleic acid/nucleotide metabolism	2.3	(deoxy)ribose 1-phosphate biosynthesis	Y	Y	Y
dihydroorotate dehydrogenase A	BN194_19150	PyrDA	Nucleic acid/nucleotide metabolism	2.3	UMP/uridine/uracil biosynthesis	N	Y	Y
xanthine phosphoribosyltransferase	BN194_12490	Xpt	Nucleic acid/nucleotide metabolism	2.3	GMP biosynthesis	N	Y	Y
dihydrolipoyl dehydrogenase	BN194_16400	BFmBC	Lipid-related metabolism	2.4	BCFA primer synthesis	N	Y	Y
glycerol-3-phosphate dehydrogenase	BN194_10350	GpsA	Lipid-related metabolism	2.4	phospholipid biosynthesis	N	Y	Y

hydroxymethylglutaryl-CoA synthase	BN194_19680	MvaS	Lipid-related metabolism	2.4	mevalonate pathway for isoprenoid backbones	N	Y	Y
acyl carrier protein	BN194_22590	AcpP2	Lipid-related metabolism	2.4	fatty acid biosynthesis	Y	N	Y
Presumptive biotin carboxylase, ATP-grasp and biotin carboxylation domains	BN194_22500	AccC?	Lipid-related metabolism	2.4	unknown function, (fatty acid biosynthesis)	N	N	Y
acetyl-CoA carboxylase biotin carboxylase subunit	BN194_22510	AccC	Lipid-related metabolism	2.4	fatty acid biosynthesis	N	N	Y
3-oxoacyl-ACP reductase	BN194_22560	FabG	Lipid-related metabolism	2.4	fatty acid biosynthesis	Y	N	Y
(3R)-hydroxymyristoyl-ACP dehydratase	BN194_22520	FabZ	Lipid-related metabolism	2.4	fatty acid biosynthesis	Y	N	Y
(3R)-hydroxymyristoyl-ACP dehydratase	BN194_22620	FabZ_2	Lipid-related metabolism	2.4	fatty acid biosynthesis	N	N	Y
malonyl CoA-acyl carrier protein transacylase	BN194_22570	FabD	Lipid-related metabolism	2.4	fatty acid biosynthesis	Y	N	Y
3-oxoacyl-[acyl-carrier-protein] reductase 4	BN194_22550	Bkr4	Lipid-related metabolism	2.4	fatty acid biosynthesis	N	N	Y
acetyl-CoA carboxylase biotin carboxyl carrier protein	BN194_22530	AccB	Lipid-related metabolism	2.4	fatty acid biosynthesis	Y	N	Y
branched-chain amino acid aminotransferase	BN194_21620	IlvE	Lipid-related metabolism	2.4	L-leucine/L-isoleucine /L-valine metabolism	N	Y	Y
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase	BN194_07650	ThiD2	Cofactor-related metabolism	2.5	thiamine biosynthesis	N	N	Y
Replicative DNA helicase	BN194_01140	DnaC	DNA replication related	3.1	DNA replication initiation	N	L	L
DNA helicase IV	BN194_21130	PcrA	DNA repair/recombination	3.2	nucleotide excision, mismatch repair	N	Y	Y
DEAD/DEAH box helicase	BN194_08460	CshB	tRNA/Ribosome assembly/processing	3.6	ribosome processing (LSU); RNA chaperone	N	Y	Y
ribosomal RNA small subunit methyltransferase H	BN194_14680	RsmH	tRNA/Ribosome assembly/processing	3.6	ribosomal RNA processing (SSU)	N	Y	Y
ribosome stabilisation protein, Iojap_YbeB family	BN194_18710	YqeL/RsfS	tRNA/Ribosome assembly/processing	3.6	unknown ribosome-associated function, silencing factor?	N	Y	Y
tRNA-dihydrouridine synthase 1	BN194_26390	Dus1	tRNA/Ribosome assembly/processing	3.6	tRNA modification	N	Y	Y
23S rRNA methyltransferase, SpoU_sub_bind/SpoU_methylase superfamily	BN194_18610	YsgA	tRNA/Ribosome assembly/processing	3.6	ribosomal RNA processing (LSU)	N	Y	Y
[citrate (pro-3S)-lyase] ligase	BN194_20340	CitC	Posttranslational modification	3.8	citrate utilisation	N	N	Y
ATP-dependent Clp protease ATP-binding subunit ClpE	BN194_19450	ClpE	Protein folding/turnover	3.9	recycling defective proteins	N	Y	Y
ATP-dependent protease ATPase subunit HslU	BN194_16010	HslU	Protein folding/turnover	3.9	recycling defective proteins	N	Y	Y
Clp endopeptidase ATP-binding subunit	BN194_26350	ClpB2	Protein folding/turnover	3.9	recycling defective proteins	N	Y	Y

ATP-dependent chaperone/Clp protease	BN194_19460	ClpB	Protein folding/turnover	3.9	recycling defective proteins	N	Y	Y
Chaperone ClpB, ClpA/ClpB family	BN194_15500	ClpB	Protein folding/turnover	3.9	recycling defective proteins	Y	Y	Y
ATP-dependent protease ATPase subunit HslU	BN194_16010	HslU	Protein folding/turnover	3.9	recycling defective proteins	N	Y	Y
acetyltransferase (GNAT) family protein	BN194_08200		General prediction only	5	unknown function	N	Y	Y
ABM/COG1359 superfamily protein YcnE/LsrG, putative monooxygenase	BN194_13230	YcnE	General prediction only	5	unknown function	N	Y	Y
tRNA-binding protein, tRNA_domain_binding superfamily, phenylalanine tRNA synthase	BN194_18970	YtpR	General prediction only	5	unknown function (tRNA-associated?)	N	Y	Y
NADPH-dependent FMN reductase, fumarate reductase? Succinate dehydrogenase?	BN194_06540	YieF	General prediction only	5	unknown function (butanoate and pyruvate metabolism?)	N	N	Y
RNA-binding protein, ASCH superfamily	BN194_17420		General prediction only	5	unknown function	N	Y	Y
Putative quinone oxidoreductase YdhH/YhfP, alcohol dehydrogenase, acryly-CoA reductase, ADH_	BN194_07740		General prediction only	5	unknown function (membrane bioenergetics?)	N	N	Y
peptidoglycan-binding lysin	BN194_00330	BacA/ybfG	General prediction only	5	unknown function (glycosyl hydrolase? Cell wall processes)	N	Y	Y
acetyltransferase GNAT family protein	BN194_03130		General prediction only	5	unknown function (transcriptional regulator, TetR family?)	N	N	Y
NADH-flavin reductase, BVR-B_like_SDR_a family	BN194_07680	ywnB	General prediction only	5	unknown function	N	Y	Y
3-hydroxyisobutyrate dehydrogenase family protein Or phosphogluconate dehydrogenase (decarboxylating) activity	BN194_02520	ykwC	General prediction only	5	unknown function (oxidoreductase, phosphogluconate dehydrogenase (decarboxylating) activity?			
3-hydroxyisobutyrate dehydrogenase family protein Or phosphogluconate dehydrogenase (decarboxylating) activity	BN194_30100	glyr1	General prediction only	5	unknown function (oxidoreductase, phosphogluconate dehydrogenase (decarboxylating) activity?	N	N	Y
6-phosphogluconate dehydrogenase	BN194_18660	Gnd[1]	Central glycolytic/intermediary pathways	2.1.2	pentose phosphate pathway	Y	Y	Y
short chain dehydrogenase/reductase family protein	BN194_15480	yqjQ	General prediction only	5	unknown function (oxidoreductase)	N	Y	Y

hydrolase, HAD_like superfamily, uncharacterised phosphatase	BN194_11320	YwpJ	General prediction only	5	unknown function (phosphatase)	N	Y	Y
DUF322 superfamily protein	BN194_18230	YqhY	Unknown/uncharacterized	6	unknown function cell wall stress? Lipid metabolism?	N	N	Y
DUF3800 superfamily protein Transcription	BN194_07060		Unknown/uncharacterized	6	unknown function initiation/termination function?	N	Y	Y
UPF0145 protein, YbjQ_1 superfamily	BN194_07140		Unknown/uncharacterized	6	unknown function (heavy metal binding?)	N	L	Y
hypothetical protein BN194_08190, transmembrane	BN194_08190		Unknown/uncharacterized	6	unknown function	N	Y	Y
DUF965 superfamily protein Phosphotransferase?	BN194_08510		Unknown/uncharacterized	6	unknown function	N	Y	Y
DUF964 superfamily protein	BN194_19080, yheA		Unknown/uncharacterized	6	unknown function biofilm formation?	N	Y	Y
DUF1292 superfamily protein	BN194_08530		Unknown/uncharacterized	6	unknown function	N	Y	Y
Hypothetical protein	BN194_25890		Unknown/uncharacterized	6	unknown function	N	Y	Y
Hypothetical protein	BN194_07660		Unknown/uncharacterized	6	unknown function	N	Y	Y
hypothetical protein	BN194_11770		Unknown/uncharacterized	6	unknown function	N	Y	Y
DegV superfamily protein	BN194_14170		Unknown/uncharacterized	6	unknown function	N	N	Y
PTS(Glucose/Mannose family) IIB, fructose-specific phosphotransferase enzyme IIB component	BN194_02970	LevE/ManX	Phosphotransferase systems	1.2.1	fructose uptake	N	Y	Y
PTS(Glucose/Mannose family) IID	BN194_02990	LevG/ManZ	Phosphotransferase systems	1.2.1	glucose/mannose uptake	N	Y	Y
PTS(Glucose/Mannose family) IIA, Putative mannose-specific EIIAB component	BN194_03000	LevD/ManX	Phosphotransferase systems	1.2.1	mannose uptake	N	Y	Y
PTS (Mannose/Fructose/Sorbose family) IIC	BN194_29710	ManY/SorA_4	Phosphotransferase systems	1.2.1	sorbose uptake	N	Y	Y
PTS (fructose family) subunit IIABC	BN194_27690	FruA	Phosphotransferase systems	1.2.1	fructose uptake	N	Y	Y
PTS (Mannose/Fructose/Sorbose family) IID, mannose permease IID component	BN194_29700	ManZ_9	Phosphotransferase systems	1.2.1	mannose uptake	Y	Y	Y
PTS (Mannose/Fructose/Sorbose family) IIAB, mannose-specific EIIAB component	BN194_29720	ManX_5	Phosphotransferase systems	1.2.1	mannose uptake	Y	Y	Y
PTS (Fructose/Mannitol family) subunit IIA	BN194_30410	MtlA/MtlF	Phosphotransferase systems	1.2.1	mannitol uptake	N	Y	Y
phosphonate ABC transporter substrate-binding protein	BN194_25680	PhnD	ABC-type transporter systems	1.2.2	phosphate/phosphonate uptake	N	Y	Y
ABC-type transporter, ATP-binding component, Nod factor export ATP-binding protein I	BN194_06850, Nod1		ABC-type transporter systems	1.2.2	unknown transport	N	Y	Y

DL-methionine uptake ABC transporter, substrate binding protein, metQ lipoprotein	BN194_13740, MetN/metQ		ABC-type transporter systems	1.2.2	Methionine transport	N	N	Y
oligopeptide transport ATP-binding protein OppD	BN194_17920	OppD	ABC-type transporter systems	1.2.2	oligopeptide uptake	N	Y	Y
spermidine/putrescine import ATP-binding protein PotA	BN194_11290	PotA	ABC-type transporter systems	1.2.2	polyamine uptake?	N	Y	Y
ABC transporter, ATP-binding component	BN194_07730		ABC-type transporter systems	1.2.2	unknown transport	N	Y	Y
maltogenic amylase	BN194_11150	BbmA	Carbohydrate-related metabolism	2.1.1	maltodextrin catabolism	N	Y	Y
pyruvate formate-lyase activating enzyme	BN194_16090	PflA/Act	Carbohydrate-related metabolism	2.1.1	fermentation; end-product formation	N	Y	Y
tagatose 1,6-diphosphate aldolase 2	BN194_07480	LacD2	Carbohydrate-related metabolism	2.1.1	galactose/tagatose catabolism	N	Y	Y
6-phospho-beta-galactosidase	BN194_07320	LacG	Carbohydrate-related metabolism	2.1.1	lactose catabolism	N	Y	Y
N-acetylglucosamine-6-phosphate deacetylase	BN194_02950	ManD	Carbohydrate-related metabolism	2.1.1	N-acetylglucosamine catabolism, cell wall processes	N	N	Y
fructose-1,6-bisphosphatase class 3	BN194_21660	Fpb	Carbohydrate-related metabolism	2.1.1	glycolysis	N	N	Y
apo-citrate lyase phosphoribosyl-dephospho-CoA transferase	BN194_20300	CitX	Tricarboxylic acid pathway	2.1.3	Citrate utilisation	N	N	Y
Phosphate-specific transport system accessory protein	BN194_10290	PhoU	Transcriptional regulation	3.5.2	Regulation of phosphate uptake	N	N	Y
HTH_XRE family transcriptional regulator, MerR family from BLAST/UniProt	BN194_21960		Transcriptional regulation	3.5.2	regulatory role unknown	N	N	Y
MerR family transcriptional regulator	BN194_25900	MerR	Transcriptional regulation	3.5.2	regulation of drug resistance transporter (other function unknown)	N	N	Y
Cold shock protein 1	BN194_06990	Csp	Transcription-associated proteins	3.5.4	RNA chaperone	N	Y	Y
50S ribosomal protein L7/L12	BN194_24080	RplL	Ribosomal proteins	3.7.1	50S (LSU) ribosome	N	Y	Y
phenylalanine--tRNA ligase subunit beta	BN194_18560	PheS	tRNA aminoacyl synthesis	3.7.2	protein synthesis; tRNA charging	N	Y	Y
Putative purine nucleoside phosphoramidase, HIT protein	BN194_19040	HinT2	tRNA aminoacyl synthesis	3.7.2	protein synthesis; tRNA charging	N	N	Y
tryptophan--tRNA ligase	BN194_27360	TrpS	tRNA aminoacyl synthesis	3.7.2	protein synthesis; tRNA charging	N	Y	Y
cysteinyl-tRNA synthetase	BN194_24430	CysS	tRNA aminoacyl synthesis	3.7.2	protein synthesis; tRNA charging	N	N	Y
peptide chain release factor 1	BN194_13510	PrfA	Protein translation (peptide release)	3.7.5	protein synthesis; translation release	N	Y	Y

ribosome-recycling factor	BN194_17650	Frr	Protein translation (peptide release)	3.7.5	protein synthesis; translation release	N	Y	Y

Type equation here.

Annexure 06(a): Proteins found in extracellular fluids (ECF) only and absent in CFE of corresponding Experiment P2 and/or acid stress

Gene locus	Entry	Protein name UniProt	Functional class W56	Function W56	Evidence of signal sequence/ transmembrane/coiled coils	Alternative name and information	Category on the basis of specific growth condition or experiments according to the Key (A/B/C/D)[a]
BN194_02430	K0N547	Alternansucrase	Cell wall biogenesis	peptidoglycan turnover?	Sig. seq,	100kDa, Lysozyme M1 (1,4-beta-N-acetylmuramidase), glycohydrolase	ACID ECF pH4.5>UC, NaN pH6.5; IN CFE but low LFQ FOUND IN TWEEN ECF, ND CFE P2 (A)
BN194_02820	K0N7S8	Putative secreted protein	cell wall biogenesis	peptidoglycan turnover?	Sig. seq.	Putative secreted protein; domain NLPC/P60, endopeptidase; cell wall-associated hydrolase	FOUND IN CITRATE ONLY IN P2 (B) LOW IN ACID CFE; ECF pH4.5 AND UC>>pH6.5
BN194_05270	K0N8C9	Uncharacterized protein	Cell surface proteins/internalins	unknown function	Transmembrane	surface anchor protein? Pilin-related? Pilin adhesin subunit SpaC, LPXTG-anchored	ECF unique to acid stress only (D); UC>pH4.5 = 6.5
BN194_05290	K0MSU3	Cell wall surface anchor family protein	Cell surface proteins/internalins	unknown function	Sig. seq., transmembrane		FOUND IN all ECF P2 and acid stress (C) ND CFE P2, detected CFE acid stress
BN194_06750	K0N2I6	Uncharacterized protein	Cell surface proteins/internalins	unknown function	Sig. seq.	uncharacterized, WxL domain	ECF unique to acid stress UC (D) ND P2 or acid CFE
BN194_24580	K0NAB9	Uncharacterized protein	Cell surface proteins/internalins	cell adhesion	transmembrane	LPXTG-motif cell wall anchor domain	ECF unique to acid stress only (D); UC>pH4.5, NaN pH6.5 ND P2 or acid CFE
BN194_30520	K0NDR4	Uncharacterized protein	Cell surface proteins/internalins	Adhesion	signal peptide	Adhesion exoprotein, MW 135kDa	ECF unique to acid stress only (D), UC only ND P2 or acid CFE
BN194_29460	K0N8D9	PA Serine protease Do-like HtrA,	Protein folding/turnover	recycling defective proteins; protein	Transmembrane		FOUND IN ALL EFC P2 AND ACID STRESS (C); pH6.5>UC>pH4.5

				folding; stress response			ND CFE P2; in CFE acid stress
BN194_01080	K0N4J7	Uncharacterized protein	Unknown/uncharacterized	unknown function	Sig. seq.	13.7 kDa	ECF unique to acid stress only (D) ND CFE pH6.5 or UC; ND ECF or CFE P2; ECF UC NaN
BN194_02560	K0N1V5	Uncharacterized protein	Unknown/uncharacterized	unknown function	Sig seq., coiled coil	cell wall associated hydrolase	ECF unique to acid stress only (D); UC>pH6.5>pH4.5 ND P2 or acid CFE
BN194_05260	K0N2E5	Uncharacterized protein	Unknown/uncharacterized	unknown function	YvcC protein, has signal sequence, secreted protein	multi-drug resistance ABC transporter, BmrA, in *B. subtilis*	FOUND IN ALL EFC P2 AND ACID STRESS ND in P1 and P2 CFEs, detected in CFE acid (C)
BN194_06730	K0N647	Uncharacterized protein	Unknown/uncharacterized	unknown function	Sig. seq	FliK family flagellar hook-length control protein	ECF unique to acid stress only (D), pH4.5/UC>pH6.5 ND P2 CFE or ECF
BN194_21380	K0N9Y1	Uncharacterized protein	Unknown/uncharacterized	unknown function	Sig. seq.		FOUND IN TW, ND CFEs P2 ECF UC>pH4.5, NaN pH6.5; in CFE acid stress, low LFQs
BN194_23630	K0NA78	Uncharacterized protein	Unknown/uncharacterized	unknown function	Sig seq, coiled coil	cell wall associated hydrolase	FOUND IN CIT ECF ONLY, IN ECFs ALL ACID STRESS, LOW LFQs IN CFEs (B)
BN194_29380	K0NB76	Uncharacterized protein	Unknown/uncharacterized	unknown function	Uncharacterized		ECF unique to acid stress only (D); UC>pH 4.5=6.5 ND ECF or CFE P2;
BN194_29420	K0NDJ8	Uncharacterized protein	Unknown/uncharacterized	unknown function	Transmembrane	FliK family flagella hook-length control protein	ECF unique to acid stress only (D) ND ECF or CFE P2
BN194_07700	K0N2V5	Uncharacterized protein	ABC-type transporter systems	unknown transport	Sig. seq.	ABC transporter substrate-binding protein	FOUND IN ECF IN TWEEN (A), ND CFE P2 In ECF pH6.5only; in CFE, pH6.5>>UC=pH4.5
BN194_25450	K0N7Y2	Manganese ABC transporter	ABC-type transporter systems	Mn/Zn ion uptake	Transmembrane		FOUND IN ECF IN ALL P2 ECF; ND ECF acid stress; ND CFE pH4.5 and UC

		substrate-binding lipoprotein					
BN194_02540	K0MS94	Transcriptional regulator lytR	Transcriptional regulation	unknown regulation	Transmembrane	transcriptional regulator	FOUND IN ECF Pe IN CITRATE ONLY (B) In all ECF, pH4.5>, acid stress; in CFE ND P2 CFE
BN194_21700	K0N6U3	Transcriptional regulator lytR	Transcriptional regulation	regulatory role (unknown)	Transmembrane protein		ONLY FOUND IN ECF pH 4.5
BN194_23780	K0NA85	transcriptional regulator	Transcriptional regulation	regulatory role unknown		LytR_4 transcriptional regulator	ECF unique to acid stress only(D)
BN194_12300	K0N472	Predicted Zn-dependent protease		Predicted Zn-dependent protease	Sig. seq. so secreted		ECF unique to acid stress only(D)
BN194_26300	K0N883	PA LPXTG-motif cell wall anchor domain protein		LPXTG-motif cell wall anchor domain protein	Transmembrane, transmembrane helix	250 kDa	ECF unique to acid stress only(D)

[a] Key

A) ECF unique to Tween
B) ECF unique to citrate
C) ECF common in P2 and acid stress
D) ECF unique to acid stress only

UC = uncontrolled pH; ND = not detected; if differences in LFQ varied in ECFs, the relative order of magnitude is shown as > to >>>; NaN = LFQ below detection.

Annexure (6b): Proteins found in in ECF that were also found in the corresponding CFE (Experiment P2 and acid stress)

Gene Locus	**Entry**	**Protein name (UniProt)**	**Putative annotation PA, Sig. seq. or transmembrane?**	**Functional Class**	**Comment**
BN194_01390	K0MRY4	D-alanine--D-alanine ligase		Cell wall biogenesis	Found in CFEs of all, moderate expression
BN194_02140	K0MS53	D-alanyl-D-alanine carboxypeptidase dacA	Sig. seq.	Cell wall biogenesis	Found in CFEs of all, low, 2 NaNs in control
BN194_07350	K0N2R3	UDP-glucose 4-epimerase	GalE	Cell wall biogenesis	Found in all CFEs, very high level of expression, similar in all; cell wall processes

BN194_11560	K0N3V9	glucosamine--fructose-6-phosphate aminotransferase		Cell wall biogenesis	Found in all CFEs, moderate level of expression, same in all
BN194_12550	K0N496	Lipoteichoic acid synthase 1	Transmembrane	Cell wall biogenesis	ND CFE or ECF P2, in pH4.5 ECF only
BN194_16720	K0NAU3	Penicillin-binding protein 1A, PonA	Transmembrane	Cell wall biogenesis	ND CFE or ECF P2; ECF pH4.5>UC, NaN pH6.5
BN194_17200	K0N5G4	Putative N-acetylmuramoyl-L-alanine amidase YrvJ		Cell wall biogenesis	ND CFE or ECF P2; ECF pH4.5>UC, NaN pH6.5
BN194_21500	K0N6S2	Surface antigen	peptidoglycan hydrolase, cell wall amidase, Sig. Seq.	Cell wall biogenesis	ND CFE or ECF P2; ECF pH4.5>>>pH6.5>UC
BN194_21780	K0N6Q5	dTDP-4-dehydrorhamnose 3,5-epimerase	dTDP-4-dehydrorhamnose 3,5-epimerase	Cell wall biogenesis	Found in all CFEs, low expression in all
BN194_05410	K0N2F5	aminopeptidase N	PepN	Amino acid-related metabolism	Found in CFEs, low level of expression, no sig seq, degradation of peptides - see paper that claims Tween enhances peptide degradation
BN194_05520	K0N8E6	cysteine synthase	Cysteine synthase	Amino acid-related metabolism	Found in all CFEs, lower in Tw and Cit relative to control, so differentially represented here; relationship with providing S groups for other protein?
BN194_13540	K0MV12	serine hydroxymethyltransferase	Serine hydroxymethyltransferase	Amino acid-related metabolism	found in all CFEs, slightly up in Tw
BN194_16630	K0N8Q0	neutral endopeptidase	pepO	Amino acid-related metabolism	found in all CFEs, low expression in all; endopeptidase doesn't appear to have a sig seq
BN194_24680	K0NAC2	aminopeptidase C	PepC_2 no signal sequence	Amino acid-related metabolism	Found in all CFEs, mooderate level of expression
BN194_13550	K0N4J8	uracil phosphoribosyltransferase	Uracil phosphoribosyltransferase	Nucleic acid/nucleotide metabolism	Found in all CFEs, moderate expression, slightly higher in Cit & Tw
BN194_21070	K0NBJ2	GMP synthase	GMP synthase	Nucleic acid/nucleotide metabolism	Found in all CFE, moderate expression, higher in Tw
BN194_26010	K0N7F0	adenylate kinase	Adenylate kinase	Nucleic acid/nucleotide metabolism	NOT FOUND in CFE of control, found in other two at low level
BN194_26790	K0MXZ1	CTP synthase	CTP synthase	Nucleic acid/nucleotide metabolism	Found in all CFEs, slightly up in Tw in CFE, minor proteins, normally cytoplasmic - lysis indication?
BN194_22520	K0NBS8	(3R)-hydroxymyristoyl-ACP dehydratase	fabZ	Lipid-related metabolism	Not found in Tw, higher in Cit than control, moderately higly expressed in cit
BN194_15740	K0MVF4	DNA-binding protein HU	Hup haem-utilization protein, DNA binding	DNA replication-related	found in all CFEs, slightly up in Tw
BN194_08960	K0N387	bifunctional phosphatase/peptidyl-prolyl *cis-trans* isomerase	Peptidyl-prolyl cis-trans isomerase	Protein folding/turnover	Found in all CFEs, even expression, NOT seen in MRS. interconverts the *cis* and *trans* isomers of peptide bonds with the amino acid proline
BN194_15330	K0N884	trigger factor Tig	cytosolic ribosome-associated chaperone	Protein folding/turnover	Found in CFE Undetected ECF P2
BN194_17460	K0N5C7	chaperone protein DnaK	DnaK	Protein folding/turnover	found in all CFE, similar level of expression in all
BN194_19060	K0N5Q8	foldase protein prsA	PrsA, foldase	Protein folding/turnover	Undetected in ECF

BN194_23760	K0N700	class I heat-shock protein (chaperonin) small subunit	GroS	Protein folding/turnover	Found in all CFE, abscent in ECF control
BN194_04740	K0MSP8	NADH peroxidase	Npr protein NADH oxidase	Cell defense/detoxification	highly expressed in all in CFE
BN194_18760	K0N5N7	hydroquinone dioxygenase-like GLO_EDI_BRP_like superfamily protein	Putative ring-cleaving dioxygenase mhqA	General prediction only	Found in all CFEs, low expression, similar in all
BN194_24320	K0NC29	sex pheromone lipoprotein (similar to cAD1 in E. faecalis)	Putative FMN-binding domain protein, sig seq, membrane location	General prediction only	Found in all CFEs, low expression, lower in Tw; sex pheromone?
BN194_00240	K0MRM8	Possible TrsG protein	Putative peptidoglycan hydrolase, surface antigen, SibA domain; sig. seq., coiled coils	Unknown/uncharacterized	ND CFE or ECF P2; ECF pH4.5>>>pH6.5>UC
BN194_20240	K0MWI3	Uncharacterized protein	Sig. seq., MW 20kDa	Unknown/uncharacterized	ND CFE or ECF P2; ECF C>pH4.5=pH6.5
BN194_27250	K0N8I3	Uncharacterized protein	YpuA, DUF1002, uncharacterized extracellular protein	Unknown/uncharacterized	ND CFE or ECF P2; ECF UC>pH4.5, NaN pH6.5
BN194_15780	K0N8E8	DUF161/DUF2179 superfamily protein	uncharacterized	Unknown/uncharacterized	Found in CFEs, moderate expression
BN194_19430	K0N9I2	phosphocarrier protein HPr	ptsH phosphoenolpyruvate-dependent sugar phosphotransferase system	Phosphotransferase systems	Found in all CFEs, up in Tw; PTS for what? No sig seq, labelled as cytoplasmic but this is anomalous given transport happens at the surface
BN194_29720	K0NDL4	PTS (Mannose/Fructose/Sorbose family) IIAB	ManX, PTS glucose/mannose family	Phosphotransferase systems	NOT detected in Control CFE, low level of expression in Tw and Cit; low expression levels. NOT seen in ECF for MRS cultures cells
BN194_17880	K0N983	oligopeptide-binding protein OppA	OppA, Oligopeptide-binding protein, sig. seq.	ABC-type transporter systems	Found in CFEs, moderate expression
BN194_07710	K0N2Z3	Uncharacterized protein	ABC transporter substrate-binding protein; sig. seq.	ABC-type transporter systems	ND CFE or ECF P2; ECF _pH6.
BN194_20640	K0MWL6	oligopeptide ABC-type transporter, substrate-binding protein	OppA_2, sig. seq., second OppA later	ABC-type transporter systems	Found in all CFE Tw expt, low level of expression, found in water wash in Adu's heat growth expt
BN194_01410	K0N1L0	D-lactate dehydrogenase, putative	PA D-Ldh or D-2-hydroxyisocaproate dehydrogenase	Carbohydrate-related metabolism	Found in all CFE, not found in acid growth expt, so related to suppression by glucose? And citrate. Leucine metabolism
BN194_06930	K0N662	trehalose-6-phosphate hydrolase	Trehalose-6-phosphate hydrolase	Carbohydrate-related metabolism	Found in all CFEs, low expression in all, related to starvation, catabolite suppressed?
BN194_07340	K0MTA3	galactokinase	GalK galactokinase	Carbohydrate-related metabolism	Found in all CFE, very high expression
BN194_11340	K0MU95	phosphate acetyltransferase	Pta, Phosphate acetyltransferase	Carbohydrate-related metabolism	found in all CFEs, moderate expr
BN194_16080	K0N8I5	formate acetyltransferase	plfB Formate acetyltransferase or pyruvate formate lyase	Carbohydrate-related metabolism	found in all CFEs, highest in Cit, Tw higher than control; highly expressed
BN194_19890	K0MWF9	N-acetylglucosamine-6-phosphate deacetylase	NagA N-acetylglucosamine-6-phosphate deacetylase	Carbohydrate-related metabolism	found in all CFEs, similar expression in all

BN194_26560	K0N7J5	L-lactate dehydrogenase	L-lactate dehydrogenase	Carbohydrate-related metabolism	Found in all CFEs, highly abundant protein. Enriched in LiCl but not in acid-grown cells in ECF. 2nd Ldh = K0N8S5, low expression in CFEs.
BN194_27060	K0N7P0	tagatose 1,6-diphosphate aldolase 2	LacD2 Tagatose 1,6-diphosphate aldolase	Carbohydrate-related metabolism	Note 2 LacD2 in CFE; this protein highly expressed in all, up in Control
BN194_30440	K0MYW0	glucosamine-6-phosphate deaminase	Nag B	Carbohydrate-related metabolism	Found in all CFEs, slightly up in Tw
BN194_05060	K0N2C9	fructose-bisphosphate aldolase	Fba_2 protein fructose bisphosphate aldolase	Central glycolytic/intermediary pathways	found in all CFEs, very highly expressed
BN194_07390	K0MTA8	galactose 1-epimerase, aldos_epim superfamily	Gal M PA aldose 1-epimerase	Central glycolytic/intermediary pathways	found in all CFE, slightly up in Tw and Cit Vs Control
BN194_11010	K0N3R3	glyceraldehyde-3-phosphate dehydrogenase	Gap	Central glycolytic/intermediary pathways	Found in all CFEs, very highly expressed in all, even expression
BN194_11020	K0N9R1	phosphoglycerate kinase	phosphoglycerate kinase	Central glycolytic/intermediary pathways	Found in all CFEs, highly abundant
BN194_11030	K0N736	triosephosphate isomerase	Triosephosphate isomerase	Central glycolytic/intermediary pathways	Found in all CFEs, moderately highly expressed, even expression - slightly higher in Cit and Tw?
BN194_11040	K0MU67	enolase	Enolase	Central glycolytic/intermediary pathways	found in all CFE, highly expressed, slightly down in Tw and Cit Vs Control
BN194_12580	K0N7I6	glucose-6-phosphate isomerase	Glucose-6-phosphate isomerase	Central glycolytic/intermediary pathways	Found in all CFE Undetected in ECF
BN194_15080	K0N860	Pyruvate dehydrogenase E1 component subunit alpha	PdhA	Central glycolytic/intermediary pathways	Found in all CFE, moderate expressing, up in Cit
BN194_15090	K0MVA7	pyruvate dehydrogenase E1 component subunit beta	PdhB	Central glycolytic/intermediary pathways	found in all CFEs, slightly up in Tw
BN194_15100	K0N4W5	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	PdhC	Central glycolytic/intermediary pathways	Found in all CFEs, highly expressed, higher in Cit
BN194_15110	K0N4P1	dihydrolipoyl dehydrogenase	PdhD	Central glycolytic/intermediary pathways	found in all CFEs, moderate expr, higher in Cit
BN194_15570	K0NAK6	6-phosphofructokinase	6 phosphofructokinase	Central glycolytic/intermediary pathways	Found in all CFEs, even expression
BN194_15580	K0N8B6	pyruvate kinase	Pyruvate kinase pyk	Central glycolytic/intermediary pathways	Found in all CFE, even expression, high level of expression
BN194_18420	K0NB57	glucokinase	GlcK glucokinase	Central glycolytic/intermediary pathways	Found in all CFEs, slightly higher in Tw, low-moderate expression
BN194_18660	K0N5N2	6-phosphogluconate dehydrogenase	6-phosphogluconate dehydrogenase, PPP	Central glycolytic/intermediary pathways	Found in all CFEs, moderately high level of expression, not up against control in Cit, forms ribulose 5-phosphate from 6-phosphogluconate
BN194_22740	K0MX58	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	Central glycolytic/intermediary pathways	Found in CFE, moderate level of expressioin, similar for all
BN194_20290	K0MWI8	oxaloacetate decarboxylase, alpha subunit	PycB protein - pyruvate carboxylase, towards oxaloacetate	Tricarboxylic acid pathway	found in all CFEs, highly expressed in Cit, slightly up in Tw, (S)-methylmalonyl-CoA + pyruvate = propanoyl-CoA + oxaloacetate

BN194_20310	K0N607	citrate lyase alpha subunit	CitF	Tricarboxylic acid pathway	Found in all CFEs, moderately high in Tw and Control, very high in Cit
BN194_26330	K0NAN3	DNA-directed RNA polymerase subunit beta'	rpoC	RNA polymerase	Found in all CFEs, moderate expression
BN194_11600	K0N3Z3	DNA-binding regulatory protein, YebC/PmpR family	PA Probable transcriptional regulatory protein	Transcriptional regulation	Found in all CFEs, low level of expression; NOT seen in MRS -
BN194_06990	K0MT67	Cold shock protein 1	csp, DNA binding trans reg	Transcription-associated proteins	NaN in control CFE, low expression level in Tw/Cit
BN194_12460	K0N438	Cold shock-like protein CspLA	CspLA protein, RNA chaperone	Transcription-associated proteins	Found in all CFEs, Cold shock-like; low level of expression in all
BN194_17580	K0N927	transcription elongation protein NusA	nusA transcription termination and antitermination	Transcription-associated proteins	found in CFEs, up in Cit
BN194_21700	K0N6U3	Transcriptional regulator lytR	LytR_3, transmembrane	Transcriptional regulation	ND ECF or CFE P2; in pH4.5 ECF only
BN194_15720	K0NAL9	30S ribosomal protein S1	YpdF 30S ribosomal protein S1 homolog	Ribosomal proteins	Found in all CFE and ECF
BN194_26110	K0N7F9	50S ribosomal protein L24	50S ribosomal protein L24	Ribosomal proteins	Found in all CFE Undetected in EFC
BN194_11960	K0N3Z6	glutamyl-tRNA(Gln) amidotransferase subunit A	Glutamyl-tRNA(Gln) amidotransferase subunit	tRNA aminoacyl synthesis	Found in all CFEs, same expression in all; NOT seen in MRS
BN194_11970	K0NA01	aspartyl/glutamyl-tRNA amidotransferase subunit B	gatB Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit	tRNA aminoacyl synthesis	Allows the formation of correctly charged Asn-tRNA(Asn) or Gln-tRNA(Gln) through the transamidation of misacylated Asp-tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both of asparaginyl-tRNA or glutaminyl-tRNA synthetases. Lysis indicator? low abundance, no sig seq
BN194_14810	K0N4L9	isoleucine--tRNA ligase	Isoleucine--tRNA ligase	tRNA aminoacyl synthesis	found in all CFEs, moderate expression, similar expression in all Tw/Cit/C
BN194_16760	K0N569	asparagine--tRNA ligase	Asparagine--tRNA ligase	tRNA aminoacyl synthesis	found in all CFE, moderate exp, same in all
BN194_17610	K0N5E2	Proline--tRNA ligase	Proline--tRNA ligase	tRNA aminoacyl synthesis	Allows the formation of correctly charged Asn-tRNA(Asn) or Gln-tRNA(Gln) through the transamidation of misacylated Asp-tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both of asparaginyl-tRNA or glutaminyl-tRNA synthetases. Lysis indicator?
BN194_18860	K0N5P5	threonine--tRNA ligase	Threonine--tRNA ligase	tRNA aminoacyl synthesis	Found in all CFEs, moderate expression, up in cit and Tw Vs control
BN194_24470	K0NC38	glutamate--tRNA ligase	Glutamate--tRNA ligase	tRNA aminoacyl synthesis	Found in all CFEs, low expression, higher in Cit than Tw
BN194_26380	K0NAN7	lysine--tRNA ligase	lysS Lysine-tRNA ligase	tRNA aminoacyl synthesis	Found in all CFEs, low level of expression
BN194_27130	K0NAU5	methionine--tRNA ligase	metG Methionine-tRNA ligase	tRNA aminoacyl synthesis	Found in all CFEs, low level of expression but higher in Cit
BN194_15150	K0N4W9	GTP-binding protein TypA/BipA	TypA Belongs to the TRAFAC class translation factor GTPase superfamily. Classic translation	Protein translation (elongation)	

			factor GTPase family. TypA subfamily.		
BN194_15310	K0N4R1	elongation factor Tu	Elongation factor Tu	Protein translation (elongation)	Found in all CFE, very highly expressed, slightly up in Cit, control and Tw identical
BN194_17670	K0NB01	elongation factor Ts	Elongation factor Ts	Protein translation (elongation)	Found in all CFEs, even expression, moderate level of expression
BN194_26270	K0NCN8	elongation factor G	Elongation factor G	Protein translation (elongation)	Found in all CFEs, higher in Tw, highly expressed.

Annexure 07: CHAPTER 05

(7a)Protein FC CFE pH 4.5 vs CFE pH 6.5

Protein names	Functional Class	Gene	Gene locus	Protein IDs	-Log t-test p-value	t-test difference	Fold change
Putative thiamine pyrophosphate-containing protein ydaP	Carbohydrate-related metabolism	*ydaP*	BN194_05070	K0N8B1	5.91	7.53	184.81
Probable dipeptidase A (EC 3.4.-.-)	Amino acid-related metabolism	*pepDA*	BN194_00410	K0N1E0	5.40	6.58	95.66
Esterase/lipase	General prediction only	*yneB*	BN194_20230	K0N9P7	4.36	6.40	84.31
Uncharacterized aminotransferase SSO0104 (EC 2.6.1.-)	*Amino acid-related metabolism*		BN194_27600	K0N8N4	2.53	4.87	29.20
Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	4.29	4.70	26.08
Acid shock protein	Protein folding/turnover		BN194_29440	K0MYM2	4.94	4.61	24.41
Deoxyguanosine kinase (EC 2.7.1.113)	*Nucleic acid/nucleotide metabolism*		BN194_14000	K0N4M7	4.32	4.61	24.39
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	*accA*	BN194_22470	K0NBS6	6.74	4.57	23.71
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*pip_2*	BN194_27140	K0MY30	4.66	4.55	23.51
Uncharacterized protein	Unknown/uncharacterized		BN194_16570	K0NAT3	2.52	4.51	22.82
Hydroxyacid oxidase (EC 1.1.3.15)	Central glycolytic/intermediary pathways	*haox*	BN194_24790	K0MXH5	7.27	4.49	22.49

5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Cobalamin-independent methionine synthase) (Methionine synthase, vitamin-B12 independent isozyme)	Amino acid-related metabolism	*metE*	BN194_06880	K0N658	6.20	4.38	20.87
4-hydroxy-tetrahydrodipicolinate synthase (HTPA synthase) (EC 4.3.3.7)	Amino acid-related metabolism	*dapA*	BN194_01010	K0N1I2	4.71	4.34	20.28
Peptidase T (EC 3.-.-.-) (EC 3.4.11.-) (EC 3.4.11.4)	Amino acid-related metabolism	*pepT*	BN194_03110	K0N213	5.28	4.11	17.24
Uncharacterized protein	Unknown/uncharacterized		BN194_25890	K0MXR4	3.66	4.09	17.08
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (ACCase subunit beta) (Acetyl-CoA carboxylase carboxyltransferase subunit beta) (EC 6.4.1.2)	Lipid-related metabolism	*accD*	BN194_22480	K0NA32	1.84	3.93	15.23
Probable amino-acid ABC transporter-binding protein HI_1080	*ABC-type transporter systems*		BN194_06710	K0N2R6	5.92	3.91	15.08
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_2*	BN194_03120	K0N7V6	5.46	3.80	13.96
D-alanine--poly(phosphoribitol) ligase subunit 2 (EC 6.1.1.13) (D-alanyl carrier protein)	Cell wall biogenesis	*dltC*	BN194_08610	K0N361	3.30	3.69	12.87
30S ribosomal protein S14	Ribosomal proteins	*rpsN*	BN194_09950	K0N3D1	2.00	3.42	10.72
Transaldolase (EC 2.2.1.2)	Central glycolytic/intermediary pathways	*fsa*	BN194_28440	K0MYF0	2.94	3.35	10.21
Phage capsid protein	Prophage genome		BN194_30330	K0NBD3	2.65	3.20	9.21
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	*pepDB*	BN194_21110	K0N678	4.86	3.19	9.14
Uncharacterized protein ybbP	Unknown/uncharacterized	*ybbP*	BN194_11530	K0N776	1.43	3.00	8.02
Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase)	Nucleic acid/nucleotide metabolism	*pyrB*	BN194_16480	K0N8N2	5.06	2.99	7.93
Uncharacterized protein				K0N2Q1;K0MXJ1	4.22	2.93	7.60
Glycolate oxidase subunit glcD	General prediction only	*glcD*	BN194_24440	K0MXF3	2.88	2.90	7.48
LexA repressor (EC 3.4.21.-) (EC 3.4.21.88)	DNA repair/recombination	*lexA*	BN194_07970	K0N944	1.20	2.86	7.27

Cytochrome d ubiquinol oxidase subunit 1 (EC 1.10.3.-)	Membrane bioenergetics	*cydA_2*	BN194_23410	K0N6Y2	1.74	2.80	6.98
Uncharacterized protein	Unknown/uncharacterized		BN194_20070	K0NBE0	4.76	2.78	6.87
Penicillin acylase (EC 3.5.1.11)	Cell defense/detoxification		BN194_04910	K0N2B8	4.20	2.76	6.79
Glucose 1-dehydrogenase 2 (EC 1.1.1.47)	Central glycolytic/intermediary pathways	*gdhII*	BN194_23130	K0NA64	2.51	2.76	6.79
Uncharacterized protein yeaO	Unknown/uncharacterized	*yeaO*	BN194_08040	K0MTJ2	1.90	2.73	6.65
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	2.30	2.69	6.45
Uncharacterized protein yxjH	Amino acid-related metabolism	*yxjH*	BN194_08320	K0N962	3.51	2.63	6.18
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E_2,P100*	BN194_05160	K0N2D7	3.47	2.62	6.14
Uncharacterized protein	Unknown/uncharacterized		BN194_19210	K0N5R7	1.71	2.60	6.08
Pyridoxine 5'-phosphate oxidase V related favin-nucleotide-binding protein	Cofactor-related metabolism		BN194_01900	K0N1E7	3.14	2.59	6.02
Lipoprotein	ABC-type transporter systems	*metQ_2*	BN194_13740	K0MV23	6.19	2.59	6.01
Methionine import ATP-binding protein MetN (EC 3.6.3.-)	ABC-type transporter systems	*metN*	BN194_13750	K0N4L1	5.43	2.55	5.84
Protein lacX, plasmid	Carbohydrate-related metabolism	*lacX*	BN194_27070	K0NCY0	4.32	2.53	5.77
Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) (Peptide-methionine (R)-S-oxide reductase)	Posttranslational modification	*msrB*	BN194_17090	K0MVR6	1.49	2.52	5.75
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE*	BN194_01720	K0N7C1	5.95	2.52	5.73
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	*mco*	BN194_25410	K0N7A4	4.69	2.51	5.69
Putative secreted protein	cell wall biogenesis		BN194_02820	K0N7S8	1.66	2.50	5.67
GTPase HflX (GTP-binding protein HflX)	tRNA/Ribosome assembly/processing	*hflX*	BN194_21260	K0N689	4.59	2.50	5.66
Uncharacterized protein	Unknown/uncharacterized		BN194_29450	K0N932	4.96	2.42	5.36

S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	*luxS*	BN194_08330	K0N6J0	4.34	2.41	5.31
tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	tRNA/Ribosome assembly/processing	*mnmG,gidA*	BN194_30590	K0MYX4	3.29	2.36	5.15
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA1, greA*	BN194_02150	K0N1G7	2.12	2.36	5.12
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO*	BN194_12030	K0N7B7	4.63	2.30	4.92
Uncharacterized protein	Unknown/uncharacterized		BN194_15520	K0NAK2	4.65	2.29	4.87
Ribonuclease P protein component (RNase P protein) (RNaseP protein) (EC 3.1.26.5) (Protein C5)	tRNA/Ribosome assembly/processing	*rnpA*	BN194_30620	K0NDS2	1.10	2.27	4.84
Uncharacterized protein	Unknown/uncharacterized		BN194_17360	K0N5B9	1.43	2.26	4.79
NAD-dependent epimerase/dehydratase:3-beta hydroxysteroid dehydrogenase/isomerase:NmrA-like	General prediction only		BN194_25520	K0NCC8	3.78	2.24	4.71
Uncharacterized protein	Unknown/uncharacterized		BN194_28350	K0N8V3	4.16	2.24	4.71
Dumpy	Cell surface proteins/internalins	*dp*	BN194_05390	K0MSV0	0.52	2.21	4.61
Uncharacterized protein yqeY	Unknown/uncharacterized	*yqeY*	BN194_17040	K0MVR2	4.19	2.16	4.46
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	*tpiA*	BN194_11030	K0N736	4.08	2.12	4.36
Chaperone protein DnaJ	Protein folding/turnover	*dnaJ*	BN194_17450	K0N5J4	4.09	2.12	4.35
Uncharacterized peptidase yqhT (EC 3.4.-.-)	Amino acid-related metabolism	*yqhT*	BN194_18260	K0N5K4	4.64	2.11	4.32
CBS domain-containing protein	Unknown/uncharacterized		BN194_26610	K0N7J7	3.72	2.08	4.24
Xre-like DNA-binding protein	Transcriptional regulation		BN194_10050	K0N3E1	0.62	2.05	4.14
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	*BN194_21350*	BN194_21780	K0N6Q5	3.90	2.02	4.04
Uncharacterized protein yhfI	General prediction only	*yhfI*	BN194_19200	K0N627	3.80	2.00	4.00

Uncharacterized protein	Unknown/uncharacterized		BN194_20190	K0MWI0	3.95	1.99	3.98
Malolactic enzyme (EC 1.-.-.-)	Tricarboxylic acid pathway	*mleA*	BN194_08070	K0N949	3.13	1.99	3.96
30S ribosomal protein S9	Ribosomal proteins	*rpsI*	BN194_25840	K0MXR0	0.31	1.98	3.94
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	4.82	1.96	3.88
Zinc-type alcohol dehydrogenase-like protein SE_1777	General prediction only		BN194_07910	K0N329	3.05	1.92	3.79
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC*	BN194_24670	K0NC50	4.90	1.92	3.77
ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136) (ADP-dependent NAD(P)HX dehydratase)	Cofactor-related metabolism	*nnrD*	BN194_09250	K0N360	2.97	1.86	3.64
Cysteine desulfurase (EC 2.8.1.7)	Cofactor-related metabolism	*csd*	BN194_13790	K0MV25	3.43	1.84	3.59
Integral membrane protein	Unknown/uncharacterized		BN194_07890	K0MTI0	1.45	1.83	3.56
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	*agaS*	BN194_02940	K0MSD9	5.66	1.83	3.55
Uncharacterized protein	Unknown/uncharacterized		BN194_05660	K0N2I2	1.42	1.82	3.53
Uncharacterized protein YPL245W	Unknown/uncharacterized		BN194_25000	K0N7U3	4.25	1.79	3.46
50S ribosomal protein L33	Ribosomal proteins	*rpmG*	BN194_20200	K0N697	0.37	1.78	3.44
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	*groS,grES*	BN194_23760	K0N700	4.66	1.77	3.42
S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	*metK*	BN194_09150	K0N352	6.20	1.76	3.38
Uncharacterized protein ynbB	Cell defense/detoxification	*ynbB*	BN194_18380	K0N9B7	3.58	1.75	3.36
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_02890	K0MSD4	3.05	1.75	3.35
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB*	BN194_17900	K0N5S3	0.84	1.75	3.35
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_4*	BN194_22020	K0NBQ1	4.97	1.74	3.34
Sorbose permease IIC component	Phosphotransferase systems	*sorA_4*	BN194_29710	K0N8G4	4.79	1.73	3.33
DltD protein	Cell wall biogenesis		BN194_08620	K0N978	4.33	1.72	3.30

Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA*	BN194_17880	K0N983	3.94	1.70	3.26
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	2.39	1.70	3.25
Uncharacterized protein	Unknown/uncharacterized		BN194_25540	K0MXN3	0.98	1.70	3.24
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	*map*	BN194_12230	K0N7E0	4.28	1.69	3.23
Beta-galactosidase 17 (EC 3.2.1.23)	Carbohydrate-related metabolism	*BGAL17*	BN194_02960	K0N204	0.74	1.69	3.22
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	*pepQ*	BN194_08740	K0MTP0	3.52	1.69	3.22
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_3*	BN194_21990	K0MWY0	2.32	1.68	3.21
Ferredoxin--NADP reductase (FNR) (Fd-NADP(+) reductase) (EC 1.18.1.2)	Membrane bioenergetics		BN194_08950	K0N337	3.59	1.65	3.14
Mannose permease IID component	Phosphotransferase systems	*manZ_9*	BN194_29700	K0N954	4.51	1.64	3.12
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP*	BN194_17930	K0N988	0.77	1.62	3.07
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	*clpC*	BN194_21680	K0N9Z7	5.40	1.61	3.05
Predicted pyrophosphatase	General prediction only		BN194_15360	K0N4R6	3.57	1.59	3.02
Exodeoxyribonuclease 7 small subunit (EC 3.1.11.6) (Exodeoxyribonuclease VII small subunit)	DNA repair/recombination	*xseB*	BN194_18190	K0MW55	3.03	1.59	3.01
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	*dltA*	BN194_08590	K0MTN0	4.65	1.59	3.01
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE*	BN194_13710	K0N4D8	2.81	1.58	2.98
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA_2*	BN194_29210	K0N8B2	4.00	1.57	2.98
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	*alsS*	BN194_20150	K0N695	2.92	1.55	2.93
Uncharacterized protein			BN194_21520	K0NBL8	0.58	1.55	2.93

Ribonuclease Z (RNase Z) (EC 3.1.26.11) (tRNA 3 endonuclease) (tRNase Z)	tRNA/Ribosome assembly/processing	*rnz*	BN194_15470	K0NAK0	1.34	1.55	2.92
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*manX_5*	BN194_29720	K0NDL4	3.80	1.55	2.92
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP*	BN194_08180	K0N6I0	4.70	1.54	2.91
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	*dhaM*	BN194_04960	K0N2C2	4.26	1.54	2.91
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	*fabK*	BN194_22580	K0NA38	5.43	1.54	2.90
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	*atpH*	BN194_13590	K0MV16	4.38	1.53	2.89
Virulence factor mviM	General prediction only	*mviM*	BN194_13310	K0N4B2	4.76	1.53	2.89
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism		BN194_22460	K0N6M0	3.76	1.50	2.84
Uncharacterized protein	Unknown/uncharacterized		BN194_24220	K0NC21	0.97	1.50	2.83
Uncharacterized protein	Unknown/uncharacterized		BN194_27210	K0N7Q6	2.97	1.50	2.83
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	*atpD*	BN194_13620	K0NAB3	4.20	1.50	2.82
GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	4.56	1.49	2.82
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	*queA*	BN194_08370	K0N965	5.74	1.49	2.81
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrDA, pyrD*	BN194_19150	K0N623	4.45	1.48	2.79
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ_2*	BN194_20470	K0NBG3	1.30	1.48	2.78
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*manD*	BN194_02950	K0N1P4	6.26	1.43	2.70
Uncharacterized protein	*Cell surface proteins/internalins*		BN194_20060	K0N5Y7	2.65	1.41	2.66
Uncharacterized protein	Unknown/uncharacterized		BN194_07550	K0N2T9	1.28	1.41	2.65

TPR repeat-containing protein ypiA	Unknown/uncharacterized	*ypiA*	BN194_15750	K0N517	3.97	1.38	2.61
Uncharacterized protein	General prediction only		BN194_30000	K0N979	2.07	1.38	2.61
Uncharacterized protein ytxK	DNA repair/recombination	*ytxK*	BN194_11680	K0N791	3.38	1.37	2.59
Protein veg	Unknown/uncharacterized	*veg*	BN194_27010	K0N7N4	1.54	1.37	2.58
L-sorbose 1-phosphate reductase (EC 1.1.1.-)	Carbohydrate-related metabolism	*sorE*	BN194_04300	K0N1W2	1.58	1.34	2.53
Large-conductance mechanosensitive channel	Other transporter proteins	*mscL*	BN194_26890	K0MY02	2.83	1.34	2.53
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	*pepN*	BN194_05410	K0N2F5	4.76	1.34	2.52
Surface antigen	Cell wall biogenesis		BN194_21500	K0N6S2	3.31	1.33	2.52
Probable calcium-transporting ATPase (EC 3.6.3.8)	Other transporter proteins	*pacL*	BN194_11490	K0MUB1	2.75	1.33	2.51
Transcriptional regulator, PadR-like family	Transcriptional regulation		BN194_26580	K0NAQ3	1.11	1.32	2.50
Uncharacterized protein	Unknown/uncharacterized		BN194_01870	K0N7D4	4.65	1.31	2.49
Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	*Steap4*	BN194_01990	K0MS41	4.56	1.31	2.48
Uncharacterized protein ACIAD3023	Cell defense/detoxification		BN194_07010	K0N2T5	0.67	1.31	2.48
Uncharacterized protein	General prediction only		BN194_28370	K0NDC5	2.52	1.31	2.48
Uncharacterized protein	RNA degradation		BN194_11250	K0N3V2	3.16	1.30	2.46
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	*atpG*	BN194_13610	K0N4D3	4.06	1.27	2.41
Guanine deaminase (EC 3.5.4.3)	Nucleic acid/nucleotide metabolism	*guaD*	BN194_13320	K0NA96	5.51	1.27	2.40
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*fruA_3*	BN194_15410	K0N4S1	1.12	1.26	2.39
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI*	BN194_07860	K0N327	2.96	1.26	2.39
Uncharacterized protein	Unknown/uncharacterized		BN194_15540	K0MVD8	2.19	1.26	2.39

Type I restriction enzyme EcoR124II M protein (EC 2.1.1.72)	IS elements/foreign DNA defense	*hsdM*	BN194_22340	K0MX17	3.44	1.26	2.39
Cytidine deaminase (EC 3.5.4.5)	Nucleic acid/nucleotide metabolism	*cdd*	BN194_17000	K0N5D8	1.79	1.22	2.34
Esterase/lipase	General prediction only		BN194_30390	K0MYV7	3.83	1.22	2.33
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	*ppaC*	BN194_16110	K0N4Z4	4.76	1.22	2.33
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_3*	BN194_14020	K0NAD1	2.39	1.22	2.33
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	*msrA_2,msrA*	BN194_15860	K0N4W6	0.39	1.21	2.32
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		BN194_08960	K0N387	3.17	1.21	2.32
Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase (EC 4.2.-.-)	*tRNA/Ribosome assembly/processing*		BN194_17370	K0NAY4	1.73	1.20	2.29
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB_2*	BN194_29110	K0N8A4	3.13	1.18	2.27
Uncharacterized protein	Unknown/uncharacterized		BN194_20720	K0NBH5	5.38	1.18	2.26
Uncharacterized protein	Unknown/uncharacterized		BN194_30140	K0MYT6	2.62	1.17	2.25
Uncharacterized protein yxkA	General prediction only	*yxkA*	BN194_27230	K0NAV1	3.74	1.16	2.23
Uncharacterized protein	Unknown/uncharacterized		BN194_21380	K0N9Y1	2.14	1.14	2.20
Kinase, putative	General prediction only		BN194_29890	K0MYR0	3.03	1.13	2.19
Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	*nfo*	BN194_17070	K0NAW5	2.50	1.13	2.19
Uncharacterized protein yqgF	Cell wall biogenesis	*yqgF*	BN194_18440	K0MW71	2.42	1.13	2.18
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	*dhaK_2*	BN194_04980	K0N5Q3	4.32	1.12	2.18
Uncharacterized protein yjbK	General prediction only	*yjbK*	BN194_09860	K0N3G6	2.95	1.12	2.17
ErfK family protein	Cell wall biogenesis		BN194_26570	K0NCS1	2.21	1.12	2.17

tRNA modification GTPase MnmE (EC 3.6.-.-)	tRNA/Ribosome assembly/processing	*mnmE,trmE*	BN194_30600	K0N9F0	2.79	1.11	2.15
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrD*	BN194_16440	K0MVL3	3.76	1.08	2.12
Carboxy-terminal processing protease CtpA (EC 3.4.21.102)	Protein folding/turnover	*ctpA*	BN194_15880	K0N8G1	4.19	1.08	2.12
Uridine phosphorylase (EC 2.4.2.3)	Nucleic acid/nucleotide metabolism	*udp*	BN194_24830	K0NAD0	2.88	1.08	2.12
NADH-dependent butanol dehydrogenase A (EC 1.1.1.-)	Carbohydrate-related metabolism	*bdhA*	BN194_22640	K0MX50	3.00	1.08	2.11
Alanine racemase (EC 5.1.1.1)	Amino acid-related metabolism	*alr*	BN194_26680	K0NAR1	4.37	1.07	2.09
Uncharacterized protein	Unknown/uncharacterized		BN194_01080	K0N4J7	1.24	1.06	2.09
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacA*	BN194_07500	K0N2T4	2.28	1.06	2.09
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	*yabR*	BN194_26500	K0N8A7	2.41	1.06	2.08
UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.3.1.98) (UDP-N-acetylmuramate dehydrogenase)	Cell wall biogenesis	*murB*	BN194_11400	K0N3X0	2.95	1.05	2.07
Glutamate--cysteine ligase/gamma-glutamylcysteine synthetase	Cofactor-related metabolism	*gshAB*	BN194_13910	K0N4F0	4.21	1.04	2.06
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP_2, acpP*	BN194_22590	K0MX45	2.38	1.03	2.05
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_27170	K0NCZ6	3.78	1.02	2.02
Septum site-determining protein DivIVA	Cytokinesis	*divIVA*	BN194_14800	K0N4T8	3.20	1.01	2.02
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA*	BN194_09090	K0MTR3	2.75	0.99	1.99
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	*rpoZ*	BN194_18100	K0N5T7	0.95	0.99	1.98

Ribosome maturation factor RimP	tRNA/Ribosome assembly/processing	*rimP*	BN194_17590	K0MVW3	0.62	0.99	1.98
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	*accB*	BN194_22530	K0NA35	1.19	0.98	1.98
Probable glutamine ABC transporter permease protein glnP	ABC-type transporter systems	*glnP*	BN194_21410	K0N6A4	0.57	0.98	1.97
ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	*atpF*	BN194_13580	K0N7S9	3.18	0.98	1.97
Uncharacterized metallophosphoesterase yunD	Nucleic acid/nucleotide metabolism	*yunD*	BN194_08890	K0MTQ0	3.17	0.98	1.97
Uncharacterized protein	General prediction only	*gpm1*	BN194_13960	K0N4F5	0.37	0.97	1.96
FemAB family protein	General prediction only		BN194_22880	K0NA57	2.20	0.97	1.96
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	*asd*	BN194_01060	K0N1I5	3.51	0.96	1.94
Diaminopimelate decarboxylase (DAP decarboxylase) (DAPDC) (EC 4.1.1.20)	Amino acid-related metabolism	*lysA*	BN194_01030	K0N4I7	1.16	0.95	1.93
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	*dnaK*	BN194_17460	K0N5C7	4.28	0.95	1.93
Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*leuS*	BN194_09210	K0N3A9	4.37	0.95	1.93
50S ribosomal protein L21	Ribosomal proteins	*rplU*	BN194_18290	K0MW61	2.38	0.95	1.93
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	*ilvE*	BN194_21620	K0NBM4	4.87	0.94	1.92
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*pheT*	BN194_18560	K0N5M4	3.27	0.93	1.90
Uncharacterized protein ycaC	General prediction only	*ycaC*	BN194_29650	K0N948	3.91	0.92	1.90
Adapter protein MecA	Competence (DNA uptake)	*mecA*	BN194_19170	K0NB89	0.27	0.92	1.90
Putative RNA methyltransferase YpsC (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ypsC*	BN194_16670	K0NAU0	3.51	0.91	1.88
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	*fabF*	BN194_22540	K0MX40	2.28	0.91	1.88

Transcriptional regulatory protein YycF	Signal transduction	*yycF_2*	BN194_29510	K0N8E4	0.29	0.91	1.88
Cold shock protein 1	Transcription-associated proteins	*csp*	BN194_06990	K0MT67	1.91	0.91	1.88
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	*nagB*	BN194_30440	K0MYW0	3.44	0.90	1.87
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	*galE*	BN194_07350	K0N2R3	4.53	0.90	1.86
Uncharacterized protein	Unknown/uncharacterized		BN194_19470	K0NBA0	1.37	0.89	1.86
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	*gpsB*	BN194_16690	K0MVN5	3.17	0.89	1.85
Uncharacterized protein	General prediction only		BN194_01300	K0N194	3.65	0.89	1.85
Glycosyl transferase family 8	Cell wall biogenesis		BN194_11730	K0N795	2.01	0.88	1.84
Uncharacterized protein yeaE	General prediction only	*yeaE*	BN194_07040	K0MT72	3.47	0.87	1.82
Uncharacterized protein	Unknown/uncharacterized		BN194_07460	K0N2W9	2.13	0.86	1.81
NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	2.87	0.86	1.81
Protein translocase subunit SecY	Protein export	*secY*	BN194_26020	K0NCJ6	1.12	0.86	1.81
Probable GTP-binding protein EngB	tRNA/Ribosome assembly/processing	*engB*	BN194_15350	K0N4Y5	0.53	0.85	1.81
Fructoselysine kinase (EC 2.7.1.-)	Carbohydrate-related metabolism	*frlD*	BN194_22240	K0MX05	2.28	0.85	1.81
Uncharacterized protein	General prediction only		BN194_26820	K0NCV9	2.51	0.84	1.79
Probable phosphoketolase (EC 4.1.2.-)	Central glycolytic/intermediary pathways	*xpkA*	BN194_01710	K0N1M9	3.50	0.83	1.78
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	*pheS*	BN194_18570	K0NB64	3.62	0.83	1.78
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	*garB*	BN194_27400	K0N8K3	4.02	0.83	1.77
Uncharacterized protein	Unknown/uncharacterized		BN194_15370	K0NAJ2	1.46	0.83	1.77
UvrABC system protein A	DNA repair/recombination	*uvrA_2*	BN194_14920	K0NAH3	4.63	0.82	1.76

Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP_3*	BN194_21160	K0N682	3.19	0.81	1.76
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	*sph*	BN194_04930	K0N5Q0	3.06	0.80	1.75
Predicted hydrolase of the HAD superfamily	General prediction only	*mtlD*	BN194_30450	K0N9D4	2.17	0.80	1.74
Uncharacterized protein ywfO	General prediction only	*ywfO*	BN194_26840	K0MXZ5	2.87	0.80	1.74
50S ribosomal protein L7/L12	Ribosomal proteins	*rplL*	BN194_24080	K0NA98	2.66	0.80	1.74
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA*	BN194_05120	K0N8B5	3.51	0.79	1.73
Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	General prediction only	*yqiG*	BN194_25330	K0NAG4	2.43	0.79	1.73
Uncharacterized protein	*Central glycolytic/intermediary pathways*		BN194_04970	K0N8A3	3.97	0.79	1.73
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	3.80	0.79	1.73
UPF0755 protein yrrL	Unknown/uncharacterized	*yrrL*	BN194_18550	K0N5W7	2.16	0.76	1.69
Uncharacterized protein yaaQ	Unknown/uncharacterized	*yaaQ*	BN194_23940	K0MXD1	1.03	0.75	1.68
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	*fabH*	BN194_22600	K0N7B0	3.01	0.75	1.68
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*glyS*	BN194_16950	K0N5D3	3.21	0.74	1.67
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE_2*	BN194_19740	K0MWF1	3.45	0.73	1.66
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	*atpA*	BN194_13600	K0N4K1	4.60	0.73	1.66
NAD kinase (EC 2.7.1.23) (ATP-dependent NAD kinase)		*nadK*	ppnK	K0N6U5	0.55	0.72	1.65
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	*deoB*	BN194_02800	K0N1N0	2.87	0.72	1.65
Predicted hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	3.50	0.72	1.65

Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	*hisS*	BN194_17110	K0N5A0	3.63	0.72	1.64
Ribosome maturation factor RimM	tRNA/Ribosome assembly/processing	*rimM*	BN194_17790	K0MVZ6	3.53	0.71	1.63
SsrA-binding protein (Small protein B)	Posttranslational modification	*smpB*	BN194_11110	K0N3S3	0.19	0.69	1.62
Uncharacterized protein	Unknown/uncharacterized		BN194_19810	K0N5W5	2.31	0.69	1.61
Probable flavodoxin-1	General prediction only	*ykuN*	BN194_01860	K0N1P2	1.85	0.68	1.61
HTH-type transcriptional repressor yvoA	Transcriptional regulation	*yvoA_2*	BN194_19880	K0N9L8	1.41	0.68	1.60
Protein QmcA	Unknown/uncharacterized	*qmcA*	BN194_12070	K0NA10	2.62	0.68	1.60
Site-determining protein	Cytokinesis	*minD*	BN194_14590	K0MV70	2.31	0.68	1.60
UbiE/COQ5 family methyltransferase	General prediction only		BN194_23620	K0NBY4	0.98	0.67	1.59
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC_2,deoC*	BN194_02790	K0MSB5	1.34	0.66	1.58
D-lactate dehydrogenase (EC 1.1.1.28)	Carbohydrate-related metabolism	*dld*	BN194_06590	K0MT28	2.06	0.66	1.58
DNA-binding protein HU	DNA replication-related	*hup*	BN194_15740	K0MVF4	3.14	0.66	1.58
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	*prsA*	BN194_19060	K0N5Q8	2.97	0.66	1.58
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	*yjlD*	BN194_24330	K0NAA7	3.40	0.65	1.57
L-asparaginase (EC 3.5.1.1)	Amino acid-related metabolism	*ansA*	BN194_23900	K0N7L6	2.43	0.65	1.57
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	*murC*	BN194_18950	K0N600	3.31	0.65	1.57
Protein hit	tRNA aminoacyl synthesis	*hit*	BN194_19040	K0MWA8	2.24	0.65	1.57
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	*mtlD_3mtlD*	BN194_30400	K0N9C8	2.70	0.65	1.57
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	*groL,groEL*	BN194_23750	K0N7K7	2.71	0.65	1.57

50S ribosomal protein L20	Ribosomal proteins	*rplT*	BN194_18800	K0N5Y4	2.00	0.63	1.55
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacB*	BN194_07490	K0MTB7	1.41	0.63	1.54
Cell growth regulatory protein	*IS elements/foreign DNA defense*		BN194_00940	K0MRU4	0.82	0.63	1.54
Uncharacterized protein	General prediction only		BN194_21910	K0N6F1	1.40	0.63	1.54
Uncharacterized protein	Unknown/uncharacterized		BN194_27530	K0NAX5	1.49	0.62	1.53
Uncharacterized lipoprotein yerH	General prediction only	*yerH*	BN194_11940	K0MUH2	3.03	0.61	1.53
Glycine betaine/carnitine/choline-binding protein OpuCC	ABC-type transporter systems	*opuCC*	BN194_00670	K0N6Z3	2.58	0.61	1.53
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	*ung*	BN194_11330	K0N758	1.58	0.61	1.53
Uncharacterized protein	Unknown/uncharacterized		BN194_25820	K0NCG9	0.60	0.61	1.53
Nucleoid occlusion protein	Cytokinesis	*noc*	BN194_02030	K0N4Z1	0.80	0.61	1.53
Putative competence-damage inducible protein	General prediction only	*cinA*	BN194_10070	K0N9I3	1.08	0.60	1.52
Uncharacterized protein	Unknown/uncharacterized		BN194_29850	K0N968	1.60	0.59	1.51
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_2*	BN194_15390	K0MVD0	0.47	0.58	1.50
Putative integral membrane protein	Unknown/uncharacterized		BN194_01660	K0N1M7	1.28	0.58	1.50
UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	3.09	0.58	1.50
Nucleoid-associated protein BN194_23980	General prediction only		BN194_23980	K0NA95	3.50	0.58	1.50
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	*carB*	BN194_16450	K0N587	4.06	0.58	1.50
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh*	BN194_26560	K0N7J5	2.60	0.58	1.49
NAD-dependent protein deacetylase (EC 3.5.1.-)	General prediction only	*cobB*	BN194_27190	K0MY36	1.79	0.58	1.49
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdE2*	BN194_16600	K0N5A1	4.65	0.58	1.49
GCN5-related N-acetyltransferase	General prediction only		BN194_19760	K0N5W1	0.81	0.58	1.49

Uncharacterized protein	Unknown/uncharacterized		BN194_22290	K0MX11	2.21	0.57	1.48
18 kDa heat shock protein	Protein folding/turnover	*hsp18*	BN194_07570	K0N8Z3	0.37	0.57	1.48
Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	2.34	0.57	1.48
Oligoendopeptidase F homolog (EC 3.4.24.-)	Amino acid-related metabolism	*yjbG*	BN194_02530	K0N560	3.92	0.57	1.48
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdF*	BN194_16610	K0N552	2.54	0.56	1.48
DegV domain-containing protein CPE0026	Unknown/uncharacterized		BN194_12060	K0N405	1.90	0.56	1.48
Uncharacterized protein ykuJ	Unknown/uncharacterized	*ykuJ*	BN194_09100	K0N348	1.12	0.56	1.48
Fumarate hydratase class II (Fumarase C) (EC 4.2.1.2)	Tricarboxylic acid pathway	*fumC*	BN194_25340	K0MXL5	2.18	0.56	1.48
30S ribosomal protein S21	Ribosomal proteins	*rpsU*	BN194_17050	K0N5E5	0.63	0.56	1.47
Uncharacterized protein ydcI	General prediction only	*ydcI*	BN194_14310	K0N4I1	0.19	0.56	1.47
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2_2,lacD*	BN194_27060	K0N7P0	3.56	0.55	1.47
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	*aspS*	BN194_17100	K0N5F3	3.04	0.55	1.47
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	*agl*	BN194_27950	K0N8T1	3.42	0.55	1.46
Sortase	Cell wall biogenesis		BN194_22780	K0NA48	1.52	0.54	1.46
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	2.39	0.53	1.45
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	*deoD*	BN194_02810	K0N1Z0	1.72	0.53	1.45
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1_2*	BN194_12550	K0N496	2.13	0.53	1.45
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	*pcp*	BN194_01980	K0N4Y4	2.61	0.53	1.44
30S ribosomal protein S13	Ribosomal proteins	*rpsM*	BN194_25980	K0NAK3	0.91	0.53	1.44
Uncharacterized protein	Unknown/uncharacterized		BN194_19530	K0N9J0	1.88	0.52	1.44

RNA polymerase sigma factor SigA	RNA polymerase	*rpoD,sigA*	BN194_16920	K0NAV6	1.83	0.52	1.44
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	*eno*	BN194_11040	K0MU67	3.93	0.52	1.44
Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Phosphoglucose isomerase) (Phosphohexose isomerase)	Central glycolytic/intermediary pathways	*pgi*	BN194_12580	K0N7I6	3.54	0.52	1.43
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*gnd*	BN194_18660	K0N5N2	2.98	0.52	1.43
Multifunctional protein: 5-nucleotidase 2,3-cyclic-nucleotide 2-phosphodiesterase	Nucleic acid/nucleotide metabolism	*ushA*	BN194_15530	K0N8A9	2.79	0.51	1.43
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	*pth*	BN194_26550	K0N8B3	1.02	0.51	1.43
Uncharacterized protein			BN194_19420	K0NB98	3.20	0.51	1.42
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC*	BN194_17890	K0MW34	1.77	0.51	1.42
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF*	BN194_17910	K0N5I3	3.18	0.51	1.42
50S ribosomal protein L33	Ribosomal proteins	*rpmG2,rpmG*	BN194_24280	K0NAA5	0.39	0.51	1.42
Phosphohydrolase (MutT/nudix family protein)	General prediction only		BN194_27160	K0N7P9	0.42	0.50	1.42
Histidinol-phosphatase	General prediction only		BN194_14010	K0N4F8	1.10	0.50	1.42
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	2.60	0.50	1.41
Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain)	Nucleic acid/nucleotide metabolism	*carA*	BN194_16460	K0N535	2.78	0.49	1.41
Uncharacterized protein RP368	*ABC-type transporter systems*		BN194_07720	K0N914	0.35	0.49	1.40
CCA-adding enzyme (EC 2.7.7.72) (CCA tRNA nucleotidyltransferase) (tRNA CCA-pyrophosphorylase) (tRNA adenylyl-/cytidylyl- transferase) (tRNA nucleotidyltransferase) (tRNA-NT)	tRNA/Ribosome assembly/processing	*cca*	BN194_15770	K0NAM4	0.31	0.48	1.39
Putative nrdI-like protein	*Nucleic acid/nucleotide metabolism*		BN194_08250	K0N300	1.68	0.48	1.39
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_01410	K0N1L0	3.17	0.48	1.39
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine	Cell wall biogenesis	*murG*	BN194_14730	K0N819	1.82	0.47	1.39

transferase (EC 2.4.1.227) (Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase)							
Translation initiation factor IF-3	Protein translation (initiation)	*infC*	BN194_18820	K0NB73	2.42	0.47	1.38
Arginine repressor	Transcriptional regulation	*argR1,argR*	BN194_19110	K0N5R1	0.13	0.47	1.38
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhB*	BN194_15090	K0MVA7	2.87	0.46	1.37
Uncharacterized protein	Unknown/uncharacterized		BN194_21450	K0N6R7	2.34	0.45	1.37
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	*typA*	BN194_15150	K0N4W9	1.73	0.45	1.37
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA2,gpmA*	BN194_22740	K0MX58	1.85	0.44	1.36
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	*pepV*	BN194_08800	K0N324	2.40	0.44	1.36
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	*proS*	BN194_17610	K0N5E2	2.68	0.44	1.35
30S ribosomal protein S19	Ribosomal proteins	*rpsS*	BN194_26180	K0NAM1	1.29	0.43	1.35
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	*mhqA_3*	BN194_18760	K0N5N7	1.46	0.43	1.35
Transport protein	Other transporter proteins		BN194_00630	K0N4D9	0.49	0.43	1.35
Putative tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207) (tRNA (cytidine/uridine-2'-O-)-methyltransferase)	*tRNA/Ribosome assembly/processing*		BN194_09990	K0MTX9	1.28	0.43	1.35
Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Phosphotransferase system, enzyme I)		*ptsI*	BN194_19410	K0N5T2	1.60	0.43	1.35
30S ribosomal protein S1 homolog	Ribosomal proteins	*ypfD*	BN194_15720	K0NAL9	2.72	0.42	1.34
Possible TrsG protein	Unknown/uncharacterized		BN194_00240	K0MRM8	0.30	0.41	1.33
Transcriptional regulator	*Posttranslational modification*		BN194_29310	K0N8C2	2.63	0.41	1.33
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	2.46	0.41	1.33
Uncharacterized protein ylxR	General prediction only	*ylxR*	BN194_17570	K0NAZ6	1.65	0.41	1.33

Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	*fhs*	BN194_16520	K0NAT0	2.49	0.40	1.32
Uncharacterized protein MJ0282	Cofactor-related metabolism		BN194_03700	K0N1T2	1.70	0.40	1.32
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	2.09	0.39	1.31
Ribosomal RNA small subunit methyltransferase G (EC 2.1.1.-) (16S rRNA 7-methylguanosine methyltransferase)	tRNA/Ribosome assembly/processing	*rsmG*	BN194_02020	K0N7F1	0.84	0.39	1.31
50S ribosomal protein L17	Ribosomal proteins	*rplQ*	BN194_25950	K0N841	1.93	0.39	1.31
Xanthine/uracil/vitamin C permease	Other transporter proteins		BN194_01470	K0N796	3.24	0.39	1.31
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25510	K0N7B2	3.53	0.38	1.30
Uncharacterized protein yqhL	General prediction only	*yqhL*	BN194_18410	K0N5L5	1.31	0.38	1.30
Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	*rp2*	BN194_17060	K0N598	0.51	0.37	1.29
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	*pgcA*	BN194_10370	K0N9K8	4.37	0.37	1.29
Protein ytsP	Signal transduction	*ytsP*	BN194_14450	K0N4Q9	1.11	0.37	1.29
Hydrolase of the alpha/beta superfamily	General prediction only		BN194_08240	K0MTK6	1.25	0.36	1.29
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD*	BN194_17920	K0NB35	2.29	0.35	1.27
Septation ring formation regulator EzrA	Cytokinesis	*ezrA*	BN194_14460	K0N4J2	2.31	0.35	1.27
Glycosyl transferase family protein	Cell wall biogenesis		BN194_02420	K0N7L2	1.19	0.35	1.27
Uncharacterized protein	Cell wall biogenesis		BN194_02360	K0N1U1	0.09	0.34	1.27
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	*tpx*	BN194_08090	K0MTJ5	1.20	0.34	1.27
Transcriptional regulator, xre family	Transcriptional regulation		BN194_05600	K0N260	1.08	0.34	1.26
Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	0.68	0.34	1.26
Uncharacterized protein	Unknown/uncharacterized		BN194_29560	K0N8E9	0.19	0.34	1.26

tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	*dus1*	BN194_26390	K0MXV9	1.60	0.33	1.26
Protein translocase subunit SecA	Protein export	*secA*	BN194_10170	K0N9J2	2.44	0.33	1.26
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		BN194_18780	K0N9E0	0.19	0.33	1.26
Uncharacterized protein	Transcriptional regulation		BN194_22670	K0NBT5	1.14	0.33	1.26
50S ribosomal protein L24	Ribosomal proteins	*rplX*	BN194_26110	K0N7F9	0.94	0.33	1.25
Acyltransferase 3			BN194_15460	K0N4S6	0.19	0.33	1.25
Sorbitol PTS, EIIA	Phosphotransferase systems		BN194_09940	K0MTX4	0.71	0.32	1.25
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	1.24	0.32	1.25
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification		BN194_25280	K0NAG2	1.23	0.32	1.25
Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-)		*rsmB*	BN194_18040	K0MW45	3.41	0.31	1.24
Uncharacterized RNA methyltransferase lp_1151 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_11990	K0MUI2	2.45	0.31	1.24
Dehydrogenase	General prediction only		BN194_24480	K0NAB4	0.88	0.31	1.24
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	*murD*	BN194_14720	K0NAG5	3.46	0.31	1.24
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*fruK*	BN194_15420	K0NAJ6	0.67	0.31	1.24
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	*pgk*	BN194_11020	K0N9R1	2.15	0.31	1.24
Heat-inducible transcription repressor HrcA	Transcriptional regulation	*hrcA*	BN194_17480	K0N915	1.03	0.30	1.23
Putative transcriptional regulator (DtxR family)	Transcriptional regulation		BN194_08410	K0N354	2.13	0.29	1.22
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)	Nucleic acid/nucleotide metabolism	*ntd*	BN194_24240	K0MXE6	0.65	0.29	1.22
Uncharacterized ABC transporter ATP-binding protein YdbJ	ABC-type transporter systems	*ydbJ*	BN194_24600	K0N7Q8	0.56	0.29	1.22

UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	1.09	0.29	1.22
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	*alaS*	BN194_08480	K0N6K2	2.21	0.29	1.22
Penicillin-binding protein 2B	Cytokinesis	*pbpB*	BN194_14700	K0N4S9	0.76	0.29	1.22
Response regulator ArlR	Signal transduction	*arlR*	BN194_18650	K0N5X3	0.23	0.28	1.22
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_3*	BN194_21440	K0MWS9	2.45	0.28	1.22
Glutathione peroxidase	Cell defense/detoxification	*gpo*	BN194_09780	K0N6T6	1.76	0.28	1.21
Exodeoxyribonuclease (EC 3.1.11.2)	DNA repair/recombination	*exoA*	BN194_11390	K0MUA0	0.25	0.28	1.21
Uncharacterized protein	Unknown/uncharacterized		BN194_02900	K0N1P1	2.05	0.27	1.21
Phosphoesterase (EC 3.1.4.-)	General prediction only	*ysnB*	BN194_08650	K0N317	1.18	0.27	1.21
Uncharacterized protein	Unknown/uncharacterized		BN194_16650	K0N5A4	0.10	0.27	1.21
Uncharacterized protein			BN194_22500	K0N788	2.38	0.27	1.20
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	*ptsH*	BN194_19430	K0N9I2	2.26	0.26	1.20
Membrane protein insertase YidC 1	Protein export	*yidC1*	BN194_18630	K0N9D1	0.23	0.26	1.20
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE*	BN194_02970	K0N7U7	2.04	0.26	1.20
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	*dnaN*	BN194_00020	K0N6S3	1.88	0.26	1.20
GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*relA*	BN194_17230	K0N8Y0	0.40	0.26	1.20
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*bglP*	BN194_06940	K0MT60	0.49	0.26	1.19
Ribosome biogenesis GTPase A	tRNA/Ribosome assembly/processing	*rbgA*	BN194_15940	K0MVH2	1.32	0.25	1.19
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	Central glycolytic/intermediary pathways	*gap*	BN194_11010	K0N3R3	1.62	0.25	1.19
30S ribosomal protein S12	Ribosomal proteins	*rpsL*	BN194_26290	K0MXV0	1.49	0.24	1.18

Uncharacterized protein	Unknown/uncharacterized		BN194_11770	K0N9Y6	0.11	0.24	1.18
50S ribosomal protein L23	Ribosomal proteins	*rplW*	BN194_26200	K0N869	1.61	0.24	1.18
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	3.50	0.24	1.18
50S ribosomal protein L6	Ribosomal proteins	*rplF*	BN194_26070	K0NCK5	2.69	0.23	1.17
Uncharacterized protein ywnB	General prediction only	*ywnB_2*	BN194_20050	K0N687	0.84	0.23	1.17
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatC*	BN194_11950	K0N436	1.52	0.23	1.17
50S ribosomal protein L31 type B	Ribosomal proteins	*rpmE2*	BN194_26770	K0NCV4	1.61	0.23	1.17
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*ileS*	BN194_14810	K0N4L9	2.09	0.22	1.17
Glycine betaine/carnitine/choline transport ATP-binding protein OpuCA	ABC-type transporter systems	*opuCA*	BN194_00680	K0N4E4	1.98	0.21	1.16
Transcriptional regulator, xre family	Transcriptional regulation		BN194_23510	K0N6Y7	1.29	0.21	1.16
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	*ykwC*	BN194_02520	K0N7M3	1.79	0.21	1.16
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhA*	BN194_15080	K0N860	1.51	0.21	1.15
50S ribosomal protein L18	Ribosomal proteins	*rplR*	BN194_26060	K0N7F4	0.57	0.21	1.15
Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	1.51	0.20	1.15
tRNA-specific adenosine deaminase (EC 3.5.4.33)	tRNA/Ribosome assembly/processing	*tadA*	BN194_24000	K0N7M1	1.06	0.20	1.15
Peptide chain release factor 3 (RF-3)	Protein translation (peptide release)	*prfC*	BN194_19480	K0N9I7	0.53	0.20	1.15
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*rluB*	BN194_15650	K0N509	0.08	0.20	1.15
Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	*bceA_2*	BN194_21230	K0N9X1	2.11	0.19	1.14
5'-nucleotidase (EC 3.1.3.5)	General prediction only		BN194_08220	K0N957	3.53	0.19	1.14

Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI_2*	BN194_16210	K0N508	0.98	0.19	1.14
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO_2*	BN194_16630	K0N8Q0	1.82	0.19	1.14
Probable catabolite control protein A	Transcriptional regulation	*ccpA*	BN194_08750	K0N323	0.89	0.18	1.14
50S ribosomal protein L16	Ribosomal proteins	*rplP*	BN194_26150	K0N863	0.30	0.18	1.13
Penicillin-binding protein 1A	Cell wall biogenesis	*ponA*	BN194_16720	K0NAU3	1.80	0.18	1.13
Oligo-1,6-glucosidase (EC 3.2.1.10)	Carbohydrate-related metabolism	*malL*	BN194_04830	K0N5P4	0.53	0.17	1.13
Uncharacterized protein MJ1445	General prediction only		BN194_08880	K0N6M7	0.93	0.17	1.13
Monooxygenase	General prediction only		BN194_07600	K0N2U5	0.98	0.17	1.13
50S ribosomal protein L35	Ribosomal proteins	*rpmI*	BN194_18810	K0N5P1	0.23	0.17	1.13
Probable phosphoketolase (EC 4.1.2.-)	*Central glycolytic/intermediary pathways*		BN194_28700	K0N8X7	0.89	0.16	1.12
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	1.59	0.16	1.12
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	*rpoB*	BN194_26340	K0MXV4	0.70	0.16	1.12
PTS family mannose/fructose/sorbose porter component IIC	Phosphotransferase systems		BN194_02980	K0N5D0	1.18	0.16	1.12
Uncharacterized protein	Lipid-related metabolism		BN194_11980	K0N7B3	0.64	0.15	1.11
Uncharacterized protein	Unknown/uncharacterized		BN194_11890	K0MUG0	0.55	0.15	1.11
50S ribosomal protein L29	Ribosomal proteins	*rpmC*	BN194_26140	K0MXT6	1.58	0.15	1.11
50S ribosomal protein L15	Ribosomal proteins	*rplO*	BN194_26030	K0NAK7	0.67	0.15	1.11
30S ribosomal protein S20	Ribosomal proteins	*rpsT*	BN194_15250	K0N4X9	0.29	0.14	1.10
DNA polymerase III PolC-type (PolIII) (EC 2.7.7.7)	DNA replication-related	*polC*	BN194_17600	K0N5L6	0.64	0.14	1.10
30S ribosomal protein S7	Ribosomal proteins	*rpsG*	BN194_26280	K0NAM9	0.77	0.14	1.10
MarR family transcriptional regulator	Transcriptional regulation		BN194_22610	K0N6N9	0.05	0.14	1.10

2,3-bisphosphoglycerate-dependent phosphoglycerate mutase 2 (EC 5.4.2.1)	Central glycolytic/intermediary pathways	*gpmA2_2*	BN194_27560	K0N7W0	0.45	0.14	1.10
Transcription termination/antitermination protein NusG	Transcription-associated proteins	*nusG*	BN194_24260	K0N730	0.26	0.14	1.10
50S ribosomal protein L13	Ribosomal proteins	*rplM*	BN194_25850	K0N828	2.51	0.14	1.10
Probable L-serine dehydratase, alpha chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAA*	BN194_13950	K0N4M4	0.27	0.13	1.10
50S ribosomal protein L4	Ribosomal proteins	*rplD*	BN194_26210	K0N7H0	1.17	0.13	1.10
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	*yuxL*	BN194_19910	K0N5X4	0.85	0.13	1.10
50S ribosomal protein L19	Ribosomal proteins	*rplS*	BN194_17770	K0NB12	1.61	0.12	1.09
UvrABC system protein A	DNA repair/recombination	*uvrA_3*	BN194_27500	K0N8M1	0.46	0.12	1.09
Uncharacterized protein	Unknown/uncharacterized		BN194_00400	K0N116	0.31	0.12	1.09
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	*pdhD*	BN194_15110	K0N4P1	0.14	0.12	1.09
50S ribosomal protein L30	Ribosomal proteins	*rpmD*	BN194_26040	K0MXS6	0.43	0.12	1.09
30S ribosomal protein S8	Ribosomal proteins	*rpsH*	BN194_26080	K0NAL1	0.77	0.12	1.09
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	*prfB*	BN194_10180	K0N6W9	1.93	0.12	1.08
Adenosylcobalamin-dependent ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*rtpR*	BN194_24230	K0NAA3	0.38	0.12	1.08
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	*nadE*	BN194_19840	K0MWF6	0.56	0.11	1.08
Probable tRNA sulfurtransferase (EC 2.8.1.4) (Sulfur carrier protein ThiS sulfurtransferase) (Thiamine biosynthesis protein ThiI) (tRNA 4-thiouridine synthase)	Cofactor-related metabolism	*thiI*	BN194_14480	K0N7Z7	0.58	0.11	1.08
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-	Amino acid-related metabolism	*mtnN*	BN194_14890	K0MV90	0.63	0.11	1.08

methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)							
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)		*accC*	BN194_22510	K0N6M5	0.39	0.11	1.08
Ribonuclease H (EC 3.1.26.4)	DNA repair/recombination	*rnhA*	BN194_27580	K0NAX8	0.07	0.10	1.07
50S ribosomal protein L3	Ribosomal proteins	*rplC*	BN194_26220	K0NCN1	0.36	0.10	1.07
MreB-like protein	Cytokinesis	*mbl*	BN194_13650	K0N4K5	0.56	0.10	1.07
Single-stranded DNA-binding protein (SSB)	DNA replication-related	*ssb*	BN194_00110	K0N1C2	0.51	0.10	1.07
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	*npr*	BN194_04740	K0MSP8	0.44	0.10	1.07
6-phospho-beta-galactosidase (EC 3.2.1.85) (Beta-D-phosphogalactoside galactohydrolase) (P-beta-Gal)	Carbohydrate-related metabolism	*lacG*	BN194_07320	K0N8W7	0.12	0.09	1.07
Uncharacterized protein	Unknown/uncharacterized		BN194_08190	K0MTK3	0.02	0.09	1.07
Uncharacterized glycosyltransferase HI_0868 (EC 2.4.-.-)	Cell wall biogenesis		BN194_02410	K0N1U3	0.15	0.09	1.06
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	*trpS*	BN194_27360	K0N7S4	0.61	0.08	1.06
Probable flavodoxin-1	Membrane bioenergetics	*ykuN_2*	BN194_12220	K0NA19	0.32	0.08	1.06
Uncharacterized RNA methyltransferase lp_3226 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_19580	K0N9J4	0.25	0.08	1.06
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	*ftsY*	BN194_17850	K0N5R8	1.47	0.08	1.06
30S ribosomal protein S18	Ribosomal proteins	*rpsR*	BN194_00120	K0N6T2	0.06	0.08	1.06
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	*proC*	BN194_19900	K0N677	0.18	0.08	1.06
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB1,pstB*	BN194_10270	K0N9K1	0.07	0.08	1.06
30S ribosomal protein S2	Ribosomal proteins	*rpsB*	BN194_17680	K0N936	0.63	0.08	1.05
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*ytzG*	BN194_09230	K0N6P7	0.02	0.07	1.05

Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	*ptp3*	BN194_23520	K0NBX6	0.74	0.07	1.05
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	*treA*	BN194_06930	K0N662	0.10	0.07	1.05
30S ribosomal protein S5	Ribosomal proteins	*rpsE*	BN194_26050	K0N853	0.32	0.07	1.05
50S ribosomal protein L1	Ribosomal proteins	*rplA*	BN194_24150	K0N7M7	0.56	0.07	1.05
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1*	BN194_09110	K0N399	1.28	0.06	1.05
UPF0473 protein BN194_08530	Unknown/uncharacterized		BN194_08530	K0N6K6	0.19	0.05	1.04
FeS cluster assembly protein sufD	Cofactor-related metabolism	*sufD*	BN194_13780	K0N7U0	0.23	0.05	1.04
Uncharacterized MscS family protein YkuT	Other transporter proteins	*ykuT*	BN194_08700	K0N322	0.03	0.05	1.04
Cell division protein FtsA	Cytokinesis	*ftsA*	BN194_14750	K0N4T3	0.20	0.05	1.03
Oligoendopeptidase, pepF/M3 family	*Amino acid-related metabolism*		BN194_11580	K0N779	0.21	0.05	1.03
Translation initiation factor IF-2	Protein translation (initiation)	*infB*	BN194_17550	K0N5K7	0.07	0.05	1.03
Putative gluconeogenesis factor	General prediction only	*yjiF*	BN194_10480	K0N6Z4	0.01	0.04	1.03
Protein RibT (EC 2.3.1.-)	Cofactor-related metabolism	*ribT*	BN194_15620	K0NAL0	0.10	0.04	1.03
Uncharacterized protein	*ABC-type transporter systems*		BN194_21220	K0NBK2	0.46	0.03	1.02
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	0.07	0.03	1.02
Transcription termination/antitermination protein NusA	Transcription-associated proteins	*nusA*	BN194_17580	K0N927	0.14	0.03	1.02
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC_2*	BN194_20620	K0NBH0	0.01	0.03	1.02
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.-)	Lipid-related metabolism	*plsC*	BN194_17710	K0N5F1	0.02	0.03	1.02
FMN-binding domain protein	General prediction only		BN194_24320	K0NC29	0.19	0.03	1.02
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	*serS*	BN194_20080	K0N9N4	0.13	0.03	1.02

Cell shape-determining protein MreC (Cell shape protein MreC)	Cytokinesis	*mreC*	BN194_14560	K0N4K0	0.08	0.02	1.02
Zinc metalloprotease (EC 3.4.24.-)	General prediction only	*eep*	BN194_17620	K0NAZ9	0.05	0.02	1.02
Membrane protein	Unknown/uncharacterized		BN194_22700	K0N7C6	0.01	0.02	1.02
Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	ABC-type transporter systems	*ecfA2, ecfA*	BN194_25920	K0NCI4	0.04	0.02	1.01
Transcriptional regulator lytR	Transcriptional regulation	*lytR_3*	BN194_21700	K0N6U3	0.21	0.02	1.01
50S ribosomal protein L5	Ribosomal proteins	*rplE*	BN194_26100	K0N859	0.07	0.02	1.01
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	*rnjA*	BN194_15020	K0NAH6	0.06	0.01	1.01
30S ribosomal protein S6	Ribosomal proteins	*rpsF*	BN194_00100	K0N0Z1	0.07	0.01	1.01
Spermidine/putrescine-binding periplasmic protein	ABC-type transporter systems	*potD*	BN194_11460	K0N3U9	0.02	0.01	1.01
UPF0659 protein YMR090W	General prediction only	*ylbE*	BN194_07030	K0N671	0.09	0.01	1.01
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*yqeC*	BN194_02330	K0N532	0.00	0.01	1.01
Uncharacterized protein	Unknown/uncharacterized		BN194_23650	K0N7J8	0.06	0.01	1.01
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	0.05	0.01	1.01
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_13380	K0N7S0	0.04	0.01	1.00
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	*metG*	BN194_27130	K0NAU5	0.04	0.01	1.00
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		BN194_13770	K0NAC0	0.01	0.01	1.00
Threonylcarbamoyl-AMP synthase (TC-AMP synthase) (EC 2.7.7.87) (L-threonylcarbamoyladenylate synthase)	tRNA/Ribosome assembly/processing	*ywlC*	BN194_13530	K0N7S6	0.01	0.00	1.00
Uncharacterized protein ysxB	Ribosomal proteins	*ysxB*	BN194_18280	K0N9A9	0.00	0.00	1.00
Tyrosine--tRNA ligase (EC 6.1.1.1)		*tyrS*	BN194_21510	K0N6A9	0.02	0.00	1.00
30S ribosomal protein S16	Ribosomal proteins	*rpsP*	BN194_17810	K0N5H1	0.01	0.00	1.00
Signal peptidase I (EC 3.4.21.89)	Protein export	*lepB*	BN194_02610	K0N1V9	0.01	0.00	1.00

30S ribosomal protein S10	Ribosomal proteins	*rpsJ*	BN194_26230	K0NAM5	0.01	-0.01	-1.01
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	*clpE*	BN194_19450	K0N644	0.05	-0.01	-1.01
Putative 2-hydroxyacid dehydrogenase SH0752 (EC 1.1.1.-)	General prediction only		BN194_01890	K0MS33	0.02	-0.01	-1.01
UPF0092 membrane protein yrbF	Protein export	*yrbF*	BN194_08390	K0MTL6	0.01	-0.01	-1.01
Uncharacterized protein	Unknown/uncharacterized	*yvcC*	BN194_05260	K0N2E5	0.06	-0.01	-1.01
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	*rpoC*	BN194_26330	K0NAN3	0.13	-0.01	-1.01
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	Cell wall biogenesis	*glmS*	BN194_11560	K0N3V9	0.13	-0.02	-1.01
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	*cysS*	BN194_24430	K0NAB2	0.06	-0.02	-1.01
30S ribosomal protein S4	Ribosomal proteins	*rpsD*	BN194_14440	K0MV63	0.16	-0.02	-1.02
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	*rbfA*	BN194_17540	K0MVV7	0.07	-0.02	-1.02
Cadmium efflux system accessory protein	Other transporter proteins	*cadC*	BN194_21540	K0MWU0	0.13	-0.03	-1.02
PhoH-like protein	General prediction only	*phoH*	BN194_17020	K0NAW2	0.15	-0.03	-1.02
UPF0342 protein yheA	Unknown/uncharacterized	*yheA*	BN194_19080	K0N9F7	0.03	-0.03	-1.02
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC_2*	BN194_24680	K0NAC2	0.19	-0.03	-1.02
Uncharacterized protein YqhY	Unknown/uncharacterized	*yqhY*	BN194_18230	K0N9A7	0.03	-0.03	-1.02
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	*pdhC*	BN194_15100	K0N4W5	0.13	-0.04	-1.03
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	*rny*	BN194_10100	K0N3E5	0.04	-0.04	-1.03

Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	*gatA*	BN194_11960	K0N3Z6	0.77	-0.04	-1.03
Uncharacterized protein yaaA	General prediction only	*yaaA*	BN194_00040	K0MRL5	0.22	-0.05	-1.03
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		BN194_24180	K0NAA2	0.22	-0.05	-1.03
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	*valS*	BN194_14510	K0N4J6	1.15	-0.05	-1.04
Uncharacterized protein	Phosphotransferase systems		BN194_04820	K0N885	0.27	-0.06	-1.04
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	*glmM*	BN194_11550	K0N3Y7	0.49	-0.06	-1.04
Regulatory protein vanR	Signal transduction	*vanR*	BN194_02120	K0N7G4	0.26	-0.06	-1.04
30S ribosomal protein S11	Ribosomal proteins	*rpsK*	BN194_25970	K0NCJ0	0.18	-0.07	-1.05
30S ribosomal protein S3	Ribosomal proteins	*rpsC*	BN194_26160	K0N7G5	0.92	-0.07	-1.05
Uncharacterized protein yitL	General prediction only	*yitL*	BN194_15600	K0N505	0.02	-0.08	-1.06
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	*rpoA*	BN194_25960	K0N7E5	0.79	-0.08	-1.06
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatB*	BN194_11970	K0NA01	0.79	-0.08	-1.06
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	*tig*	BN194_15330	K0N884	0.25	-0.08	-1.06
Phosphoenolpyruvate-dependent sugar phosphotransferase system EIIA, galactitol/fructose specific	Phosphotransferase systems		BN194_27050	K0N8F9	0.39	-0.09	-1.06
Uncharacterized protein	Unknown/uncharacterized		BN194_12100	K0N456	0.10	-0.09	-1.06
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E,P100*	BN194_02180	K0N513	1.41	-0.09	-1.06
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA*	BN194_11290	K0MU90	0.67	-0.09	-1.07
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	*gltX*	BN194_24470	K0NC38	0.83	-0.09	-1.07
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	*polA*	BN194_18930	K0N9E7	0.58	-0.10	-1.07

Uncharacterized protein	Unknown/uncharacterized		BN194_13400	K0N4I9	0.07	-0.10	-1.07
50S ribosomal protein L27	Ribosomal proteins	*rpmA*	BN194_18270	K0NB51	0.32	-0.10	-1.07
Acylphosphatase	Carbohydrate-related metabolism	*acyP*	BN194_18620	K0NB65	0.44	-0.10	-1.07
50S ribosomal protein L14	Ribosomal proteins	*rplN*	BN194_26120	K0NCL3	0.27	-0.10	-1.08
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*gmuB*	BN194_23840	K0MXC7	0.33	-0.11	-1.08
Signal recognition particle protein (Fifty-four homolog)	Protein export	*ffh*	BN194_17820	K0NB27	0.09	-0.11	-1.08
Segregation and condensation protein B	Cytokinesis	*scpB*	BN194_15640	K0MVE6	0.24	-0.11	-1.08
Phosphate-binding protein pstS 1	ABC-type transporter systems	*pstS1*	BN194_10240	K0MTZ5	0.12	-0.11	-1.08
Glycerol-3-phosphate ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_11260	K0N3T6	1.73	-0.11	-1.08
SPFH/Band 7/PHB domain protein	Unknown/uncharacterized		BN194_29820	K0NDM1	0.06	-0.11	-1.08
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	1.10	-0.11	-1.08
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	*rex_2,rex*	BN194_23820	K0NBZ5	0.59	-0.12	-1.08
Transcriptional regulator, TetR family	Transcriptional regulation		BN194_12190	K0MUM1	0.15	-0.12	-1.09
Spore coat polysaccharide biosynthesis protein spsK				K0N9X8;K0N6D6	0.50	-0.12	-1.09
Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)	Nucleic acid/nucleotide metabolism	*pdp*	BN194_23430	K0NA73	0.86	-0.13	-1.09
50S ribosomal protein L22	Ribosomal proteins	*rplV*	BN194_26170	K0NCM1	0.42	-0.13	-1.09
Penicillin-binding protein 3	Cell wall biogenesis	*pbpC*	BN194_03320	K0N7W9	0.30	-0.13	-1.09
Uncharacterized protein	Unknown/uncharacterized		BN194_20240	K0MWI3	0.11	-0.13	-1.09
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	*nusB*	BN194_18220	K0NB49	0.49	-0.13	-1.09
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	*dkgB*	BN194_08260	K0N347	0.45	-0.14	-1.10

FeS cluster assembly protein sufB	Cofactor-related metabolism	*sufB*	BN194_13810	K0N4E5	0.22	-0.14	-1.10
50S ribosomal protein L9	Ribosomal proteins	*rplI*	BN194_01130	K0N4K3	0.51	-0.14	-1.10
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	*ispA*	BN194_18180	K0N9A2	0.09	-0.14	-1.10
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	0.25	-0.14	-1.10
Lipopolysaccharide synthesis sugar transferase	Cell wall biogenesis		BN194_21390	K0MWS4	0.26	-0.14	-1.10
Inner membrane amino-acid ABC transporter permease protein yecS	ABC-type transporter systems	*yecS_3*	BN194_29780	K0NB99	0.13	-0.14	-1.10
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	0.86	-0.14	-1.10
30S ribosomal protein S17	Ribosomal proteins	*rpsQ*	BN194_26130	K0NAL6	0.50	-0.14	-1.10
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	*ddl*	BN194_01390	K0MRY4	0.67	-0.14	-1.11
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	*def*	BN194_15060	K0N4N6	0.99	-0.15	-1.11
Predicted acetyltransferase			BN194_11820	K0N9Y9	0.44	-0.15	-1.11
Uncharacterized protein ypmR	General prediction only	*ypmR*	BN194_15840	K0MVG3	0.48	-0.15	-1.11
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yutF*	BN194_08910	K0N383	1.57	-0.15	-1.11
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	*iolS*	BN194_29680	K0NB94	1.35	-0.15	-1.11
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	0.31	-0.16	-1.12
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	*hpt*	BN194_26470	K0NCR2	0.49	-0.16	-1.12
Ribosome-binding ATPase YchF	Protein translation (peptide release)	*engD,ychF*	BN194_02070	K0N7F7	0.87	-0.16	-1.12
Glycosyl transferase group 1	Cell wall biogenesis		BN194_09760	K0N3F8	0.25	-0.16	-1.12
Uncharacterized protein	Cell wall biogenesis		BN194_21890	K0MWX1	0.34	-0.17	-1.12

Putative transcriptional regulator, MarR family	Transcriptional regulation		BN194_27490	K0MY64	0.43	-0.17	-1.12
Sporulation initiation inhibitor protein soj	Cytokinesis	*soj*	BN194_02040	K0MS45	1.04	-0.17	-1.13
Transcriptional repressor CcpN	Transcriptional regulation	*ccpN*	BN194_24740	K0MXH2	1.02	-0.18	-1.13
Uncharacterized protein	Unknown/uncharacterized		BN194_23540	K0MXB4	0.50	-0.18	-1.13
50S ribosomal protein L10	Ribosomal proteins	*rplJ*	BN194_24090	K0MXD8	1.05	-0.18	-1.14
Sensory transduction protein BceR	Signal transduction	*bceR_2*	BN194_19250	K0N630	0.61	-0.19	-1.14
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_29810	K0N8H4	1.63	-0.19	-1.14
Anaerobic ribonucleoside-triphosphate reductase-activating protein (EC 1.97.1.-)	Nucleic acid/nucleotide metabolism	*nrdG*	BN194_19270	K0NB93	0.18	-0.19	-1.14
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	*murA2,murA*	BN194_26780	K0NAR9	0.68	-0.19	-1.14
LPXTG-motif cell wall anchor domain protein			BN194_26300	K0N883	1.57	-0.19	-1.14
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	0.22	-0.19	-1.14
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_19800	K0N670	0.44	-0.20	-1.15
Mannose permease IID component	Phosphotransferase systems	*manZ*	BN194_02990	K0MSE1	1.52	-0.20	-1.15
50S ribosomal protein L2	Ribosomal proteins	*rplB*	BN194_26190	K0MXU1	0.90	-0.20	-1.15
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	*ssdA*	BN194_24140	K0MXE0	1.51	-0.20	-1.15
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	*grpE*	BN194_17470	K0NAZ2	2.03	-0.21	-1.15
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	*mnmA*	BN194_14930	K0N844	1.40	-0.21	-1.15
Transcriptional regulator, XRE family	Transcriptional regulation		BN194_30170	K0NDP4	2.25	-0.21	-1.16
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	*rpoE*	BN194_26810	K0N7L4	0.55	-0.22	-1.16
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	*trxB*	BN194_10360	K0N3L1	2.92	-0.22	-1.16

Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA*	BN194_08450	K0N309	1.99	-0.22	-1.17
Chromosomal replication initiator protein DnaA	DNA replication-related	*dnaA*	BN194_00010	K0N1B5	1.31	-0.22	-1.17
Alkyl hydroperoxide reductase subunit C (EC 1.11.1.15)	Cell defense/detoxification	*ahpC*	BN194_26250	K0N876	0.47	-0.22	-1.17
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	*zwf*	BN194_08420	K0N966	2.65	-0.23	-1.17
Translation initiation factor IF-1	Protein translation (initiation)	*infA*	BN194_26000	K0N847	0.65	-0.23	-1.17
Uncharacterized protein	Unknown/uncharacterized		BN194_24010	K0N715	0.95	-0.23	-1.17
NifU-like protein	Cofactor-related metabolism	*nifU*	BN194_13800	K0N4L4	0.47	-0.23	-1.18
TPR repeats containing protein	Unknown/uncharacterized		BN194_14960	K0N4M8	1.17	-0.24	-1.18
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*asnS*	BN194_16760	K0N569	2.62	-0.24	-1.18
DNA translocase SftA	Cytokinesis	*sftA*	BN194_18960	K0N5Q1	0.87	-0.24	-1.18
Isoprenyl transferase (EC 2.5.1.-)	Lipid-related metabolism	*uppS*	BN194_17640	K0MVX1	0.12	-0.24	-1.18
Gluconate 5-dehydrogenase (EC 1.1.1.69)	General prediction only	*idnO*	BN194_08150	K0N2Z5	0.14	-0.24	-1.18
Glutamate dehydrogenase	Amino acid-related metabolism	*gdh*	BN194_06980	K0N666	1.82	-0.24	-1.18
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	*pyrH*	BN194_17660	K0N5E6	0.75	-0.24	-1.18
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	*yqjQ*	BN194_15480	K0N8A1	0.26	-0.25	-1.19
Alpha-galactosidase 2 (EC 3.2.1.22)	Carbohydrate-related metabolism	*agaS_2*	BN194_22160	K0N6I2	1.55	-0.25	-1.19
Dihydrofolate reductase (EC 1.5.1.3)	Cofactor-related metabolism	*folA*	BN194_15810	K0N4W0	0.39	-0.25	-1.19
Calcium-transporting ATPase lmo0841 (EC 3.6.3.8)	Other transporter proteins		BN194_19820	K0NBC5	2.04	-0.25	-1.19
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	*rnr*	BN194_11100	K0N3S4	2.88	-0.25	-1.19

Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	*pmi*	BN194_02920	K0N7U2	2.04	-0.26	-1.20
Rod shape-determining protein MreB	Cytokinesis	*mreB*	BN194_14550	K0N4R7	1.64	-0.26	-1.20
Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	Nucleic acid/nucleotide metabolism	*add*	BN194_23440	K0MXB1	0.61	-0.27	-1.20
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	1.09	-0.27	-1.21
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		BN194_11600	K0N3Z3	0.86	-0.28	-1.21
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*yacO*	BN194_24420	K0NC34	0.81	-0.28	-1.21
ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	*clpX*	BN194_15340	K0MVC6	1.43	-0.28	-1.22
GTPase Era	tRNA/Ribosome assembly/processing	*era*	BN194_16990	K0MVQ8	0.76	-0.28	-1.22
Uncharacterized ABC transporter ATP-binding protein TM_0288	*ABC-type transporter systems*		BN194_06900	K0N2K4	0.14	-0.29	-1.23
Nucleotide-binding protein BN194_10470	General prediction only		BN194_10470	K0N9L7	1.88	-0.29	-1.23
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ysgA*	BN194_18610	K0N5M8	0.27	-0.29	-1.23
Uncharacterized protein	Unknown/uncharacterized		BN194_01150	K0N181	0.41	-0.30	-1.23
Transcriptional regulator, xre family	Transcriptional regulation		BN194_13860	K0N4E8	0.24	-0.30	-1.23
Septum formation inhibitor MinC, C-terminal domain family	Cytokinesis	*minC*	BN194_14580	K0N805	1.75	-0.30	-1.23
50S ribosomal protein L11	Ribosomal proteins	*rplK*	BN194_24160	K0N724	0.62	-0.30	-1.23
Serine/threonine-protein kinase PrkC (EC 2.7.11.1)	Posttranslational modification	*prkC*	BN194_18020	K0NB40	0.20	-0.31	-1.24
DNA replication protein dnaD	DNA replication-related	*dnaD*	BN194_16750	K0N5B1	0.51	-0.31	-1.24
Uncharacterized protein	Posttranslational modification	*pp2C*	BN194_18030	K0N993	0.12	-0.31	-1.24
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	*tuf*	BN194_15310	K0N4R1	1.23	-0.31	-1.24

Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	*pyk*	BN194_15580	K0N8B6	3.70	-0.32	-1.24
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_3*	BN194_29920	K0NDN0	0.87	-0.32	-1.25
Uncharacterized protein	Prophage genome		BN194_09330	K0N6Q4	1.70	-0.32	-1.25
Queuosine transporter QueT	General prediction only	*queT*	BN194_21930	K0NA07	0.13	-0.33	-1.26
Transcriptional regulator	Transcriptional regulation		BN194_08230	K0N6I4	2.15	-0.33	-1.26
Uncharacterized protein	Unknown/uncharacterized	*FNV1452*	BN194_18830	K0N9E3	0.20	-0.33	-1.26
3-keto-L-gulonate-6-phosphate decarboxylase sgbH (EC 4.1.1.85)	Carbohydrate-related metabolism	*sgbH*	BN194_28550	K0N8W6	0.23	-0.34	-1.26
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	0.71	-0.34	-1.27
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	*ybeY*	BN194_17010	K0N594	0.36	-0.34	-1.27
Microcin C7 self-immunity protein mccF			BN194_01360	K0N1K5	2.34	-0.34	-1.27
Thioredoxin	Posttranslational modification	*trxA_2*	BN194_08570	K0N975	0.80	-0.35	-1.27
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	*ohrR*	BN194_10500	K0N3J7	0.45	-0.35	-1.27
DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	DNA replication-related	*dnaX*	BN194_23990	K0MXD3	1.76	-0.35	-1.28
Putative carboxypeptidase SCO6489 (EC 3.4.16.-)			BN194_01370	K0N787	1.10	-0.35	-1.28
Cell division ATP-binding protein FtsE	Cytokinesis	*ftsE*	BN194_10190	K0MTZ2	2.89	-0.35	-1.28
Chaperone protein ClpB	Protein folding/turnover	*clpB*	BN194_15500	K0N4Z8	0.56	-0.35	-1.28
Uncharacterized protein	Unknown/uncharacterized		BN194_02470	K0N7L7	1.82	-0.36	-1.28
ABC-type antimicrobial peptide transport system,ATPase component	*ABC-type transporter systems*		BN194_19940	K0MWG2	1.10	-0.36	-1.28
Probable L-serine dehydratase, beta chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAB*	BN194_13940	K0MV34	1.20	-0.36	-1.28
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		BN194_21400	K0N6R1	3.46	-0.36	-1.28

Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	*glpK_2,glpK*	BN194_27720	K0ND65	0.95	-0.37	-1.29
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	*thrS*	BN194_18860	K0N5P5	5.99	-0.37	-1.29
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	*pepS*	BN194_12180	K0N7D5	1.27	-0.37	-1.29
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	*lysS*	BN194_26380	K0NAN7	1.66	-0.37	-1.29
Stage 0 sporulation protein J	Cytokinesis	*spo0J*	BN194_02050	K0N1F9	2.57	-0.38	-1.30
Uncharacterized protein	Unknown/uncharacterized		BN194_13840	K0MV29	0.36	-0.38	-1.30
Maf-like protein maf	General prediction only	*maf*	BN194_23700	K0N7K3	0.16	-0.39	-1.31
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	*fabD*	BN194_22570	K0NBT1	1.88	-0.39	-1.31
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB2,pstB*	BN194_10280	K0N6X8	1.32	-0.39	-1.31
Uncharacterized protein			BN194_16060	K0N4Y8	0.37	-0.40	-1.32
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	*asnB*	BN194_22990	K0MX90	3.03	-0.40	-1.32
Probable cation-transporting ATPase exp7 (EC 3.6.3.-)	Other transporter proteins	*exp7*	BN194_08170	K0N955	0.90	-0.40	-1.32
Ribosomal RNA small subunit methyltransferase F (EC 2.1.1.178)	tRNA/Ribosome assembly/processing	*rsmF*	BN194_16850	K0N5C0	0.95	-0.41	-1.33
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	*maa*	BN194_30010	K0N8I9	2.08	-0.41	-1.33
Uncharacterized ABC transporter ATP-binding protein YfiB	ABC-type transporter systems	*yfiB*	BN194_06890	K0MT56	1.67	-0.41	-1.33
UvrABC system protein B (Protein UvrB) (Excinuclease ABC subunit B)	DNA repair/recombination	*uvrB*	BN194_10440	K0MU09	2.27	-0.41	-1.33
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	3.85	-0.41	-1.33
Cell division protein FtsZ	Cytokinesis	*ftsZ*	BN194_14760	K0N4L6	3.60	-0.42	-1.33
30S ribosomal protein S14 type Z	Ribosomal proteins	*rpsZ,rpsN*	BN194_26090	K0MXS9	0.99	-0.42	-1.34

3'-5' exoribonuclease yhaM (EC 3.1.-.-)	RNA degradation	*yhaM*	BN194_19070	K0NB84	1.65	-0.42	-1.34
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	*glgC*	BN194_21600	K0N6T3	0.30	-0.42	-1.34
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	*uvrA*	BN194_10450	K0N3J2	2.15	-0.42	-1.34
Cold shock-like protein CspLA	Transcription-associated proteins	*cspLA*	BN194_12460	K0N438	0.48	-0.42	-1.34
Glycosyltransferase	Cell wall biogenesis		BN194_09050	K0N346	0.20	-0.43	-1.34
Replicative DNA helicase (EC 3.6.4.12)	DNA replication-related	*dnaC*	BN194_01140	K0MRW2	1.35	-0.43	-1.34
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	*yqeL,rsfS*	BN194_18710	K0N5N6	1.40	-0.43	-1.35
4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase) (EC 1.17.1.8)	Amino acid-related metabolism	*dapB*	BN194_01000	K0N166	0.58	-0.43	-1.35
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	*ycnE*	BN194_13230	K0N7R3	0.43	-0.43	-1.35
Putative tRNA-binding protein ytpR	General prediction only	*ytpR*	BN194_18970	K0NB80	2.90	-0.43	-1.35
N5-carboxyaminoimidazole ribonucleotide mutase (N5-CAIR mutase) (EC 5.4.99.18) (5-(carboxyamino)imidazole ribonucleotide mutase)	Nucleic acid/nucleotide metabolism	*purE*	BN194_19380	K0N9H9	2.14	-0.44	-1.35
Uncharacterized protein	Unknown/uncharacterized		BN194_15850	K0N527	2.28	-0.44	-1.36
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	*mhqD*	BN194_18770	K0NB71	1.31	-0.44	-1.36
Archaeal fructose-1,6-bisphosphatase related enzyme of inositol monophosphatase family	*Carbohydrate-related metabolism*		BN194_15140	K0MVB0	1.70	-0.44	-1.36
ABC transporter glutamine-binding protein glnH	ABC-type transporter systems	*glnH*	BN194_21430	K0N9Y4	2.09	-0.44	-1.36
Glycosyl transferase family 2	Cell wall biogenesis		BN194_02460	K0N1U7	0.83	-0.44	-1.36
Uncharacterized isochorismatase family protein pncA (EC 3.-.-.-)	General prediction only	*pncA*	BN194_29120	K0NDH8	0.21	-0.44	-1.36
Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	0.21	-0.44	-1.36

Uncharacterized protein ybxB	tRNA/Ribosome assembly/processing	*ybxB*	BN194_24020	K0NC08	2.58	-0.45	-1.36
Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	*plsX*	BN194_17940	K0MW37	0.55	-0.45	-1.37
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA*	BN194_18520	K0NB62	2.67	-0.46	-1.37
Uncharacterized zinc protease ymfH (EC 3.4.24.-)	Amino acid-related metabolism	*ymfH*	BN194_10030	K0N6V9	0.99	-0.46	-1.37
Transcriptional regulator lytR	Transcriptional regulation	*lytR*	BN194_02540	K0MS94	3.10	-0.46	-1.37
Uncharacterized protein	Unknown/uncharacterized		BN194_19050	K0N613	1.47	-0.46	-1.37
Uncharacterized protein	Signal transduction		BN194_18490	K0MW74	0.64	-0.46	-1.38
Transcriptional repressor smtB homolog	Transcriptional regulation	*ziaR*	BN194_01180	K0N4L0	0.25	-0.47	-1.38
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ*	BN194_11360	K0N3U2	1.29	-0.47	-1.39
Uncharacterized protein ypgQ	General prediction only	*ypgQ*	BN194_27480	K0NAX0	0.44	-0.47	-1.39
CBS domain-containing protein ykuL	Unknown/uncharacterized	*ykuL*	BN194_08670	K0N981	1.07	-0.48	-1.39
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	*thiD_2*	BN194_07650	K0N2U9	1.89	-0.48	-1.39
Uncharacterized protein	Unknown/uncharacterized		BN194_20160	K0N5Z4	2.90	-0.48	-1.39
Acyl-ACP thioesterase	Lipid-related metabolism		BN194_23910	K0N709	2.43	-0.49	-1.40
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	*prfA*	BN194_13510	K0N4C6	1.74	-0.49	-1.40
Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*nrdD*	BN194_01250	K0N190	1.54	-0.50	-1.41
Uncharacterized protein YwcC	Carbohydrate-related metabolism	*ywcC*	BN194_09930	K0N6V0	1.85	-0.50	-1.41
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	*obg*	BN194_15440	K0MVD3	2.00	-0.51	-1.42

Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF_2*	BN194_19090	K0MWB2	1.12	-0.51	-1.42
DNA polymerase III subunit delta (EC 2.7.7.7)	DNA replication-related	*holB*	BN194_23930	K0NA93	1.19	-0.52	-1.43
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	2.69	-0.52	-1.44
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB*	BN194_21340	K0MWS0	2.24	-0.52	-1.44
30S ribosomal protein S15	Ribosomal proteins	*rpsO*	BN194_15260	K0N4Q6	1.09	-0.53	-1.44
Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	*aspC*	BN194_16770	K0NAU6	2.93	-0.53	-1.45
5-bromo-4-chloroindolyl phosphate hydrolysis protein	General prediction only		BN194_14860	K0N4M3	2.99	-0.54	-1.45
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA_2, potA*	BN194_11430	K0N765	2.44	-0.54	-1.45
Transcriptional regulator lytR	Transcriptional regulation	*lytR_4*	BN194_23780	K0NA85	2.19	-0.54	-1.46
Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	0.17	-0.55	-1.46
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	*tsf*	BN194_17670	K0NB01	3.34	-0.56	-1.47
Glycine cleavage system H protein	Amino acid-related metabolism	*gcvH*	BN194_13700	K0N4K8	1.25	-0.56	-1.47
Elongation factor 4 (EF-4) (EC 3.6.5.n1) (Ribosomal back-translocase LepA)	Protein translation (elongation)	*lepA*	BN194_17440	K0MVU5	2.00	-0.56	-1.47
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB*	BN194_19860	K0N5X0	3.62	-0.56	-1.48
Uncharacterized protein			BN194_02080	K0N4Z7	0.86	-0.57	-1.48
Elongation factor G (EF-G)	Protein translation (elongation)	*fusA*	BN194_26270	K0NCN8	2.88	-0.57	-1.48
Bifunctional protein GlmU	Cell wall biogenesis	*glmU*	BN194_26940	K0MY10	2.47	-0.57	-1.48
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	*glcK*	BN194_18420	K0NB57	4.05	-0.58	-1.49
Uncharacterized protein	General prediction only		BN194_13850	K0N4L8	2.20	-0.58	-1.50

Uncharacterized protein ytoI	Transcriptional regulation	*ytoI*	BN194_08440	K0MTM0	1.31	-0.58	-1.50
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	*ywpJ*	BN194_11320	K0N9U2	4.19	-0.59	-1.50
HTH-type transcriptional repressor glcR	Transcriptional regulation	*glcR*	BN194_02570	K0N7M8	1.54	-0.59	-1.50
Elongation factor P	Protein translation (elongation)	*efp*	BN194_18240	K0MW57	2.75	-0.60	-1.51
Glucose-1-phosphate thymidylyltransferase		*rmlA*		K0N699;K0MWW4	3.00	-0.60	-1.52
Uncharacterized protein yghZ	General prediction only	*yghZ*	BN194_27510	K0N7U8	4.02	-0.61	-1.53
Endonuclease MutS2 (EC 3.1.-.-)	DNA repair/recombination	*mutS2*	BN194_08560	K0N359	2.43	-0.64	-1.55
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	*citX*	BN194_20300	K0N6A3	2.30	-0.64	-1.56
Cell division protein FtsX	Cytokinesis	*ftsX*	BN194_10200	K0N3G0	4.11	-0.64	-1.56
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	*lplJ*	BN194_16640	K0MVN0	0.88	-0.64	-1.56
Predicted Zn-dependent peptidase	*Amino acid-related metabolism*		BN194_10020	K0N9H8	2.94	-0.64	-1.56
Ribosomal RNA small subunit methyltransferase H (EC 2.1.1.199) (16S rRNA m(4)C1402 methyltransferase) (rRNA (cytosine-N(4)-)-methyltransferase RsmH)	tRNA/Ribosome assembly/processing	*rsmH*	BN194_14680	K0N814	0.74	-0.65	-1.57
Integral membrane protein	Unknown/uncharacterized		BN194_02590	K0MS97	0.85	-0.65	-1.57
Primosomal protein DnaI	DNA replication-related	*dnaI*	BN194_18880	K0N9E5	1.13	-0.67	-1.59
Putative sporulation transcription regulator WhiA	Transcriptional regulation	*whiA*	BN194_10490	K0MU14	0.61	-0.67	-1.59
1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157)	Cell wall biogenesis		BN194_09040	K0MTQ9	2.22	-0.67	-1.59
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	*ftsH*	BN194_26460	K0N7I8	4.46	-0.67	-1.59
ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease RexB)	DNA repair/recombination	*rexB*	BN194_16810	K0N573	3.64	-0.67	-1.59
Glucitol operon repressor	Transcriptional regulation	*srlR*	BN194_28690	K0MYG3	3.63	-0.67	-1.59
Hypothetical lipoprotein	Unknown/uncharacterized		BN194_12440	K0MUR1	0.85	-0.68	-1.60

DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	2.44	-0.68	-1.60
Zinc-transporting ATPase (EC 3.6.3.5)	Other transporter proteins	*zosA_2*	BN194_29430	K0NB79	2.89	-0.68	-1.60
Xanthine permease	Other transporter proteins	*pbuX*	BN194_12500	K0N490	0.34	-0.68	-1.61
UPF0478 protein SAOUHSC_01855	Signal transduction		BN194_08710	K0N365	3.25	-0.69	-1.61
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC*	BN194_00080	K0N486	4.65	-0.69	-1.61
Uncharacterized protein	Unknown/uncharacterized		BN194_21170	K0NBJ9	1.84	-0.69	-1.61
Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	DNA repair/recombination	*recJ*	BN194_17390	K0MVT7	0.47	-0.70	-1.62
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_4*	BN194_29900	K0N971	2.92	-0.70	-1.62
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	*murF*	BN194_26720	K0NCU5	1.97	-0.70	-1.63
DNA topoisomerase 4 subunit A (EC 5.99.1.-)		*parC*	BN194_16070	K0NAP8	2.06	-0.71	-1.63
GNAT family acetyltransferase	General prediction only		BN194_29620	K0NDL0	0.32	-0.71	-1.63
Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	*rpiA_2, ripA*	BN194_28600	K0N8W9	2.04	-0.72	-1.65
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF*	BN194_08770	K0N987	2.38	-0.72	-1.65
DNA mismatch repair protein MutL	DNA repair/recombination	*mutL*	BN194_23710	K0N6Z8	2.94	-0.72	-1.65
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	*iscS1*	BN194_14900	K0N4U8	3.54	-0.73	-1.66
Uncharacterized protein yslB	Unknown/uncharacterized	*yslB*	BN194_08630	K0N6L4	1.59	-0.73	-1.66
Cell division protein DivIB	Cytokinesis	*divIB*	BN194_14740	K0MV80	0.55	-0.73	-1.66
Uncharacterized protein SE_0534	*tRNA/Ribosome assembly/processing*		BN194_10150	K0N3F2	1.88	-0.74	-1.67
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	3.29	-0.75	-1.68
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	4.17	-0.76	-1.69
Uncharacterized protein	Unknown/uncharacterized		BN194_05550	K0N257	0.42	-0.76	-1.70

YbbR-like domain-containing protein ybbR	Unknown/uncharacterized	*ybbR*	BN194_11540	K0MUB6	0.89	-0.77	-1.70
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	*aldB*	BN194_20140	K0MWH5	2.67	-0.77	-1.71
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	*dacA*	BN194_02140	K0MS53	4.68	-0.78	-1.71
UPF0237 protein BN194_09820	Unknown/uncharacterized		BN194_09820	K0N9F9	0.93	-0.78	-1.71
Chromosome partition protein Smc	Cytokinesis	*smc*	BN194_17860	K0N5H9	2.52	-0.78	-1.72
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*yfmL*	BN194_12120	K0NA13	2.14	-0.79	-1.72
Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase)	Cofactor-related metabolism	*coaA*	BN194_21080	K0N9V9	3.33	-0.79	-1.72
Uncharacterized protein ypuA	Unknown/uncharacterized	*ypuA*	BN194_27250	K0N8I3	2.60	-0.79	-1.73
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	*thyA*	BN194_15800	K0N522	3.23	-0.80	-1.74
Uncharacterized protein	Unknown/uncharacterized		BN194_08270	K0N959	0.52	-0.80	-1.74
Chaperone protein ClpB	Protein folding/turnover	*clpB_2*	BN194_26350	K0N887	1.85	-0.81	-1.76
ABC-type Na+ efflux pump permease component-like protein	*ABC-type transporter systems*		BN194_11370	K0N9U5	2.60	-0.82	-1.76
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	*cmk*	BN194_15710	K0N4V1	3.87	-0.82	-1.76
Aldose 1-epimerase	*Central glycolytic/intermediary pathways*		BN194_16020	K0NAP4	3.84	-0.82	-1.77
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	*der*	BN194_15730	K0N8E1	2.89	-0.82	-1.77
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	2.25	-0.82	-1.77
Bifunctional protein BirA (EC 6.3.4.15)	Lipid-related metabolism	*birA*	BN194_08790	K0MTP3	3.21	-0.83	-1.78
Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	*phoP*	BN194_10220	K0N9J6	2.86	-0.84	-1.79
Transcriptional regulator GltC	Transcriptional regulation	*nac*	BN194_16620	K0NAT7	3.87	-0.84	-1.79
Uncharacterized amino acid permease YfnA	Other transporter proteins	*yfnA*	BN194_06960	K0N2T0	0.95	-0.84	-1.79

DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	*gyrB*	BN194_00060	K0N1B8	2.13	-0.84	-1.79
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	*HBN1*	BN194_16550	K0N597	2.81	-0.84	-1.79
Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.193)	tRNA/Ribosome assembly/processing	*rsmE*	BN194_17250	K0N5G8	1.69	-0.84	-1.79
Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	Carbohydrate-related metabolism	*scrB*	BN194_22440	K0MX27	1.60	-0.84	-1.79
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD(+)])	DNA replication-related	*ligA*	BN194_11930	K0N7A9	1.24	-0.84	-1.80
Uncharacterized RNA pseudouridine synthase YhcT (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*yhcT_2*	BN194_20220	K0NBE7	1.13	-0.85	-1.80
Probable copper-transporting P-type ATPase B (EC 3.6.3.-)	Other transporter proteins	*copB*	BN194_19280	K0N9H1	0.82	-0.85	-1.80
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	*guaB*	BN194_02100	K0N1G3	3.23	-0.85	-1.80
HTH-type transcriptional regulator yodB	Transcriptional regulation	*yodB*	BN194_18590	K0MW80	0.48	-0.85	-1.81
Transcriptional repressor NrdR	Transcriptional regulation	*nrdR*	BN194_18900	K0N5Z5	2.26	-0.86	-1.81
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh1,ldh*	BN194_06970	K0N8S5	2.53	-0.87	-1.83
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	*yclJ*	BN194_11790	K0MUE5	1.52	-0.87	-1.83
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	*hslO*	BN194_26400	K0N893	1.21	-0.88	-1.83
Mevalonate kinase (EC 2.7.1.36)	Lipid-related metabolism	*mvk*	BN194_12270	K0NA23	3.86	-0.88	-1.84
Uncharacterized protein yjdJ	General prediction only	*yjdJ*	BN194_24650	K0N7R2	1.57	-0.88	-1.84
DNA topoisomerase 4 subunit B (EC 5.99.1.3) (Topoisomerase IV subunit B)	DNA replication-related	*parE*	BN194_16050	K0N545	4.86	-0.89	-1.85
GNAT family acetyltransferase	General prediction only		BN194_01510	K0N1L8	1.74	-0.89	-1.85
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*lacC*	BN194_07470	K0N8Y4	3.37	-0.89	-1.85
Uncharacterized protein	General prediction only		BN194_17420	K0NAY8	1.56	-0.89	-1.86

DNA mismatch repair protein MutS	DNA repair/recombination	*mutS*	BN194_23720	K0NBY9	2.64	-0.89	-1.86
Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase)	Cofactor-related metabolism	*coaE*	BN194_18910	K0N5P8	2.72	-0.89	-1.86
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	*mtlF*	BN194_30410	K0N8N0	2.62	-0.90	-1.86
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	*pta*	BN194_11340	K0MU95	4.97	-0.90	-1.86
Uncharacterized oxidoreductase YbdH (EC 1.1.-.-)	Carbohydrate-related metabolism	*ybdH*	BN194_30540	K0MYX0	3.18	-0.90	-1.86
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	*pyrG*	BN194_26790	K0MXZ1	2.67	-0.90	-1.87
Nuclease sbcCD subunit D	DNA repair/recombination	*sbcD*	BN194_07530	K0N6B1	0.59	-0.90	-1.87
Uncharacterized protein yieF	General prediction only	*yieF_2*	BN194_06540	K0MT25	1.73	-0.91	-1.88
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	*galK*	BN194_07340	K0MTA3	3.71	-0.91	-1.88
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	*apt*	BN194_17380	K0N902	3.44	-0.92	-1.89
ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	DNA repair/recombination	*addA*	BN194_16800	K0N5B6	3.53	-0.92	-1.89
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	*patB_2*	BN194_09790	K0MTW3	3.60	-0.92	-1.89
Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	*adk*	BN194_26010	K0N7F0	6.22	-0.92	-1.89
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB_2*	BN194_21770	K0NBN4	2.99	-0.93	-1.90
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	*fbp*	BN194_21660	K0N6C3	1.63	-0.93	-1.90
Aldose 1-epimerase (EC 5.1.3.3)	*Central glycolytic/intermediary pathways*		BN194_07390	K0MTA8	2.67	-0.93	-1.91

Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	*upp*	BN194_13550	K0N4J8	3.39	-0.93	-1.91
Uncharacterized ABC transporter ATP-binding protein YfmR (EC 3.6.3.-)	ABC-type transporter systems	*yfmR*	BN194_15790	K0MVF8	2.57	-0.95	-1.93
Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (EC 5.3.3.2) (Isopentenyl diphosphate:dimethylallyl diphosphate isomerase) (Isopentenyl pyrophosphate isomerase) (Type 2 isopentenyl diphosphate isomerase)	Lipid-related metabolism	*fni*	BN194_16840	K0MVP7	0.99	-0.96	-1.95
Methionyl-tRNA formyltransferase (EC 2.1.2.9)	Protein translation (initiation)	*fmt*	BN194_18060	K0N5J2	3.24	-0.97	-1.97
Double-stranded beta-helix related protein	Transcriptional regulation		BN194_11420	K0N9U8	0.80	-0.98	-1.97
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	*msmK*	BN194_11180	K0N747	0.86	-0.99	-1.99
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	*cap4C*	BN194_12280	K0N7E3	5.06	-0.99	-1.99
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	0.61	-1.00	-1.99
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	2.61	-1.00	-2.00
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*argS*	BN194_19120	K0NB86	5.67	-1.00	-2.00
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	*bkr4*	BN194_22550	K0N799	1.90	-1.01	-2.01
tRNA N6-adenosine threonylcarbamoyltransferase (EC 2.3.1.234) (N6-L-threonylcarbamoyladenine synthase) (t(6)A37 threonylcarbamoyladenosine biosynthesis protein TsaD) (tRNA threonylcarbamoyladenosine biosynthesis protein TsaD)	General prediction only	*tsaD,gcp*	BN194_23850	K0N7L3	2.62	-1.01	-2.01
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	*yhaA*	BN194_30550	K0N9E4	0.72	-1.03	-2.04
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_2*	BN194_29910	K0N8I1	3.77	-1.03	-2.04
Oligoendopeptidase F	Amino acid-related metabolism	*yjbG_2*	BN194_08130	K0N6H7	4.25	-1.03	-2.05
HTH-type transcriptional regulator galR	Transcriptional regulation	*galR*	BN194_03780	K0N5G9	0.64	-1.03	-2.05
Guanylate kinase (EC 2.7.4.8)	Nucleic acid/nucleotide metabolism	*gmk_2*	BN194_21480	K0N9Y7	1.72	-1.04	-2.06

Protein LemA	Unknown/uncharacterized	*lemA*	BN194_27350	K0N8J7	3.51	-1.05	-2.07
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	*gyrA*	BN194_00070	K0N6S7	1.26	-1.06	-2.08
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	*glyr1*	BN194_30100	K0N992	3.17	-1.06	-2.08
Cell wall surface anchor family protein	*Cell surface proteins/internalins*		BN194_05290	K0MSU3	2.15	-1.07	-2.09
tRNA pseudouridine synthase B (EC 5.4.99.25) (tRNA pseudouridine(55) synthase) (tRNA pseudouridylate synthase) (tRNA-uridine isomerase)	tRNA/Ribosome assembly/processing	*truB*	BN194_17520	K0NAZ5	0.87	-1.07	-2.10
Thioredoxin-like protein ytpP	Posttranslational modification	*ytpP*	BN194_18980	K0N9F1	3.13	-1.08	-2.12
41 kDa protein		*repA*	BN194_P0550	K0NBI6	2.03	-1.09	-2.13
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	*ykpA*	BN194_07220	K0N8V6	3.46	-1.09	-2.13
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	*prs1_2*	BN194_30370	K0NDQ5	1.52	-1.10	-2.15
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	*fabG*	BN194_22560	K0N6N3	3.28	-1.11	-2.15
Uncharacterized protein IRC4	Unknown/uncharacterized	*IRC4*	BN194_30110	K0N8K0	1.87	-1.11	-2.17
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox_2*	BN194_02850	K0N1N9	4.19	-1.12	-2.17
D-2-hydroxyacid dehydrogenase (EC 1.1.1.-)	General prediction only	*ddh*	BN194_16660	K0N557	2.38	-1.12	-2.18
Ribosomal RNA small subunit methyltransferase A (EC 2.1.1.182) (16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase) (16S rRNA dimethyladenosine transferase) (16S rRNA dimethylase) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase)	tRNA/Ribosome assembly/processing	*rsmA,ksgA*	BN194_27020	K0NCX3	3.38	-1.15	-2.22
Putative N-acetylmuramoyl-L-alanine amidase YrvJ (EC 3.5.1.28)	Cytokinesis	*yrvJ*	BN194_17200	K0N5G4	0.89	-1.15	-2.22
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_23190	K0MXA1	3.09	-1.15	-2.23
PspC domain-containing protein	Unknown/uncharacterized	*ythC*	BN194_10300	K0N3H5	4.35	-1.17	-2.25
Acetyltransferase	General prediction only		BN194_08200	K0N2Z8	2.12	-1.17	-2.25
Predicted ORF			BN194_P0560	K0MZ29	0.75	-1.17	-2.25

Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	*dut*	BN194_24640	K0MXG3	2.96	-1.17	-2.25
Uncharacterized oxidoreductase YcsN (EC 1.-.-.-)	General prediction only	*ycsN*	BN194_27290	K0MY45	1.49	-1.19	-2.27
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB_2*	BN194_20630	K0N9S5	0.53	-1.19	-2.27
Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)	Nucleic acid/nucleotide metabolism	*purC*	BN194_19360	K0N5S8	3.75	-1.19	-2.29
Uncharacterized protein	Unknown/uncharacterized		BN194_23630	K0NA78	3.05	-1.20	-2.29
Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-)	Nucleic acid/nucleotide metabolism	*purK*	BN194_12510	K0N441	5.42	-1.20	-2.29
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	*yabO*	BN194_26520	K0NCR8	1.12	-1.21	-2.32
ABC transporter, ATP-binding protein	*Cell surface proteins/internalins*		BN194_15700	K0N514	0.99	-1.22	-2.32
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	3.50	-1.22	-2.33
tRNA (Adenine(22)-N(1))-methyltransferase (EC 2.1.1.217)	tRNA/Ribosome assembly/processing	*trmK*	BN194_16910	K0N584	3.17	-1.22	-2.33
Polyphosphate kinase (EC 2.7.4.1) (ATP-polyphosphate phosphotransferase) (Polyphosphoric acid kinase)	Membrane bioenergetics	*ppk*	BN194_27270	K0ND10	2.40	-1.22	-2.33
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	*glyA*	BN194_13540	K0MV12	5.40	-1.25	-2.38
Nod factor export ATP-binding protein I (EC 3.6.3.-)	ABC-type transporter systems	*nodI*	BN194_06850	K0N2J7	1.66	-1.26	-2.39
Folate transporter FolT	Unknown/uncharacterized	*folT*	BN194_23890	K0MXC9	2.79	-1.27	-2.40
Uncharacterized protein	Unknown/uncharacterized		BN194_08020	K0N947	3.99	-1.27	-2.41
Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	Nucleic acid/nucleotide metabolism	*purD*	BN194_19290	K0MWC4	3.37	-1.28	-2.43
Transcription-repair-coupling factor (TRCF) (EC 3.6.4.-)	DNA repair/recombination	*mfd*	BN194_26540	K0MXW9	1.05	-1.28	-2.43
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	*frr*	BN194_17650	K0N5M3	3.70	-1.29	-2.44

Uncharacterized protein ybfG	General prediction only	*ybfG*	BN194_00330	K0N4B3	4.01	-1.30	-2.46
Putative ribosome biogenesis GTPase RsgA (EC 3.6.1.-)	tRNA/Ribosome assembly/processing	*rsgA*	BN194_18010	K0N5J0	0.90	-1.31	-2.48
Pur operon repressor	Transcriptional regulation	*purR_2*	BN194_26960	K0N7M9	3.19	-1.31	-2.48
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	*yqeH*	BN194_18740	K0MW90	4.37	-1.32	-2.50
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	*prs1,prs*	BN194_26930	K0NAT2	3.78	-1.35	-2.55
Uncharacterized protein YdiC	General prediction only	*ydiC_3*	BN194_23870	K0NBZ8	2.39	-1.35	-2.56
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*helD*	BN194_21130	K0N9W3	4.67	-1.36	-2.57
Uncharacterized protein YneR	General prediction only	*yneR*	BN194_18480	K0N9C1	1.43	-1.36	-2.57
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	*fabZ_2*	BN194_22620	K0NBT3	3.46	-1.36	-2.57
Ribosomal protein L11 methyltransferase (L11 Mtase) (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*prmA*	BN194_17260	K0N5B0	1.71	-1.37	-2.59
Putative RNA-binding protein ylmH	General prediction only	*ylmH*	BN194_14790	K0MV84	1.08	-1.38	-2.60
GTP pyrophosphokinase yjbM (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*yjbM*	BN194_09870	K0N9G5	4.62	-1.38	-2.60
Phosphoribosylformylglycinamidine synthase subunit PurQ (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit I) (Glutaminase PurQ) (Phosphoribosylformylglycinamidine synthase subunit I)	Nucleic acid/nucleotide metabolism	*purQ*	BN194_19340	K0MWC7	4.91	-1.39	-2.61
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	*hmgCS1*	BN194_19680	K0N9K3	3.38	-1.40	-2.63
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	*guaA*	BN194_21070	K0NBJ2	4.73	-1.40	-2.64
Uncharacterized protein	*Nucleic acid/nucleotide metabolism*		BN194_27260	K0N7R1	1.81	-1.41	-2.65

DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshB*	BN194_08460	K0N356	3.63	-1.42	-2.68
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_3*	BN194_04780	K0N5N9	4.35	-1.43	-2.69
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	*fabZ*	BN194_22520	K0NBS8	3.91	-1.43	-2.69
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	*purA*	BN194_01160	K0N1J0	6.74	-1.45	-2.72
Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	*rbsK*	BN194_03300	K0N1R2	4.48	-1.45	-2.72
GMP reductase (EC 1.7.1.7) (Guanosine 5'-monophosphate oxidoreductase)	Nucleic acid/nucleotide metabolism	*guaC*	BN194_09960	K0N3H4	6.27	-1.45	-2.73
Uridine kinase (EC 2.7.1.48)		*udk*	BN194_18540	K0MW76	1.05	-1.45	-2.73
Uncharacterized protein	Unknown/uncharacterized		BN194_12110	K0N410	0.83	-1.45	-2.73
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*pcrA*	BN194_11920	K0N9Z6	2.55	-1.46	-2.74
Mannose permease IID component	Phosphotransferase systems	*manZ_4*	BN194_04510	K0N287	1.66	-1.46	-2.75
Uncharacterized protein	General prediction only		BN194_21200	K0N6M8	3.91	-1.47	-2.77
Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	*fba_2*	BN194_05060	K0N2C9	4.54	-1.47	-2.78
tRNA pseudouridine synthase A (EC 5.4.99.12) (tRNA pseudouridine(38-40) synthase) (tRNA pseudouridylate synthase I) (tRNA-uridine isomerase I)	tRNA/Ribosome assembly/processing	*truA*	BN194_25910	K0N7E2	1.70	-1.48	-2.79
Uncharacterized protein yueI	Unknown/uncharacterized	*yueI*	BN194_13920	K0NAC7	3.52	-1.50	-2.83
Exopolyphosphatase	Membrane bioenergetics		BN194_27280	K0NAV4	0.90	-1.52	-2.87
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	*clpP_2, clpP*	BN194_10510	K0N3M4	4.54	-1.54	-2.91
DegV domain-containing protein SP_1112	Unknown/uncharacterized		BN194_15830	K0N8F3	4.83	-1.54	-2.92

Uncharacterized protein yloA	Cell surface proteins/internalins	*yloA*	BN194_16340	K0MVK5	3.83	-1.55	-2.92
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	Nucleic acid/nucleotide metabolism	*tmk*	BN194_23950	K0N7L9	3.52	-1.56	-2.94
Cof protein	General prediction only		BN194_12010	K0N401	0.90	-1.56	-2.94
Uncharacterized protein	Unknown/uncharacterized		BN194_01790	K0MS25	1.07	-1.56	-2.95
Uncharacterized protein	Unknown/uncharacterized		BN194_12200	K0N464	0.60	-1.57	-2.97
Uncharacterized protein	Cofactor-related metabolism		BN194_18720	K0NB69	1.81	-1.57	-2.97
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB*	BN194_13410	K0N4C0	1.29	-1.57	-2.97
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03940	K0MSJ3	1.38	-1.58	-2.98
Protein dedA	Unknown/uncharacterized	*dedA*	BN194_08930	K0N6M9	0.36	-1.60	-3.04
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	*yfeX*	BN194_07170	K0N8U9	3.47	-1.60	-3.04
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25570	K0NCD4	2.79	-1.61	-3.05
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	*hslU*	BN194_16010	K0N4Y1	1.79	-1.62	-3.07
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshA*	BN194_26700	K0N8C7	3.48	-1.62	-3.08
HTH-type transcriptional regulator iolR	Transcriptional regulation	*iolR*	BN194_02190	K0MS58	1.23	-1.62	-3.08
Uncharacterized protein yutG	Lipid-related metabolism	*yutG*	BN194_08940	K0MTQ3	4.55	-1.63	-3.09
Thymidine kinase (EC 2.7.1.21)	Nucleic acid/nucleotide metabolism	*tdk*	BN194_13500	K0N4J4	1.19	-1.63	-3.10
Holo-[acyl-carrier-protein] synthase (Holo-ACP synthase) (EC 2.7.8.7) (4'-phosphopantetheinyl transferase AcpS)	Cofactor-related metabolism	*acpS*	BN194_26690	K0MXY2	4.03	-1.65	-3.14
Oxidoreductase YdhF (EC 1.-.-.-)	General prediction only	*ydhF*	BN194_25320	K0NCA1	1.10	-1.69	-3.22
Sorbose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*sorB_2*	BN194_29180	K0NB63	0.98	-1.69	-3.23
Lactose phosphotransferase system repressor	Transcriptional regulation	*lacR*	BN194_07510	K0N2X5	1.27	-1.70	-3.25

Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ*	BN194_14610	K0N4K4	0.87	-1.70	-3.26
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	*cysK*	BN194_05520	K0N8E6	4.05	-1.72	-3.28
Glutathione reductase, chloroplastic (EC 1.8.1.7)	Cofactor-related metabolism	*GOR*	BN194_23200	K0N7H3	4.24	-1.74	-3.33
Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)	Nucleic acid/nucleotide metabolism	*pyrF*	BN194_16430	K0N8M7	3.21	-1.75	-3.36
Diphosphomevalonate decarboxylase (EC 4.1.1.33)	Lipid-related metabolism	*mvd1*	BN194_16830	K0N8S2	1.59	-1.75	-3.37
Uncharacterized protein yeaC		*yeaC*	BN194_29960	K0N8I6	1.78	-1.75	-3.37
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2,lacD*	BN194_07480	K0N6A8	5.57	-1.75	-3.37
Uncharacterized protein YxeH	General prediction only	*yxeH*	BN194_04750	K0N1Y7	3.94	-1.76	-3.39
Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase)	Nucleic acid/nucleotide metabolism	*purM*	BN194_19320	K0NB95	4.45	-1.79	-3.45
Aspartate racemase (EC 5.1.1.13)	*Amino acid-related metabolism*		BN194_02170	K0N7H2	2.89	-1.80	-3.49
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	*gmk*	BN194_18110	K0N5J6	5.37	-1.83	-3.54
Putative beta-phosphoglucomutase (EC 5.4.2.6)	Central glycolytic/intermediary pathways	*yvdM*	BN194_11170	K0N9S7	2.35	-1.84	-3.58
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	*hslV*	BN194_16000	K0N542	3.67	-1.84	-3.59
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA*	BN194_01620	K0N7B1	2.24	-1.85	-3.61
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	*act*	BN194_16090	K0MVI3	3.16	-1.85	-3.62
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	*murI*	BN194_08640	K0MTN4	3.64	-1.86	-3.63
3-hydroxy-3-methylglutaryl coenzyme A reductase (HMG-CoA reductase) (EC 1.1.1.88)	Lipid-related metabolism	*mvaA*	BN194_19690	K0MWE8	2.40	-1.88	-3.69

Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	*pyrC*	BN194_16470	K0NAS6	3.03	-1.90	-3.72
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	*xpt*	BN194_12490	K0MUR6	3.68	-1.91	-3.77
Hex regulon repressor	Transcriptional regulation		BN194_02320	K0N7J9	1.92	-1.92	-3.78
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	*rnc*	BN194_17870	K0NB31	1.69	-1.92	-3.78
Phosphatase YbjI (EC 3.1.3.-)	General prediction only	*ybjI*	BN194_30020	K0NDN5	2.10	-1.92	-3.78
Probable transcription repressor NiaR	Transcriptional regulation	*niaR*	BN194_08730	K0N6L8	5.00	-1.93	-3.80
Putative ADP-ribose pyrophosphatase yjhB (EC 3.6.1.-)	General prediction only	*yjhB*	BN194_25530	K0NAH4	1.94	-1.94	-3.83
Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	*pox5*	BN194_19670	K0NBB6	3.45	-1.95	-3.87
Uncharacterized protein	General prediction only		BN194_14990	K0MV99	3.46	-1.95	-3.88
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	*phoU*	BN194_10290	K0MTZ9	2.98	-1.96	-3.89
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA_2*	BN194_22950	K0N7F8	4.53	-1.98	-3.95
Uncharacterized protein in fgs 3'region	General prediction only		BN194_14530	K0N802	1.60	-1.99	-3.96
Elongation factor P	Protein translation (elongation)	*efp_2*	BN194_22050	K0N712	2.56	-2.00	-4.01
Uncharacterized N-acetyltransferase ycf52-like (EC 2.3.1.-)	General prediction only	*speE1*	BN194_21490	K0MWT4	1.97	-2.03	-4.09
Phosphatase YidA (EC 3.1.3.-)	General prediction only	*yidA*	BN194_28520	K0NDD5	5.45	-2.04	-4.10
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox*	BN194_01780	K0N4U4	3.92	-2.05	-4.14
Putative HAD-hydrolase yfnB (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yfnB*	BN194_08780	K0N6M1	1.65	-2.05	-4.15
Uncharacterized protein	Unknown/uncharacterized		BN194_01600	K0N1B9	3.08	-2.06	-4.17
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	*htrA*	BN194_29460	K0N8D9	3.92	-2.09	-4.25

UPF0337 protein yhjA	General prediction only	*yhjA*	BN194_24800	K0N7S1	0.55	-2.12	-4.35
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	*hprK*	BN194_10330	K0N6Y3	5.43	-2.15	-4.43
Recombination protein RecR	DNA repair/recombination	*recR*	BN194_23970	K0NC03	1.78	-2.15	-4.43
Phosphoribosylformylglycinamidine synthase subunit PurL (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit II) (Glutamine amidotransferase PurL) (Phosphoribosylformylglycinamidine synthase subunit II)	Nucleic acid/nucleotide metabolism	*purL*	BN194_19330	K0N9H6	2.44	-2.15	-4.44
Transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	4.00	-2.16	-4.45
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*nagA*	BN194_19890	K0MWF9	5.26	-2.16	-4.46
SMC domain protein	DNA repair/recombination		BN194_07540	K0MTC3	1.02	-2.20	-4.59
Uncharacterized ABC transporter ATP-binding protein YdiF	General prediction only	*ydiF*	BN194_23830	K0NA88	5.49	-2.21	-4.61
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	*pfkA*	BN194_15570	K0NAK6	4.07	-2.21	-4.64
Protein RecA (Recombinase A)	DNA repair/recombination	*recA_2,recA*	BN194_27650	K0N8P0	2.44	-2.22	-4.66
Uncharacterized protein HI_0912	General prediction only	*thiF3*	BN194_05090	K0MSS8	1.76	-2.27	-4.84
Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	*gntK*	BN194_02340	K0MS76	3.80	-2.28	-4.87
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA_2*	BN194_18340	K0MW64	6.46	-2.34	-5.07
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	*yhfP*	BN194_07740	K0MTE1	4.76	-2.41	-5.32
Phosphoribosylformylglycinamidine synthase subunit PurS (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit III) (Phosphoribosylformylglycinamidine synthase subunit III)	Nucleic acid/nucleotide metabolism	*yexA,purS*	BN194_19350	K0N638	2.93	-2.42	-5.35
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	*glgD*	BN194_21590	K0MWU4	2.46	-2.42	-5.36

Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB_2*	BN194_21970	K0NBP6	2.52	-2.43	-5.38
Bifunctional protein FolD	Cofactor-related metabolism	*folD*	BN194_18210	K0N5K0	1.11	-2.43	-5.41
ABC-type phosphate/phosphonate transport system,periplasmic component	*ABC-type transporter systems*		BN194_25680	K0NAI1	5.33	-2.52	-5.73
50S ribosomal protein L32	Ribosomal proteins	*rpmF*	BN194_15510	K0N4T0	0.56	-2.60	-6.05
Phosphonates import ATP-binding protein PhnC (EC 3.6.3.28)	ABC-type transporter systems	*phnC_2,phnC*	BN194_25690	K0MXP5	4.62	-2.60	-6.06
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	*murE*	BN194_02160	K0N1S5	6.40	-2.60	-6.06
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	*citD*	BN194_20330	K0N9Q5	2.25	-2.62	-6.16
MFS permease-like protein	Other transporter proteins		BN194_06910	K0N2S6	2.93	-2.63	-6.21
Alternansucrase	Cell wall biogenesis		BN194_02430	K0N547	4.48	-2.69	-6.47
UPF0346 protein BN194_15870	Unknown/uncharacterized		BN194_15870	K0NAN2	1.97	-2.71	-6.53
Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		BN194_08520	K0N972	5.38	-2.73	-6.65
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		BN194_03130	K0N5D9	6.01	-2.77	-6.81
Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (EC 2.7.7.12) (UDP-glucose--hexose-1-phosphate uridylyltransferase)		*galT*	BN194_07370	K0N8X1	4.27	-2.82	-7.07
Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		BN194_20000	K0N684	6.98	-2.83	-7.11
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	*gpsA*	BN194_10350	K0N3I2	4.81	-2.84	-7.17
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citE*	BN194_20320	K0NBF4	3.46	-2.92	-7.59
tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA (guanine(46)-N(7))-methyltransferase) (tRNA(m7G46)-methyltransferase)	tRNA/Ribosome assembly/processing	*trmB*	BN194_19000	K0N606	2.76	-2.97	-7.82
DNA topoisomerase 1 (EC 5.99.1.2) (DNA topoisomerase I)	DNA replication-related	*topA*	BN194_15970	K0NAP0	1.10	-3.03	-8.15
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	*apbE_3*	BN194_21550	K0N6S8	4.43	-3.09	-8.50
Uncharacterized protein yuaG	Unknown/uncharacterized	*yuaG*	BN194_22920	K0NBV0	2.49	-3.18	-9.07

Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	Nucleic acid/nucleotide metabolism	*purN*	BN194_19310	K0N5S4	1.89	-3.21	-9.22
Maltose ABC transporter, periplasmic maltose-binding protein	*ABC-type transporter systems*		BN194_11200	K0N3U4	5.35	-3.24	-9.47
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA_2,ackA*	BN194_23060	K0N6W4	4.52	-3.25	-9.51
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_2*	BN194_04490	K0MSM9	2.35	-3.31	-9.91
Uncharacterized protein			BN194_07360	K0N2W3	6.16	-3.32	-10.01
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	*ndk*	BN194_08160	K0N340	4.32	-3.43	-10.75
Bifunctional purine biosynthesis protein PurH	Nucleic acid/nucleotide metabolism	*purH*	BN194_19300	K0N634	3.28	-3.44	-10.89
Uncharacterized protein MJ1651	General prediction only		BN194_04410	K0N281	6.04	-3.51	-11.37
UPF0039 protein SAR1027	General prediction only		BN194_19510	K0N5U0	2.82	-3.55	-11.71
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_2*	BN194_20600	K0N6C6	3.93	-3.70	-13.01
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA1,gpmA*	BN194_24750	K0N7R7	2.99	-3.94	-15.30
Coenzyme A biosynthesis bifunctional protein CoaBC (EC 4.1.1.36) (EC 6.3.2.5)		*coaBC*	BN194_18090	K0MW49	4.95	-4.01	-16.09
UPF0337 protein lp_1708	General prediction only		BN194_05810	K0N2J8	3.09	-4.11	-17.23
N5-carboxyaminoimidazole ribonucleotide synthase (N5-CAIR synthase) (EC 6.3.4.18) (5-(carboxyamino)imidazole ribonucleotide synthetase)	Nucleic acid/nucleotide metabolism	*purK_2, purK*	BN194_19370	K0NB96	7.48	-4.11	-17.26
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	*pyc*	BN194_15170	K0NAI2	6.66	-4.11	-17.29
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_07710	K0N2Z3	6.91	-4.20	-18.41
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	*purB*	BN194_12520	K0NA41	4.94	-4.21	-18.49

Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citF*	BN194_20310	K0N607	6.91	-4.37	-20.65
Manganese transport system ATP-binding protein MntB	ABC-type transporter systems	*mntB*	BN194_25460	K0N7A8	3.16	-4.76	-27.06
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA_2*	BN194_20640	K0MWL6	7.11	-4.97	-31.24
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	*coaD*	BN194_15200	K0N4X3	6.02	-4.97	-31.35
Manganese ABC transporter substrate-binding lipoprotein	ABC-type transporter systems	*fimA*	BN194_25450	K0N7Y2	5.31	-4.98	-31.61
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF_2*	BN194_20590	K0MWL1	5.36	-5.03	-32.75
D-ribose-binding protein	ABC-type transporter systems	*rbsB*	BN194_03290	K0MSF6	2.38	-5.14	-35.16
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	*rpe*	BN194_18000	K0N5T1	2.77	-5.24	-37.77
Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	*ADH2*	BN194_08400	K0N307	4.94	-5.77	-54.55
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	*pycB*	BN194_20290	K0MWI8	3.21	-5.83	-56.89
ABC-type uncharacterized transport system, ATPase component	*ABC-type transporter systems*		BN194_07730	K0N6C9	3.93	-6.44	-87.01
Uncharacterized protein	Unknown/uncharacterized		BN194_01760	K0N1N3	3.85	-6.60	-96.88
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	*pflB*	BN194_16080	K0N8I5	5.37	-7.90	-238.73
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07700	K0N2V5	4.52	-9.93	-975.64

(7b) ProteinFC UC pH Vs pH CFE 6.5

Protein names	Functional Class	Gene	Gene locus	Protein IDs	-Log t-test p-value	t-test difference	Fold change
Esterase/lipase	General prediction only	*yneB*	BN194_20230	K0N9P7	4.69	7.66	202.88
Uncharacterized aminotransferase SSO0104 (EC 2.6.1.-)	*Amino acid-related metabolism*		BN194_27600	K0N8N4	3.07	6.78	109.80
Uncharacterized protein	Unknown/uncharacterized		BN194_07550	K0N2T9	3.41	6.49	89.74
Malolactic enzyme (EC 1.-.-.-)	Tricarboxylic acid pathway	*mleA*	BN194_08070	K0N949	5.14	6.37	82.51
UPF0337 protein yhjA	General prediction only	*yhjA*	BN194_24800	K0N7S1	1.64	6.23	75.09
Uncharacterized protein	Unknown/uncharacterized		BN194_25890	K0MXR4	5.12	6.14	70.54
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*pip_2*	BN194_27140	K0MY30	5.08	6.14	70.46
Probable dipeptidase A (EC 3.4.-.-)	Amino acid-related metabolism	*pepDA*	BN194_00410	K0N1E0	5.27	5.99	63.53
D-alanine--poly(phosphoribitol) ligase subunit 2 (EC 6.1.1.13) (D-alanyl carrier protein)	Cell wall biogenesis	*dltC*	BN194_08610	K0N361	4.74	5.80	55.59
Hydroxyacid oxidase (EC 1.1.3.15)	Central glycolytic/intermediary pathways	*haox*	BN194_24790	K0MXH5	7.67	5.60	48.58
Peptidase T (EC 3.-.-.-) (EC 3.4.11.-) (EC 3.4.11.4)	Amino acid-related metabolism	*pepT*	BN194_03110	K0N213	5.51	5.23	37.64
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	*luxS*	BN194_08330	K0N6J0	5.81	5.09	33.97
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	*pepDB*	BN194_21110	K0N678	5.68	5.03	32.75
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	*mco*	BN194_25410	K0N7A4	6.17	4.97	31.41
Glycolate oxidase subunit glcD	General prediction only	*glcD*	BN194_24440	K0MXF3	4.07	4.85	28.94
Protein lacX, plasmid	Carbohydrate-related metabolism	*lacX*	BN194_27070	K0NCY0	5.38	4.79	27.76
Penicillin acylase (EC 3.5.1.11)	Cell defense/detoxification		BN194_04910	K0N2B8	5.17	4.79	27.75
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP*	BN194_17930	K0N988	2.17	4.61	24.37

NAD-dependent epimerase/dehydratase:3-beta hydroxysteroid dehydrogenase/isomerase:NmrA-like	General prediction only		BN194_25520	K0NCC8	5.29	4.59	24.15
Uncharacterized protein	General prediction only		BN194_28370	K0NDC5	5.05	4.48	22.35
4-hydroxy-tetrahydrodipicolinate synthase (HTPA synthase) (EC 4.3.3.7)	Amino acid-related metabolism	*dapA*	BN194_01010	K0N1I2	4.44	4.47	22.09
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	*BN194_21350*	BN194_21780	K0N6Q5	5.21	4.45	21.84
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	*tpiA*	BN194_11030	K0N736	5.16	4.45	21.81
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	*nagB*	BN194_30440	K0MYW0	6.25	4.33	20.12
Beta-galactosidase 17 (EC 3.2.1.23)	Carbohydrate-related metabolism	*BGAL17*	BN194_02960	K0N204	1.83	4.31	19.88
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	3.04	4.25	19.04
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	*mtlD_3mtlD*	BN194_30400	K0N9C8	5.91	4.18	18.09
Uncharacterized protein				K0N2Q1;K0MXJ1	4.93	4.07	16.74
6-phospho-beta-galactosidase (EC 3.2.1.85) (Beta-D-phosphogalactoside galactohydrolase) (P-beta-Gal)	Carbohydrate-related metabolism	*lacG*	BN194_07320	K0N8W7	3.73	4.04	16.49
Putative secreted protein	cell wall biogenesis		BN194_02820	K0N7S8	2.41	3.99	15.90
Uncharacterized protein	Unknown/uncharacterized		BN194_28350	K0N8V3	5.21	3.94	15.37
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E_2,P100*	BN194_05160	K0N2D7	4.11	3.86	14.51
Acid shock protein	Protein folding/turnover		BN194_29440	K0MYM2	4.79	3.84	14.34
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrDA, pyrD*	BN194_19150	K0N623	6.64	3.75	13.45
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI*	BN194_07860	K0N327	3.35	3.74	13.40
Uncharacterized isochorismatase family protein pncA (EC 3.-.-.-)	General prediction only	*pncA*	BN194_29120	K0NDH8	2.67	3.74	13.32
Uncharacterized protein ynbB	Cell defense/detoxification	*ynbB*	BN194_18380	K0N9B7	4.85	3.73	13.25

Probable flavodoxin-1	General prediction only	*ykuN*	BN194_01860	K0N1P2	4.03	3.70	12.97
GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	5.86	3.62	12.26
Cytidine deaminase (EC 3.5.4.5)	Nucleic acid/nucleotide metabolism	*cdd*	BN194_17000	K0N5D8	4.61	3.55	11.68
Uncharacterized protein ycaC	General prediction only	*ycaC*	BN194_29650	K0N948	5.69	3.54	11.64
Uncharacterized protein	Unknown/uncharacterized		BN194_15370	K0NAJ2	3.34	3.54	11.63
18 kDa heat shock protein	Protein folding/turnover	*hsp18*	BN194_07570	K0N8Z3	2.41	3.51	11.40
Uncharacterized protein yhfI	General prediction only	*yhfI*	BN194_19200	K0N627	4.68	3.47	11.10
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	*agaS*	BN194_02940	K0MSD9	6.59	3.45	10.92
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	*galE*	BN194_07350	K0N2R3	5.22	3.42	10.67
Pyridoxine 5'-phosphate oxidase V related favin-nucleotide-binding protein	Cofactor-related metabolism		BN194_01900	K0N1E7	3.60	3.41	10.66
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC_2,deoC*	BN194_02790	K0MSB5	4.55	3.35	10.18
UPF0342 protein yheA	Unknown/uncharacterized	*yheA*	BN194_19080	K0N9F7	4.04	3.21	9.24
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC*	BN194_24670	K0NC50	5.93	3.21	9.22
Uncharacterized protein	Phosphotransferase systems		BN194_04820	K0N885	5.04	3.18	9.06
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	*ppaC*	BN194_16110	K0N4Z4	6.12	3.16	8.92
Oligo-1,6-glucosidase (EC 3.2.1.10)	Carbohydrate-related metabolism	*malL*	BN194_04830	K0N5P4	4.71	3.12	8.66
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	*dnaK*	BN194_17460	K0N5C7	5.34	3.10	8.56
Uncharacterized protein yqeY	Unknown/uncharacterized	*yqeY*	BN194_17040	K0MVR2	5.00	3.10	8.55
Cytochrome d ubiquinol oxidase subunit 1 (EC 1.10.3.-)	Membrane bioenergetics	*cydA_2*	BN194_23410	K0N6Y2	1.90	3.09	8.51

Zinc-type alcohol dehydrogenase-like protein SE_1777	General prediction only		BN194_07910	K0N329	3.91	3.08	8.44
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	*alsS*	BN194_20150	K0N695	4.33	3.07	8.38
3-keto-L-gulonate-6-phosphate decarboxylase sgbH (EC 4.1.1.85)	Carbohydrate-related metabolism	*sgbH*	BN194_28550	K0N8W6	2.52	3.05	8.30
Putative 2-hydroxyacid dehydrogenase SH0752 (EC 1.1.1.-)	General prediction only		BN194_01890	K0MS33	4.99	3.00	7.97
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	*pepN*	BN194_05410	K0N2F5	6.17	2.96	7.76
L-sorbose 1-phosphate reductase (EC 1.1.1.-)	Carbohydrate-related metabolism	*sorE*	BN194_04300	K0N1W2	3.54	2.94	7.67
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrD*	BN194_16440	K0MVL3	4.64	2.92	7.59
Cysteine desulfurase (EC 2.8.1.7)	Cofactor-related metabolism	*csd*	BN194_13790	K0MV25	4.18	2.92	7.59
Uncharacterized protein	Unknown/uncharacterized		BN194_01870	K0N7D4	5.33	2.91	7.52
L-asparaginase (EC 3.5.1.1)	Amino acid-related metabolism	*ansA*	BN194_23900	K0N7L6	5.01	2.89	7.43
Multifunctional protein: 5-nucleotidase 2,3-cyclic-nucleotide 2-phosphodiesterase	Nucleic acid/nucleotide metabolism	*ushA*	BN194_15530	K0N8A9	5.52	2.89	7.40
Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Phosphoglucose isomerase) (Phosphohexose isomerase)	Central glycolytic/intermediary pathways	*pgi*	BN194_12580	K0N7I6	6.39	2.87	7.34
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	*deoB*	BN194_02800	K0N1N0	5.22	2.85	7.22
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*glyS*	BN194_16950	K0N5D3	5.58	2.85	7.21
Uncharacterized protein	Unknown/uncharacterized		BN194_29450	K0N932	5.35	2.83	7.10
Uncharacterized protein	*Central glycolytic/intermediary pathways*		BN194_04970	K0N8A3	6.12	2.82	7.04
Putative thiamine pyrophosphate-containing protein ydaP	Carbohydrate-related metabolism	*ydaP*	BN194_05070	K0N8B1	3.61	2.77	6.80
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB_2*	BN194_29110	K0N8A4	4.79	2.76	6.77
Uncharacterized protein ACIAD3023	Cell defense/detoxification		BN194_07010	K0N2T5	1.48	2.75	6.74

10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	*groS,grES*	BN194_23760	K0N700	6.35	2.75	6.71
Uncharacterized protein	Unknown/uncharacterized		BN194_16570	K0NAT3	1.75	2.73	6.65
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO*	BN194_12030	K0N7B7	3.74	2.73	6.64
Uncharacterized protein	RNA degradation		BN194_11250	K0N3V2	4.47	2.72	6.59
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	*deoD*	BN194_02810	K0N1Z0	4.56	2.72	6.57
Xre-like DNA-binding protein	Transcriptional regulation		BN194_10050	K0N3E1	2.47	2.71	6.53
Uncharacterized protein yxkA	General prediction only	*yxkA*	BN194_27230	K0NAV1	5.35	2.69	6.46
Uncharacterized protein	Unknown/uncharacterized		BN194_19210	K0N5R7	1.74	2.67	6.37
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	*pcp*	BN194_01980	K0N4Y4	4.09	2.66	6.33
Uncharacterized protein MJ0282	Cofactor-related metabolism		BN194_03700	K0N1T2	5.21	2.63	6.19
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	*asd*	BN194_01060	K0N1I5	4.95	2.59	6.02
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	*pepS*	BN194_12180	K0N7D5	4.64	2.57	5.94
Protein hit	tRNA aminoacyl synthesis	*hit*	BN194_19040	K0MWA8	4.56	2.57	5.92
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA_2*	BN194_29210	K0N8B2	4.68	2.56	5.88
UPF0659 protein YMR090W	General prediction only	*ylbE*	BN194_07030	K0N671	5.55	2.54	5.81
Transaldolase (EC 2.2.1.2)	Central glycolytic/intermediary pathways	*fsa*	BN194_28440	K0MYF0	2.19	2.54	5.80
Microcin C7 self-immunity protein mccF			BN194_01360	K0N1K5	6.83	2.52	5.75
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_01410	K0N1L0	6.26	2.51	5.71
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_13380	K0N7S0	6.30	2.51	5.69
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP_2, acpP*	BN194_22590	K0MX45	3.82	2.49	5.62

Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO_2*	BN194_16630	K0N8Q0	5.24	2.49	5.61
Dumpy	Cell surface proteins/internalins	*dp*	BN194_05390	K0MSV0	0.60	2.48	5.57
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	*dhaK_2*	BN194_04980	K0N5Q3	4.75	2.47	5.54
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE*	BN194_13710	K0N4D8	4.64	2.46	5.51
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	*eno*	BN194_11040	K0MU67	6.48	2.45	5.48
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	*pepV*	BN194_08800	K0N324	5.68	2.45	5.48
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	*pgcA*	BN194_10370	K0N9K8	5.78	2.42	5.35
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	*HBN1*	BN194_16550	K0N597	4.55	2.42	5.34
Maf-like protein maf	General prediction only	*maf*	BN194_23700	K0N7K3	1.46	2.40	5.27
Uncharacterized protein	Unknown/uncharacterized		BN194_20070	K0NBE0	4.40	2.38	5.21
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	*pepQ*	BN194_08740	K0MTP0	4.31	2.37	5.16
Uncharacterized protein	Unknown/uncharacterized		BN194_05660	K0N2I2	1.63	2.34	5.06
Putative carboxypeptidase SCO6489 (EC 3.4.16.-)			BN194_01370	K0N787	3.69	2.34	5.06
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	*treA*	BN194_06930	K0N662	3.87	2.31	4.97
Uncharacterized protein yaaQ	Unknown/uncharacterized	*yaaQ*	BN194_23940	K0MXD1	2.80	2.31	4.97
Uncharacterized protein	Unknown/uncharacterized		BN194_07460	K0N2W9	2.54	2.31	4.96
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	*nadE*	BN194_19840	K0MWF6	4.82	2.30	4.93
Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	*pox5*	BN194_19670	K0NBB6	5.09	2.27	4.82
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification		BN194_25280	K0NAG2	3.46	2.26	4.79
Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*leuS*	BN194_09210	K0N3A9	5.04	2.25	4.77

Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA*	BN194_08450	K0N309	6.30	2.24	4.73
Histidinol-phosphatase	General prediction only		BN194_14010	K0N4F8	3.82	2.18	4.54
Probable phosphoketolase (EC 4.1.2.-)	*Central glycolytic/intermediary pathways*		BN194_28700	K0N8X7	3.97	2.18	4.54
Uncharacterized protein	Unknown/uncharacterized		BN194_20240	K0MWI3	2.20	2.17	4.51
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_23190	K0MXA1	4.32	2.16	4.46
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	*serS*	BN194_20080	K0N9N4	6.22	2.15	4.45
Probable phosphoketolase (EC 4.1.2.-)	Central glycolytic/intermediary pathways	*xpkA*	BN194_01710	K0N1M9	5.53	2.14	4.42
Spore coat polysaccharide biosynthesis protein spsK				K0N9X8;K0N6D6	4.17	2.13	4.38
Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	Nucleic acid/nucleotide metabolism	*add*	BN194_23440	K0MXB1	3.32	2.11	4.33
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2_2,lacD*	BN194_27060	K0N7P0	5.83	2.11	4.31
Uncharacterized protein	Unknown/uncharacterized		BN194_29560	K0N8E9	1.76	2.09	4.27
Uncharacterized protein	Unknown/uncharacterized		BN194_20190	K0MWI0	4.02	2.09	4.25
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatC*	BN194_11950	K0N436	5.01	2.09	4.25
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC_2*	BN194_24680	K0NAC2	5.24	2.08	4.22
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	5.18	2.07	4.21
Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	*fhs*	BN194_16520	K0NAT0	4.47	2.06	4.18
UPF0346 protein BN194_15870	Unknown/uncharacterized		BN194_15870	K0NAN2	2.03	2.04	4.10
Diaminopimelate decarboxylase (DAP decarboxylase) (DAPDC) (EC 4.1.1.20)	Amino acid-related metabolism	*lysA*	BN194_01030	K0N4I7	3.15	2.01	4.02
Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	2.80	2.00	3.99

Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1_2*	BN194_12550	K0N496	3.99	1.99	3.98
Glucose 1-dehydrogenase 2 (EC 1.1.1.47)	Central glycolytic/intermediary pathways	*gdhII*	BN194_23130	K0NA64	1.97	1.97	3.92
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	*proC*	BN194_19900	K0N677	3.85	1.96	3.89
Uncharacterized protein YwcC	Carbohydrate-related metabolism	*ywcC*	BN194_09930	K0N6V0	4.25	1.95	3.86
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	2.57	1.91	3.76
Uncharacterized protein ykuJ	Unknown/uncharacterized	*ykuJ*	BN194_09100	K0N348	3.05	1.90	3.73
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	*gatA*	BN194_11960	K0N3Z6	6.22	1.88	3.67
Predicted hydrolase of the HAD superfamily	General prediction only	*mtlD*	BN194_30450	K0N9D4	4.30	1.87	3.67
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatB*	BN194_11970	K0NA01	6.68	1.86	3.62
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	*glpK_2,glpK*	BN194_27720	K0ND65	2.79	1.85	3.61
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	*galK*	BN194_07340	K0MTA3	3.62	1.83	3.56
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	*proS*	BN194_17610	K0N5E2	5.10	1.82	3.52
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	Central glycolytic/intermediary pathways	*gap*	BN194_11010	K0N3R3	5.69	1.80	3.48
Cell wall surface anchor family protein	*Cell surface proteins/internalins*		BN194_05290	K0MSU3	2.65	1.79	3.46
Uncharacterized protein			BN194_19420	K0NB98	5.93	1.78	3.44
Sorbose permease IIC component	Phosphotransferase systems	*sorA_4*	BN194_29710	K0N8G4	4.28	1.77	3.42
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		BN194_21400	K0N6R1	4.91	1.77	3.41
Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Phosphotransferase system, enzyme I)		*ptsI*	BN194_19410	K0N5T2	4.38	1.75	3.36
Glycine cleavage system H protein	Amino acid-related metabolism	*gcvH*	BN194_13700	K0N4K8	3.27	1.74	3.34

Guanine deaminase (EC 3.5.4.3)	Nucleic acid/nucleotide metabolism	*guaD*	BN194_13320	K0NA96	5.19	1.71	3.26
Glucose-1-phosphate thymidylyltransferase		*rmlA*		K0N699;K0MWW4	4.71	1.70	3.26
Possible TrsG protein	Unknown/uncharacterized		BN194_00240	K0MRM8	1.40	1.67	3.19
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	*pmi*	BN194_02920	K0N7U2	5.51	1.62	3.07
Probable flavodoxin-1	Membrane bioenergetics	*ykuN_2*	BN194_12220	K0NA19	3.49	1.57	2.97
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	*ilvE*	BN194_21620	K0NBM4	5.51	1.57	2.97
Mannose permease IID component	Phosphotransferase systems	*manZ_9*	BN194_29700	K0N954	4.43	1.57	2.96
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	*hpt*	BN194_26470	K0NCR2	3.86	1.53	2.88
Surface antigen	Cell wall biogenesis		BN194_21500	K0N6S2	3.57	1.51	2.85
UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	3.40	1.51	2.85
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2,lacD*	BN194_07480	K0N6A8	4.84	1.50	2.83
Cold shock protein 1	Transcription-associated proteins	*csp*	BN194_06990	K0MT67	2.42	1.50	2.83
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	4.87	1.48	2.79
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	*ptsH*	BN194_19430	K0N9I2	4.65	1.47	2.78
Dihydrofolate reductase (EC 1.5.1.3)	Cofactor-related metabolism	*folA*	BN194_15810	K0N4W0	2.81	1.46	2.75
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	*tpx*	BN194_08090	K0MTJ5	2.97	1.44	2.72
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	*npr*	BN194_04740	K0MSP8	3.72	1.44	2.71
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	4.14	1.44	2.71
Alanine racemase (EC 5.1.1.1)	Amino acid-related metabolism	*alr*	BN194_26680	K0NAR1	5.96	1.43	2.70
DltD protein	Cell wall biogenesis		BN194_08620	K0N978	3.90	1.43	2.70

Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE*	BN194_01720	K0N7C1	2.24	1.43	2.70
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox_2*	BN194_02850	K0N1N9	3.66	1.43	2.69
Sorbitol PTS, EIIA	Phosphotransferase systems		BN194_09940	K0MTX4	4.11	1.42	2.68
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_27170	K0NCZ6	4.95	1.40	2.64
LPXTG-motif cell wall anchor domain protein			BN194_26300	K0N883	1.07	1.39	2.61
NADH-dependent butanol dehydrogenase A (EC 1.1.1.-)	Carbohydrate-related metabolism	*bdhA*	BN194_22640	K0MX50	3.12	1.37	2.58
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	*atpD*	BN194_13620	K0NAB3	4.01	1.37	2.58
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	*pgk*	BN194_11020	K0N9R1	4.56	1.36	2.57
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*pheT*	BN194_18560	K0N5M4	3.82	1.36	2.56
Aldose 1-epimerase (EC 5.1.3.3)	*Central glycolytic/intermediary pathways*		BN194_07390	K0MTA8	3.81	1.34	2.54
Uncharacterized protein yueI	Unknown/uncharacterized	*yueI*	BN194_13920	K0NAC7	3.74	1.34	2.54
Uncharacterized protein	Unknown/uncharacterized	*yvcC*	BN194_05260	K0N2E5	2.96	1.33	2.52
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	4.09	1.31	2.47
Uncharacterized protein yeaE	General prediction only	*yeaE*	BN194_07040	K0MT72	3.79	1.28	2.42
Probable calcium-transporting ATPase (EC 3.6.3.8)	Other transporter proteins	*pacL*	BN194_11490	K0MUB1	2.03	1.25	2.38
Putative tRNA-binding protein ytpR	General prediction only	*ytpR*	BN194_18970	K0NB80	4.19	1.24	2.37
Uncharacterized zinc protease ymfH (EC 3.4.24.-)	Amino acid-related metabolism	*ymfH*	BN194_10030	K0N6V9	2.16	1.24	2.37
Predicted Zn-dependent peptidase	*Amino acid-related metabolism*		BN194_10020	K0N9H8	4.07	1.22	2.33
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	*pheS*	BN194_18570	K0NB64	4.50	1.21	2.31
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		BN194_18780	K0N9E0	0.85	1.20	2.29

Acetyltransferase	General prediction only		BN194_08200	K0N2Z8	2.59	1.18	2.27
Uncharacterized protein	General prediction only		BN194_30000	K0N979	1.74	1.16	2.23
Dehydrogenase	General prediction only		BN194_24480	K0NAB4	1.91	1.12	2.17
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	*fabF*	BN194_22540	K0MX40	2.24	1.09	2.13
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	*cysS*	BN194_24430	K0NAB2	3.89	1.09	2.13
Oligoendopeptidase, pepF/M3 family	*Amino acid-related metabolism*		BN194_11580	K0N779	3.64	1.08	2.12
Uncharacterized peptidase yqhT (EC 3.4.-.-)	Amino acid-related metabolism	*yqhT*	BN194_18260	K0N5K4	3.39	1.08	2.11
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	*hisS*	BN194_17110	K0N5A0	4.22	1.07	2.10
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	*glmM*	BN194_11550	K0N3Y7	5.40	1.06	2.08
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	*iscS1*	BN194_14900	K0N4U8	3.67	0.99	1.99
GNAT family acetyltransferase	General prediction only		BN194_29620	K0NDL0	0.90	0.98	1.97
Methionine import ATP-binding protein MetN (EC 3.6.3.-)	ABC-type transporter systems	*metN*	BN194_13750	K0N4L1	2.08	0.96	1.95
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*yqeC*	BN194_02330	K0N532	0.50	0.96	1.94
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA*	BN194_09090	K0MTR3	3.30	0.95	1.94
Lipoprotein	ABC-type transporter systems	*metQ_2*	BN194_13740	K0MV23	4.46	0.94	1.92
Uncharacterized protein ybbP	Unknown/uncharacterized	*ybbP*	BN194_11530	K0N776	0.21	0.93	1.90
Zinc-transporting ATPase (EC 3.6.3.5)	Other transporter proteins	*zosA_2*	BN194_29430	K0NB79	3.29	0.93	1.90
Predicted pyrophosphatase	General prediction only		BN194_15360	K0N4R6	2.18	0.92	1.89
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP*	BN194_08180	K0N6I0	3.69	0.91	1.87
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E,P100*	BN194_02180	K0N513	4.74	0.90	1.86
Transcriptional regulator	*Posttranslational modification*		BN194_29310	K0N8C2	3.16	0.89	1.85
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	*ddl*	BN194_01390	K0MRY4	3.25	0.88	1.84

PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*manX_5*	BN194_29720	K0NDL4	3.37	0.86	1.81
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB*	BN194_17900	K0N5S3	0.44	0.84	1.80
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh*	BN194_26560	K0N7J5	2.63	0.83	1.78
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	3.84	0.83	1.78
Single-stranded DNA-binding protein (SSB)	DNA replication-related	*ssb*	BN194_00110	K0N1C2	2.23	0.83	1.78
Uncharacterized protein ytxK	DNA repair/recombination	*ytxK*	BN194_11680	K0N791	2.40	0.83	1.77
Uncharacterized protein ywfO	General prediction only	*ywfO*	BN194_26840	K0MXZ5	2.70	0.82	1.76
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	*accB*	BN194_22530	K0NA35	0.79	0.82	1.76
Probable amino-acid ABC transporter-binding protein HI_1080	*ABC-type transporter systems*		BN194_06710	K0N2R6	3.44	0.81	1.76
Uncharacterized protein	Unknown/uncharacterized		BN194_23650	K0N7J8	3.14	0.81	1.75
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	*aldB*	BN194_20140	K0MWH5	2.18	0.79	1.73
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	*atpA*	BN194_13600	K0N4K1	5.04	0.78	1.72
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_02890	K0MSD4	2.92	0.78	1.72
S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	*metK*	BN194_09150	K0N352	4.09	0.78	1.72
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC*	BN194_00080	K0N486	3.71	0.78	1.72
Uncharacterized protein yghZ	General prediction only	*yghZ*	BN194_27510	K0N7U8	4.39	0.78	1.71
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	*yjlD*	BN194_24330	K0NAA7	3.71	0.77	1.71
Bifunctional protein BirA (EC 6.3.4.15)	Lipid-related metabolism	*birA*	BN194_08790	K0MTP3	2.78	0.77	1.71
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	*agl*	BN194_27950	K0N8T1	4.17	0.76	1.69

Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	*Steap4*	BN194_01990	K0MS41	3.01	0.76	1.69
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB*	BN194_21340	K0MWS0	3.49	0.74	1.67
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	*msrA_2,msrA*	BN194_15860	K0N4W6	0.22	0.73	1.66
Glutamate dehydrogenase	Amino acid-related metabolism	*gdh*	BN194_06980	K0N666	3.48	0.73	1.66
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*asnS*	BN194_16760	K0N569	4.37	0.72	1.65
tRNA-specific adenosine deaminase (EC 3.5.4.33)	tRNA/Ribosome assembly/processing	*tadA*	BN194_24000	K0N7M1	2.65	0.72	1.64
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA*	BN194_05120	K0N8B5	2.36	0.71	1.63
TPR repeat-containing protein ypiA	Unknown/uncharacterized	*ypiA*	BN194_15750	K0N517	2.37	0.68	1.60
Alkyl hydroperoxide reductase subunit C (EC 1.11.1.15)	Cell defense/detoxification	*ahpC*	BN194_26250	K0N876	1.88	0.68	1.60
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	*garB*	BN194_27400	K0N8K3	3.15	0.67	1.59
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	2.10	0.66	1.59
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	*pta*	BN194_11340	K0MU95	3.98	0.63	1.55
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA*	BN194_17880	K0N983	2.39	0.62	1.53
Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	1.60	0.62	1.53
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	*dnaN*	BN194_00020	K0N6S3	3.13	0.61	1.52
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	*dltA*	BN194_08590	K0MTN0	2.46	0.59	1.51
ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	*atpF*	BN194_13580	K0N7S9	1.55	0.58	1.50
Hydrolase of the alpha/beta superfamily	General prediction only		BN194_08240	K0MTK6	3.66	0.55	1.47
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ_2*	BN194_20470	K0NBG3	0.42	0.54	1.45

Nucleoid-associated protein BN194_23980	General prediction only		BN194_23980	K0NA95	1.41	0.51	1.43
Uncharacterized protein	*ABC-type transporter systems*		BN194_21220	K0NBK2	1.71	0.51	1.43
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_2*	BN194_03120	K0N7V6	1.19	0.50	1.41
Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase)	Nucleic acid/nucleotide metabolism	*pyrB*	BN194_16480	K0N8N2	2.03	0.49	1.40
Thioredoxin	Posttranslational modification	*trxA_2*	BN194_08570	K0N975	1.18	0.48	1.40
Exodeoxyribonuclease 7 small subunit (EC 3.1.11.6) (Exodeoxyribonuclease VII small subunit)	DNA repair/recombination	*xseB*	BN194_18190	K0MW55	1.72	0.47	1.39
FMN-binding domain protein	General prediction only		BN194_24320	K0NC29	3.01	0.46	1.38
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	*aspS*	BN194_17100	K0N5F3	2.57	0.46	1.38
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	*atpH*	BN194_13590	K0MV16	1.80	0.45	1.37
Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	*bceA_2*	BN194_21230	K0N9X1	2.90	0.43	1.34
Monooxygenase	General prediction only		BN194_07600	K0N2U5	2.09	0.43	1.34
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdE2*	BN194_16600	K0N5A1	2.97	0.42	1.33
Thioredoxin-like protein ytpP	Posttranslational modification	*ytpP*	BN194_18980	K0N9F1	2.35	0.41	1.33
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdF*	BN194_16610	K0N552	2.01	0.40	1.32
Arginine repressor	Transcriptional regulation	*argR1,argR*	BN194_19110	K0N5R1	0.09	0.39	1.31
Protein translocase subunit SecY	Protein export	*secY*	BN194_26020	K0NCJ6	0.46	0.39	1.31
Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) (Peptide-methionine (R)-S-oxide reductase)	Posttranslational modification	*msrB*	BN194_17090	K0MVR6	0.18	0.38	1.30
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	*tsf*	BN194_17670	K0NB01	1.94	0.37	1.30
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_4*	BN194_22020	K0NBQ1	2.23	0.36	1.29
Xanthine/uracil/vitamin C permease	Other transporter proteins		BN194_01470	K0N796	1.56	0.36	1.28

Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	*trpS*	BN194_27360	K0N7S4	1.88	0.36	1.28
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	*atpG*	BN194_13610	K0N4D3	1.99	0.35	1.28
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	1.63	0.35	1.27
Uncharacterized protein yqgF	Cell wall biogenesis	*yqgF*	BN194_18440	K0MW71	0.79	0.33	1.26
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	*accA*	BN194_22470	K0NBS6	0.23	0.33	1.26
Cold shock-like protein CspLA	Transcription-associated proteins	*cspLA*	BN194_12460	K0N438	0.60	0.32	1.25
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*fruK*	BN194_15420	K0NAJ6	0.82	0.31	1.24
Uncharacterized lipoprotein yerH	General prediction only	*yerH*	BN194_11940	K0MUH2	2.34	0.31	1.24
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		BN194_24180	K0NAA2	1.68	0.31	1.24
Uncharacterized protein ybfG	General prediction only	*ybfG*	BN194_00330	K0N4B3	1.70	0.31	1.24
Protein QmcA	Unknown/uncharacterized	*qmcA*	BN194_12070	K0NA10	2.17	0.30	1.24
Uncharacterized protein	Unknown/uncharacterized		BN194_15540	K0MVD8	0.32	0.30	1.23
Uncharacterized protein	Unknown/uncharacterized		BN194_27530	K0NAX5	0.67	0.28	1.21
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE*	BN194_02970	K0N7U7	0.97	0.28	1.21
Queuosine transporter QueT	General prediction only	*queT*	BN194_21930	K0NA07	0.06	0.27	1.20
Septum site-determining protein DivIVA	Cytokinesis	*divIVA*	BN194_14800	K0N4T8	1.35	0.24	1.18
Uncharacterized protein yitL	General prediction only	*yitL*	BN194_15600	K0N505	0.10	0.22	1.16
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	*glcK*	BN194_18420	K0NB57	1.59	0.20	1.15
Phosphohydrolase (MutT/nudix family protein)	General prediction only		BN194_27160	K0N7P9	0.08	0.20	1.15
Phage capsid protein	Prophage genome		BN194_30330	K0NBD3	0.40	0.20	1.15

Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	*ykwC*	BN194_02520	K0N7M3	0.68	0.20	1.15
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_3*	BN194_21990	K0MWY0	0.95	0.20	1.14
Transcriptional regulator lytR	Transcriptional regulation	*lytR*	BN194_02540	K0MS94	1.44	0.18	1.14
Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	*rbsK*	BN194_03300	K0N1R2	1.49	0.18	1.13
Signal peptidase I (EC 3.4.21.89)	Protein export	*lepB*	BN194_02610	K0N1V9	0.77	0.17	1.13
Transcriptional regulator, PadR-like family	Transcriptional regulation		BN194_26580	K0NAQ3	0.11	0.17	1.12
Zinc metalloprotease (EC 3.4.24.-)	General prediction only	*eep*	BN194_17620	K0NAZ9	0.48	0.16	1.12
Kinase, putative	General prediction only		BN194_29890	K0MYR0	0.33	0.15	1.11
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (ACCase subunit beta) (Acetyl-CoA carboxylase carboxyltransferase subunit beta) (EC 6.4.1.2)	Lipid-related metabolism	*accD*	BN194_22480	K0NA32	0.06	0.14	1.10
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_3*	BN194_14020	K0NAD1	0.10	0.12	1.09
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	0.21	0.12	1.09
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB_2*	BN194_21770	K0NBN4	0.31	0.12	1.09
D-2-hydroxyacid dehydrogenase (EC 1.1.1.-)	General prediction only	*ddh*	BN194_16660	K0N557	0.46	0.12	1.08
Uncharacterized ABC transporter ATP-binding protein YdbJ	ABC-type transporter systems	*ydbJ*	BN194_24600	K0N7Q8	0.20	0.12	1.08
UPF0755 protein yrrL	Unknown/uncharacterized	*yrrL*	BN194_18550	K0N5W7	0.43	0.10	1.07
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA*	BN194_18520	K0NB62	0.52	0.09	1.07
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	*yfeX*	BN194_07170	K0N8U9	0.30	0.09	1.06
Large-conductance mechanosensitive channel	Other transporter proteins	*mscL*	BN194_26890	K0MY02	0.15	0.08	1.06
4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase) (EC 1.17.1.8)	Amino acid-related metabolism	*dapB*	BN194_01000	K0N166	0.03	0.07	1.05
Glycine betaine/carnitine/choline-binding protein OpuCC	ABC-type transporter systems	*opuCC*	BN194_00670	K0N6Z3	0.27	0.07	1.05

Deoxyguanosine kinase (EC 2.7.1.113)	*Nucleic acid/nucleotide metabolism*		BN194_14000	K0N4M7	0.10	0.06	1.04
Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-)	Nucleic acid/nucleotide metabolism	*purK*	BN194_12510	K0N441	0.24	0.02	1.02
tRNA pseudouridine synthase A (EC 5.4.99.12) (tRNA pseudouridine(38-40) synthase) (tRNA pseudouridylate synthase I) (tRNA-uridine isomerase I)	tRNA/Ribosome assembly/processing	*truA*	BN194_25910	K0N7E2	0.00	0.00	1.00
Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	General prediction only	*yqiG*	BN194_25330	K0NAG4	0.05	-0.01	-1.01
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_3*	BN194_29920	K0NDN0	0.03	-0.01	-1.01
Uncharacterized protein YneR	General prediction only	*yneR*	BN194_18480	K0N9C1	0.02	-0.02	-1.01
Uncharacterized MscS family protein YkuT	Other transporter proteins	*ykuT*	BN194_08700	K0N322	0.02	-0.02	-1.01
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*fruA_3*	BN194_15410	K0N4S1	0.01	-0.03	-1.02
Penicillin-binding protein 1A	Cell wall biogenesis	*ponA*	BN194_16720	K0NAU3	0.17	-0.03	-1.02
Transcriptional regulator lytR	Transcriptional regulation	*lytR_3*	BN194_21700	K0N6U3	0.61	-0.04	-1.03
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25510	K0N7B2	0.42	-0.07	-1.05
Putative tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207) (tRNA (cytidine/uridine-2'-O-)-methyltransferase)	*tRNA/Ribosome assembly/processing*		BN194_09990	K0MTX9	0.21	-0.07	-1.05
Sortase	Cell wall biogenesis		BN194_22780	K0NA48	0.22	-0.07	-1.05
Uncharacterized protein	Unknown/uncharacterized		BN194_20720	K0NBH5	0.36	-0.08	-1.06
PTS family mannose/fructose/sorbose porter component IIC	Phosphotransferase systems		BN194_02980	K0N5D0	0.37	-0.09	-1.06
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	*mnmA*	BN194_14930	K0N844	0.43	-0.09	-1.06
Uncharacterized protein RP368	*ABC-type transporter systems*		BN194_07720	K0N914	0.03	-0.09	-1.07
N5-carboxyaminoimidazole ribonucleotide mutase (N5-CAIR mutase) (EC 5.4.99.18) (5-(carboxyamino)imidazole ribonucleotide mutase)	Nucleic acid/nucleotide metabolism	*purE*	BN194_19380	K0N9H9	0.63	-0.10	-1.07
Membrane protein	Unknown/uncharacterized		BN194_22700	K0N7C6	0.08	-0.10	-1.07

Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	0.54	-0.10	-1.07
D-lactate dehydrogenase (EC 1.1.1.28)	Carbohydrate-related metabolism	*dld*	BN194_06590	K0MT28	0.26	-0.11	-1.08
Uncharacterized protein yaaA	General prediction only	*yaaA*	BN194_00040	K0MRL5	0.04	-0.12	-1.09
Aldose 1-epimerase	*Central glycolytic/intermediary pathways*		BN194_16020	K0NAP4	0.86	-0.13	-1.09
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	*glyr1*	BN194_30100	K0N992	0.45	-0.13	-1.10
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	*rny*	BN194_10100	K0N3E5	0.11	-0.14	-1.10
Putative nrdI-like protein	*Nucleic acid/nucleotide metabolism*		BN194_08250	K0N300	0.35	-0.14	-1.11
UPF0337 protein lp_1708	General prediction only		BN194_05810	K0N2J8	0.11	-0.15	-1.11
Uncharacterized protein yjdJ	General prediction only	*yjdJ*	BN194_24650	K0N7R2	0.23	-0.15	-1.11
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	*rbfA*	BN194_17540	K0MVV7	0.57	-0.16	-1.12
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*gmuB*	BN194_23840	K0MXC7	0.41	-0.16	-1.12
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1*	BN194_09110	K0N399	3.84	-0.17	-1.13
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	*mhqA_3*	BN194_18760	K0N5N7	0.64	-0.18	-1.13
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	*dhaM*	BN194_04960	K0N2C2	0.72	-0.18	-1.14
SPFH/Band 7/PHB domain protein	Unknown/uncharacterized		BN194_29820	K0NDM1	0.18	-0.21	-1.16
Uncharacterized ABC transporter ATP-binding protein TM_0288	*ABC-type transporter systems*		BN194_06900	K0N2K4	0.09	-0.21	-1.16
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA1, greA*	BN194_02150	K0N1G7	0.40	-0.21	-1.16
Uncharacterized protein	*Cell surface proteins/internalins*		BN194_20060	K0N5Y7	0.58	-0.22	-1.16
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF*	BN194_17910	K0N5I3	1.08	-0.22	-1.16
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_3*	BN194_21440	K0MWS9	0.85	-0.22	-1.17

UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	1.62	-0.23	-1.17
Fructoselysine kinase (EC 2.7.1.-)	Carbohydrate-related metabolism	*frlD*	BN194_22240	K0MX05	0.99	-0.23	-1.17
Carboxy-terminal processing protease CtpA (EC 3.4.21.102)	Protein folding/turnover	*ctpA*	BN194_15880	K0N8G1	0.81	-0.23	-1.18
UPF0237 protein BN194_09820	Unknown/uncharacterized		BN194_09820	K0N9F9	0.08	-0.24	-1.18
Uncharacterized glycosyltransferase HI_0868 (EC 2.4.-.-)	Cell wall biogenesis		BN194_02410	K0N1U3	0.33	-0.24	-1.18
ABC-type antimicrobial peptide transport system,ATPase component	*ABC-type transporter systems*		BN194_19940	K0MWG2	0.92	-0.24	-1.18
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.-)	Lipid-related metabolism	*plsC*	BN194_17710	K0N5F1	0.09	-0.24	-1.18
Uncharacterized protein	General prediction only	*gpm1*	BN194_13960	K0N4F5	0.08	-0.25	-1.19
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		BN194_03130	K0N5D9	0.85	-0.25	-1.19
Uncharacterized protein ypuA	Unknown/uncharacterized	*ypuA*	BN194_27250	K0N8I3	0.93	-0.25	-1.19
NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	1.07	-0.25	-1.19
tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	tRNA/Ribosome assembly/processing	*mnmG,gidA*	BN194_30590	K0MYX4	0.34	-0.26	-1.19
Uncharacterized protein	General prediction only		BN194_21910	K0N6F1	0.49	-0.26	-1.19
Uncharacterized protein	Unknown/uncharacterized		BN194_08270	K0N959	0.69	-0.26	-1.20
Endonuclease MutS2 (EC 3.1.-.-)	DNA repair/recombination	*mutS2*	BN194_08560	K0N359	0.08	-0.28	-1.21
Mannose permease IID component	Phosphotransferase systems	*manZ*	BN194_02990	K0MSE1	1.52	-0.29	-1.22
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citE*	BN194_20320	K0NBF4	0.96	-0.29	-1.22
Ribonuclease H (EC 3.1.26.4)	DNA repair/recombination	*rnhA*	BN194_27580	K0NAX8	0.19	-0.30	-1.23
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	*yhaA*	BN194_30550	K0N9E4	0.18	-0.30	-1.23
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_19800	K0N670	0.14	-0.31	-1.24

6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*gnd*	BN194_18660	K0N5N2	2.27	-0.31	-1.24
Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	Nucleic acid/nucleotide metabolism	*purN*	BN194_19310	K0N5S4	1.14	-0.31	-1.24
Uncharacterized protein	Unknown/uncharacterized		BN194_24220	K0NC21	0.20	-0.32	-1.24
Uncharacterized metallophosphoesterase yunD	Nucleic acid/nucleotide metabolism	*yunD*	BN194_08890	K0MTQ0	0.96	-0.32	-1.25
Methionyl-tRNA formyltransferase (EC 2.1.2.9)	Protein translation (initiation)	*fmt*	BN194_18060	K0N5J2	1.36	-0.33	-1.25
Penicillin-binding protein 2B	Cytokinesis	*pbpB*	BN194_14700	K0N4S9	2.14	-0.33	-1.26
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA_2*	BN194_20640	K0MWL6	2.57	-0.33	-1.26
ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136) (ADP-dependent NAD(P)HX dehydratase)	Cofactor-related metabolism	*nnrD*	BN194_09250	K0N360	0.40	-0.33	-1.26
Inner membrane amino-acid ABC transporter permease protein yecS	ABC-type transporter systems	*yecS_3*	BN194_29780	K0NB99	0.29	-0.34	-1.26
UPF0092 membrane protein yrbF	Protein export	*yrbF*	BN194_08390	K0MTL6	1.32	-0.34	-1.27
Uncharacterized protein	Unknown/uncharacterized		BN194_02470	K0N7L7	0.97	-0.35	-1.27
Uncharacterized protein			BN194_02080	K0N4Z7	0.40	-0.35	-1.27
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*lacC*	BN194_07470	K0N8Y4	1.65	-0.35	-1.28
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase 2 (EC 5.4.2.1)	Central glycolytic/intermediary pathways	*gpmA2_2*	BN194_27560	K0N7W0	1.45	-0.36	-1.28
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	*purA*	BN194_01160	K0N1J0	3.02	-0.37	-1.30
Putative integral membrane protein	Unknown/uncharacterized		BN194_01660	K0N1M7	0.06	-0.39	-1.31
Penicillin-binding protein 3	Cell wall biogenesis	*pbpC*	BN194_03320	K0N7W9	1.64	-0.39	-1.31
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*ileS*	BN194_14810	K0N4L9	2.73	-0.39	-1.31
Mannose permease IID component	Phosphotransferase systems	*manZ_4*	BN194_04510	K0N287	0.70	-0.40	-1.32

Uncharacterized protein	Unknown/uncharacterized		BN194_17360	K0N5B9	0.20	-0.40	-1.32
Uncharacterized protein	Unknown/uncharacterized		BN194_11890	K0MUG0	1.43	-0.40	-1.32
Virulence factor mviM	General prediction only	*mviM*	BN194_13310	K0N4B2	2.12	-0.41	-1.33
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB1,pstB*	BN194_10270	K0N9K1	0.60	-0.43	-1.34
NAD kinase (EC 2.7.1.23) (ATP-dependent NAD kinase)		*nadK*	ppnK	K0N6U5	0.12	-0.43	-1.35
Transcriptional regulator lytR	Transcriptional regulation	*lytR_4*	BN194_23780	K0NA85	2.03	-0.44	-1.36
Transport protein	Other transporter proteins		BN194_00630	K0N4D9	0.41	-0.45	-1.37
Uncharacterized protein	Unknown/uncharacterized		BN194_12100	K0N456	1.50	-0.46	-1.38
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ*	BN194_11360	K0N3U2	1.75	-0.46	-1.38
50S ribosomal protein L7/L12	Ribosomal proteins	*rplL*	BN194_24080	K0NA98	2.53	-0.47	-1.39
Oligoendopeptidase F homolog (EC 3.4.24.-)	Amino acid-related metabolism	*yjbG*	BN194_02530	K0N560	3.91	-0.48	-1.40
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	*dacA*	BN194_02140	K0MS53	2.16	-0.48	-1.40
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	*murF*	BN194_26720	K0NCU5	1.45	-0.49	-1.40
Sorbose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*sorB_2*	BN194_29180	K0NB63	1.96	-0.49	-1.41
MarR family transcriptional regulator	Transcriptional regulation		BN194_22610	K0N6N9	0.17	-0.49	-1.41
Cell division ATP-binding protein FtsE	Cytokinesis	*ftsE*	BN194_10190	K0MTZ2	1.99	-0.50	-1.41
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC*	BN194_17890	K0MW34	1.44	-0.51	-1.42
Xanthine permease	Other transporter proteins	*pbuX*	BN194_12500	K0N490	0.20	-0.51	-1.42
Uncharacterized protein	Unknown/uncharacterized		BN194_23540	K0MXB4	1.38	-0.51	-1.42
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD*	BN194_17920	K0NB35	2.66	-0.52	-1.43
Uncharacterized protein yqhL	General prediction only	*yqhL*	BN194_18410	K0N5L5	1.72	-0.53	-1.44
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	*sph*	BN194_04930	K0N5Q0	2.78	-0.53	-1.45

Glycosyl transferase family protein	Cell wall biogenesis		BN194_02420	K0N7L2	1.24	-0.54	-1.45
Uncharacterized ABC transporter ATP-binding protein YfiB	ABC-type transporter systems	*yfiB*	BN194_06890	K0MT56	1.80	-0.54	-1.45
ABC transporter glutamine-binding protein glnH	ABC-type transporter systems	*glnH*	BN194_21430	K0N9Y4	2.27	-0.55	-1.46
Calcium-transporting ATPase lmo0841 (EC 3.6.3.8)	Other transporter proteins		BN194_19820	K0NBC5	3.48	-0.56	-1.48
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	4.14	-0.56	-1.48
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	3.35	-0.57	-1.48
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	*gpsB*	BN194_16690	K0MVN5	2.50	-0.59	-1.51
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI_2*	BN194_16210	K0N508	2.74	-0.59	-1.51
50S ribosomal protein L21	Ribosomal proteins	*rplU*	BN194_18290	K0MW61	0.48	-0.61	-1.53
Uncharacterized protein	Unknown/uncharacterized		BN194_15850	K0N527	2.11	-0.62	-1.53
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	*prsA*	BN194_19060	K0N5Q8	2.52	-0.62	-1.53
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*rluB*	BN194_15650	K0N509	0.31	-0.62	-1.53
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_07710	K0N2Z3	3.19	-0.63	-1.55
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Cobalamin-independent methionine synthase) (Methionine synthase, vitamin-B12 independent isozyme)	Amino acid-related metabolism	*metE*	BN194_06880	K0N658	1.47	-0.63	-1.55
Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	*ptp3*	BN194_23520	K0NBX6	5.15	-0.64	-1.56
Putative transcriptional regulator, MarR family	Transcriptional regulation		BN194_27490	K0MY64	0.53	-0.65	-1.56
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	*def*	BN194_15060	K0N4N6	3.63	-0.66	-1.58
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	1.35	-0.66	-1.58
Uncharacterized protein ypmR	General prediction only	*ypmR*	BN194_15840	K0MVG3	1.11	-0.66	-1.58
GCN5-related N-acetyltransferase	General prediction only		BN194_19760	K0N5W1	3.31	-0.68	-1.60

Hypothetical lipoprotein	Unknown/uncharacterized		BN194_12440	K0MUR1	0.38	-0.68	-1.61
Uncharacterized protein	Unknown/uncharacterized		BN194_01600	K0N1B9	2.21	-0.68	-1.61
Uncharacterized amino acid permease YfnA	Other transporter proteins	*yfnA*	BN194_06960	K0N2T0	0.56	-0.69	-1.62
Cell growth regulatory protein	*IS elements/foreign DNA defense*		BN194_00940	K0MRU4	0.44	-0.70	-1.62
Lipopolysaccharide synthesis sugar transferase	Cell wall biogenesis		BN194_21390	K0MWS4	1.43	-0.70	-1.63
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	*tuf*	BN194_15310	K0N4R1	2.90	-0.71	-1.64
Protein veg	Unknown/uncharacterized	*veg*	BN194_27010	K0N7N4	0.70	-0.72	-1.65
Uncharacterized oxidoreductase YbdH (EC 1.1.-.-)	Carbohydrate-related metabolism	*ybdH*	BN194_30540	K0MYX0	2.96	-0.73	-1.66
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	*mtlF*	BN194_30410	K0N8N0	1.98	-0.74	-1.67
Glycine betaine/carnitine/choline transport ATP-binding protein OpuCA	ABC-type transporter systems	*opuCA*	BN194_00680	K0N4E4	3.04	-0.74	-1.67
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	*trxB*	BN194_10360	K0N3L1	2.35	-0.76	-1.69
Probable glutamine ABC transporter permease protein glnP	ABC-type transporter systems	*glnP*	BN194_21410	K0N6A4	0.46	-0.76	-1.69
Cell division protein FtsX	Cytokinesis	*ftsX*	BN194_10200	K0N3G0	3.44	-0.76	-1.69
Serine/threonine-protein kinase PrkC (EC 2.7.11.1)	Posttranslational modification	*prkC*	BN194_18020	K0NB40	0.79	-0.78	-1.72
Nucleoid occlusion protein	Cytokinesis	*noc*	BN194_02030	K0N4Z1	0.46	-0.79	-1.72
Cell shape-determining protein MreC (Cell shape protein MreC)	Cytokinesis	*mreC*	BN194_14560	K0N4K0	2.94	-0.79	-1.73
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_2*	BN194_29910	K0N8I1	2.90	-0.79	-1.73
Oligoendopeptidase F	Amino acid-related metabolism	*yjbG_2*	BN194_08130	K0N6H7	3.68	-0.80	-1.74
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	*valS*	BN194_14510	K0N4J6	5.05	-0.82	-1.76
Uncharacterized protein			BN194_21520	K0NBL8	0.27	-0.83	-1.77
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA*	BN194_11290	K0MU90	2.92	-0.83	-1.78

Uncharacterized protein	Unknown/uncharacterized		BN194_21450	K0N6R7	2.83	-0.83	-1.78
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_29810	K0N8H4	3.31	-0.84	-1.78
Ribosome-binding ATPase YchF	Protein translation (peptide release)	*engD,ychF*	BN194_02070	K0N7F7	2.44	-0.84	-1.79
Membrane protein insertase YidC 1	Protein export	*yidC1*	BN194_18630	K0N9D1	0.60	-0.86	-1.81
ErfK family protein	Cell wall biogenesis		BN194_26570	K0NCS1	0.39	-0.86	-1.82
Phosphate-binding protein pstS 1	ABC-type transporter systems	*pstS1*	BN194_10240	K0MTZ5	0.49	-0.88	-1.84
UbiE/COQ5 family methyltransferase	General prediction only		BN194_23620	K0NBY4	0.80	-0.88	-1.84
Glycerol-3-phosphate ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_11260	K0N3T6	4.27	-0.88	-1.85
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE_2*	BN194_19740	K0MWF1	2.52	-0.90	-1.86
Nod factor export ATP-binding protein I (EC 3.6.3.-)	ABC-type transporter systems	*nodI*	BN194_06850	K0N2J7	1.22	-0.90	-1.86
Uncharacterized protein MJ1445	General prediction only		BN194_08880	K0N6M7	0.57	-0.90	-1.86
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC_2*	BN194_20620	K0NBH0	0.50	-0.90	-1.87
Uncharacterized protein	Unknown/uncharacterized		BN194_21380	K0N9Y1	1.77	-0.91	-1.87
Acylphosphatase	Carbohydrate-related metabolism	*acyP*	BN194_18620	K0NB65	2.86	-0.92	-1.90
Predicted acetyltransferase			BN194_11820	K0N9Y9	2.67	-0.93	-1.91
Uncharacterized protein	Unknown/uncharacterized		BN194_30140	K0MYT6	1.25	-0.94	-1.92
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	*maa*	BN194_30010	K0N8I9	3.88	-0.95	-1.93
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	*patB_2*	BN194_09790	K0MTW3	3.55	-0.96	-1.94
Uncharacterized protein	Unknown/uncharacterized		BN194_16650	K0N5A4	0.44	-0.98	-1.97
Probable cation-transporting ATPase exp7 (EC 3.6.3.-)	Other transporter proteins	*exp7*	BN194_08170	K0N955	3.39	-0.99	-1.98
Elongation factor P	Protein translation (elongation)	*efp*	BN194_18240	K0MW57	1.97	-0.99	-1.99
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_3*	BN194_04780	K0N5N9	2.35	-1.00	-2.00

Glycosyltransferase	Cell wall biogenesis		BN194_09050	K0N346	1.74	-1.01	-2.01
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)		*accC*	BN194_22510	K0N6M5	0.38	-1.02	-2.03
Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	0.83	-1.02	-2.03
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_4*	BN194_29900	K0N971	2.34	-1.04	-2.05
Integral membrane protein	Unknown/uncharacterized		BN194_02590	K0MS97	1.59	-1.04	-2.06
NifU-like protein	Cofactor-related metabolism	*nifU*	BN194_13800	K0N4L4	0.67	-1.04	-2.06
ABC transporter, ATP-binding protein	*Cell surface proteins/internalins*		BN194_15700	K0N514	0.78	-1.05	-2.08
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	*metG*	BN194_27130	K0NAU5	3.95	-1.06	-2.08
Transcriptional repressor smtB homolog	Transcriptional regulation	*ziaR*	BN194_01180	K0N4L0	0.88	-1.08	-2.11
Protein ytsP	Signal transduction	*ytsP*	BN194_14450	K0N4Q9	1.86	-1.08	-2.12
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	3.42	-1.08	-2.12
Putative competence-damage inducible protein	General prediction only	*cinA*	BN194_10070	K0N9I3	1.73	-1.13	-2.19
Uncharacterized protein	Unknown/uncharacterized		BN194_15520	K0NAK2	0.98	-1.14	-2.21
Spermidine/putrescine-binding periplasmic protein	ABC-type transporter systems	*potD*	BN194_11460	K0N3U9	1.24	-1.15	-2.22
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	*pdhC*	BN194_15100	K0N4W5	3.44	-1.16	-2.23
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	*cysK*	BN194_05520	K0N8E6	3.29	-1.16	-2.23
Glycosyl transferase family 2	Cell wall biogenesis		BN194_02460	K0N1U7	0.56	-1.16	-2.24
Uncharacterized protein	Cell wall biogenesis		BN194_21890	K0MWX1	2.00	-1.17	-2.24
Uncharacterized protein yeaO	Unknown/uncharacterized	*yeaO*	BN194_08040	K0MTJ2	0.64	-1.17	-2.26
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	*ftsH*	BN194_26460	K0N7I8	5.69	-1.18	-2.27
SsrA-binding protein (Small protein B)	Posttranslational modification	*smpB*	BN194_11110	K0N3S3	0.89	-1.20	-2.29
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	*dkgB*	BN194_08260	K0N347	3.46	-1.20	-2.29
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ*	BN194_14610	K0N4K4	3.03	-1.23	-2.34

Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase)	Cofactor-related metabolism	*coaE*	BN194_18910	K0N5P8	2.99	-1.23	-2.35
Uncharacterized protein MJ1651	General prediction only		BN194_04410	K0N281	4.51	-1.23	-2.35
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF*	BN194_08770	K0N987	3.91	-1.24	-2.35
Uncharacterized protein ywnB	General prediction only	*ywnB_2*	BN194_20050	K0N687	2.60	-1.24	-2.36
Protein LemA	Unknown/uncharacterized	*lemA*	BN194_27350	K0N8J7	3.68	-1.25	-2.38
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227) (Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase)	Cell wall biogenesis	*murG*	BN194_14730	K0N819	0.58	-1.25	-2.38
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	*citD*	BN194_20330	K0N9Q5	1.22	-1.25	-2.38
Glycosyl transferase family 8	Cell wall biogenesis		BN194_11730	K0N795	0.81	-1.25	-2.38
Anaerobic ribonucleoside-triphosphate reductase-activating protein (EC 1.97.1.-)	Nucleic acid/nucleotide metabolism	*nrdG*	BN194_19270	K0NB93	0.92	-1.27	-2.42
Septum formation inhibitor MinC, C-terminal domain family	Cytokinesis	*minC*	BN194_14580	K0N805	3.81	-1.28	-2.43
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	2.50	-1.29	-2.44
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacA*	BN194_07500	K0N2T4	1.84	-1.29	-2.44
HTH-type transcriptional regulator galR	Transcriptional regulation	*galR*	BN194_03780	K0N5G9	0.73	-1.29	-2.45
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*bglP*	BN194_06940	K0MT60	1.24	-1.31	-2.48
Nuclease sbcCD subunit D	DNA repair/recombination	*sbcD*	BN194_07530	K0N6B1	0.60	-1.33	-2.51
Acyltransferase 3			BN194_15460	K0N4S6	1.19	-1.34	-2.52
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	*murC*	BN194_18950	K0N600	3.30	-1.34	-2.54
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ysgA*	BN194_18610	K0N5M8	1.75	-1.35	-2.54

Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	*ispA*	BN194_18180	K0N9A2	0.86	-1.35	-2.55
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	3.65	-1.36	-2.57
CBS domain-containing protein	Unknown/uncharacterized		BN194_26610	K0N7J7	2.73	-1.39	-2.62
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	*thiD_2*	BN194_07650	K0N2U9	3.79	-1.39	-2.62
Ribonuclease Z (RNase Z) (EC 3.1.26.11) (tRNA 3 endonuclease) (tRNase Z)	tRNA/Ribosome assembly/processing	*rnz*	BN194_15470	K0NAK0	0.79	-1.39	-2.62
50S ribosomal protein L33	Ribosomal proteins	*rpmG2,rpmG*	BN194_24280	K0NAA5	0.89	-1.39	-2.63
Gluconate 5-dehydrogenase (EC 1.1.1.69)	General prediction only	*idnO*	BN194_08150	K0N2Z5	0.84	-1.40	-2.64
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	*glgC*	BN194_21600	K0N6T3	1.83	-1.40	-2.64
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	*clpC*	BN194_21680	K0N9Z7	4.03	-1.41	-2.65
Uncharacterized protein	Unknown/uncharacterized		BN194_25540	K0MXN3	0.62	-1.41	-2.65
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	3.42	-1.41	-2.66
Uncharacterized protein	Cell wall biogenesis		BN194_02360	K0N1U1	0.57	-1.42	-2.67
Predicted ORF			BN194_P0560	K0MZ29	1.01	-1.42	-2.67
ABC-type Na+ efflux pump permease component-like protein	*ABC-type transporter systems*		BN194_11370	K0N9U5	0.83	-1.43	-2.69
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	*htrA*	BN194_29460	K0N8D9	3.55	-1.43	-2.69
Putative N-acetylmuramoyl-L-alanine amidase YrvJ (EC 3.5.1.28)	Cytokinesis	*yrvJ*	BN194_17200	K0N5G4	1.00	-1.43	-2.70
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	*nusB*	BN194_18220	K0NB49	3.96	-1.46	-2.74
Uncharacterized protein	Unknown/uncharacterized		BN194_23630	K0NA78	2.23	-1.46	-2.74
Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase (EC 4.2.-.-)	*tRNA/Ribosome assembly/processing*		BN194_17370	K0NAY4	3.08	-1.46	-2.76
DegV domain-containing protein CPE0026	Unknown/uncharacterized		BN194_12060	K0N405	3.14	-1.47	-2.78

Uncharacterized RNA pseudouridine synthase YhcT (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*yhcT_2*	BN194_20220	K0NBE7	1.43	-1.48	-2.79
Protein translocase subunit SecA	Protein export	*secA*	BN194_10170	K0N9J2	4.50	-1.48	-2.80
Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	3.39	-1.49	-2.80
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	*alaS*	BN194_08480	K0N6K2	4.45	-1.49	-2.80
Septation ring formation regulator EzrA	Cytokinesis	*ezrA*	BN194_14460	K0N4J2	5.11	-1.49	-2.81
Fumarate hydratase class II (Fumarase C) (EC 4.2.1.2)	Tricarboxylic acid pathway	*fumC*	BN194_25340	K0MXL5	3.23	-1.49	-2.81
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	*mtnN*	BN194_14890	K0MV90	3.58	-1.51	-2.84
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yutF*	BN194_08910	K0N383	5.89	-1.52	-2.87
Ribosome maturation factor RimP	tRNA/Ribosome assembly/processing	*rimP*	BN194_17590	K0MVW3	1.72	-1.54	-2.90
tRNA modification GTPase MnmE (EC 3.6.-.-)	tRNA/Ribosome assembly/processing	*mnmE,trmE*	BN194_30600	K0N9F0	2.66	-1.58	-2.98
50S ribosomal protein L19	Ribosomal proteins	*rplS*	BN194_17770	K0NB12	3.08	-1.58	-2.99
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA_2, potA*	BN194_11430	K0N765	3.34	-1.58	-2.99
Uncharacterized protein	Unknown/uncharacterized		BN194_01080	K0N4J7	1.12	-1.58	-2.99
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*ytzG*	BN194_09230	K0N6P7	1.04	-1.61	-3.06
Acyl-ACP thioesterase	Lipid-related metabolism		BN194_23910	K0N709	4.15	-1.62	-3.07
Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (EC 5.3.3.2) (Isopentenyl diphosphate:dimethylallyl diphosphate isomerase) (Isopentenyl pyrophosphate isomerase) (Type 2 isopentenyl diphosphate isomerase)	Lipid-related metabolism	*fni*	BN194_16840	K0MVP7	1.13	-1.62	-3.07
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	*tig*	BN194_15330	K0N884	3.69	-1.63	-3.09

Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	*msmK*	BN194_11180	K0N747	1.54	-1.63	-3.09
Guanylate kinase (EC 2.7.4.8)	Nucleic acid/nucleotide metabolism	*gmk_2*	BN194_21480	K0N9Y7	2.90	-1.63	-3.10
ABC-type phosphate/phosphonate transport system,periplasmic component	*ABC-type transporter systems*		BN194_25680	K0NAI1	4.54	-1.63	-3.10
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP_3*	BN194_21160	K0N682	3.43	-1.64	-3.11
Uridine kinase (EC 2.7.1.48)		*udk*	BN194_18540	K0MW76	1.17	-1.65	-3.15
Uncharacterized protein	Unknown/uncharacterized		BN194_01790	K0MS25	0.59	-1.67	-3.18
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	*fabK*	BN194_22580	K0NA38	1.68	-1.67	-3.19
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	*fbp*	BN194_21660	K0N6C3	1.99	-1.68	-3.21
Integral membrane protein	Unknown/uncharacterized		BN194_07890	K0MTI0	1.33	-1.70	-3.24
Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	*nfo*	BN194_17070	K0NAW5	1.25	-1.70	-3.26
LexA repressor (EC 3.4.21.-) (EC 3.4.21.88)	DNA repair/recombination	*lexA*	BN194_07970	K0N944	0.68	-1.72	-3.28
Uncharacterized protein ydcI	General prediction only	*ydcI*	BN194_14310	K0N4I1	4.61	-1.72	-3.30
Transcription-repair-coupling factor (TRCF) (EC 3.6.4.-)	DNA repair/recombination	*mfd*	BN194_26540	K0MXW9	0.95	-1.72	-3.30
Uncharacterized protein	Unknown/uncharacterized		BN194_11770	K0N9Y6	1.17	-1.73	-3.31
30S ribosomal protein S18	Ribosomal proteins	*rpsR*	BN194_00120	K0N6T2	1.27	-1.73	-3.32
5'-nucleotidase (EC 3.1.3.5)	General prediction only		BN194_08220	K0N957	5.23	-1.74	-3.33
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_2*	BN194_15390	K0MVD0	0.66	-1.77	-3.41
Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	Carbohydrate-related metabolism	*scrB*	BN194_22440	K0MX27	1.09	-1.77	-3.42
Ribosomal RNA small subunit methyltransferase F (EC 2.1.1.178)	tRNA/Ribosome assembly/processing	*rsmF*	BN194_16850	K0N5C0	1.34	-1.77	-3.42
Site-determining protein	Cytokinesis	*minD*	BN194_14590	K0MV70	3.90	-1.78	-3.44

Uncharacterized protein	Unknown/uncharacterized		BN194_25820	K0NCG9	0.43	-1.78	-3.45
Tyrosine--tRNA ligase (EC 6.1.1.1)		*tyrS*	BN194_21510	K0N6A9	4.69	-1.79	-3.46
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citF*	BN194_20310	K0N607	4.83	-1.79	-3.46
Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	*aspC*	BN194_16770	K0NAU6	4.80	-1.79	-3.47
Exodeoxyribonuclease (EC 3.1.11.2)	DNA repair/recombination	*exoA*	BN194_11390	K0MUA0	2.36	-1.80	-3.48
TPR repeats containing protein	Unknown/uncharacterized		BN194_14960	K0N4M8	3.52	-1.80	-3.49
Uncharacterized protein	General prediction only		BN194_17420	K0NAY8	3.25	-1.80	-3.49
Isoprenyl transferase (EC 2.5.1.-)	Lipid-related metabolism	*uppS*	BN194_17640	K0MVX1	0.77	-1.81	-3.49
Phosphonates import ATP-binding protein PhnC (EC 3.6.3.28)	ABC-type transporter systems	*phnC_2,phnC*	BN194_25690	K0MXP5	4.57	-1.81	-3.51
Uncharacterized protein yxjH	Amino acid-related metabolism	*yxjH*	BN194_08320	K0N962	1.30	-1.82	-3.52
30S ribosomal protein S14	Ribosomal proteins	*rpsN*	BN194_09950	K0N3D1	0.96	-1.82	-3.53
Protein RibT (EC 2.3.1.-)	Cofactor-related metabolism	*ribT*	BN194_15620	K0NAL0	2.67	-1.83	-3.55
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	Nucleic acid/nucleotide metabolism	*tmk*	BN194_23950	K0N7L9	4.08	-1.85	-3.60
Esterase/lipase	General prediction only		BN194_30390	K0MYV7	4.77	-1.85	-3.61
Putative HAD-hydrolase yfnB (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yfnB*	BN194_08780	K0N6M1	0.65	-1.87	-3.66
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	*carB*	BN194_16450	K0N587	6.47	-1.87	-3.67
Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	*gntK*	BN194_02340	K0MS76	3.67	-1.88	-3.68
41 kDa protein		*repA*	BN194_P0550	K0NBI6	4.41	-1.88	-3.68
Uncharacterized protein	Posttranslational modification	*pp2C*	BN194_18030	K0N993	0.92	-1.88	-3.69
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB2,pstB*	BN194_10280	K0N6X8	1.00	-1.91	-3.75

Phosphoenolpyruvate-dependent sugar phosphotransferase system EIIA, galactitol/fructose specific	Phosphotransferase systems		BN194_27050	K0N8F9	1.19	-1.91	-3.75
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	4.29	-1.93	-3.80
NAD-dependent protein deacetylase (EC 3.5.1.-)	General prediction only	*cobB*	BN194_27190	K0MY36	1.47	-1.93	-3.82
Rod shape-determining protein MreB	Cytokinesis	*mreB*	BN194_14550	K0N4R7	4.44	-1.94	-3.84
Double-stranded beta-helix related protein	Transcriptional regulation		BN194_11420	K0N9U8	2.27	-1.94	-3.85
Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-)		*rsmB*	BN194_18040	K0MW45	1.21	-1.95	-3.85
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	*citX*	BN194_20300	K0N6A3	4.20	-1.95	-3.86
YbbR-like domain-containing protein ybbR	Unknown/uncharacterized	*ybbR*	BN194_11540	K0MUB6	4.63	-1.95	-3.86
Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	DNA repair/recombination	*recJ*	BN194_17390	K0MVT7	1.25	-1.95	-3.86
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	*cmk*	BN194_15710	K0N4V1	5.26	-1.96	-3.89
UPF0473 protein BN194_08530	Unknown/uncharacterized		BN194_08530	K0N6K6	2.99	-1.96	-3.90
Uncharacterized protein	General prediction only		BN194_01300	K0N194	1.16	-1.98	-3.94
Uncharacterized protein	Unknown/uncharacterized		BN194_13400	K0N4I9	1.59	-1.98	-3.94
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	*lysS*	BN194_26380	K0NAN7	4.69	-1.98	-3.94
Putative gluconeogenesis factor	General prediction only	*yjiF*	BN194_10480	K0N6Z4	0.97	-1.98	-3.95
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03940	K0MSJ3	2.08	-1.99	-3.96
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*nagA*	BN194_19890	K0MWF9	4.57	-1.99	-3.97
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	*ybeY*	BN194_17010	K0N594	2.53	-1.99	-3.97
Uncharacterized protein	Unknown/uncharacterized	*FNV1452*	BN194_18830	K0N9E3	1.21	-2.01	-4.03
Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	ABC-type transporter systems	*ecfA2, ecfA*	BN194_25920	K0NCI4	0.90	-2.02	-4.05

Uncharacterized protein	Unknown/uncharacterized		BN194_08020	K0N947	4.05	-2.03	-4.09
Cell division protein FtsZ	Cytokinesis	*ftsZ*	BN194_14760	K0N4L6	5.24	-2.04	-4.12
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	*yuxL*	BN194_19910	K0N5X4	3.60	-2.05	-4.13
Uncharacterized protein	Unknown/uncharacterized		BN194_24010	K0N715	4.83	-2.05	-4.14
Segregation and condensation protein B	Cytokinesis	*scpB*	BN194_15640	K0MVE6	2.39	-2.05	-4.14
Probable GTP-binding protein EngB	tRNA/Ribosome assembly/processing	*engB*	BN194_15350	K0N4Y5	1.13	-2.08	-4.22
Ribonuclease P protein component (RNase P protein) (RNaseP protein) (EC 3.1.26.5) (Protein C5)	tRNA/Ribosome assembly/processing	*rnpA*	BN194_30620	K0NDS2	0.84	-2.08	-4.24
Uncharacterized protein	Unknown/uncharacterized		BN194_19050	K0N613	2.55	-2.09	-4.26
Adapter protein MecA	Competence (DNA uptake)	*mecA*	BN194_19170	K0NB89	1.03	-2.09	-4.26
Uncharacterized protein	Unknown/uncharacterized		BN194_05550	K0N257	1.06	-2.10	-4.29
MreB-like protein	Cytokinesis	*mbl*	BN194_13650	K0N4K5	2.91	-2.11	-4.30
Transcriptional regulatory protein YycF	Signal transduction	*yycF_2*	BN194_29510	K0N8E4	0.72	-2.11	-4.30
Transcriptional regulator GltC	Transcriptional regulation	*nac*	BN194_16620	K0NAT7	2.54	-2.13	-4.38
Chaperone protein DnaJ	Protein folding/turnover	*dnaJ*	BN194_17450	K0N5J4	2.52	-2.14	-4.39
Ribosomal protein L11 methyltransferase (L11 Mtase) (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*prmA*	BN194_17260	K0N5B0	1.91	-2.14	-4.42
Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	*rp2*	BN194_17060	K0N598	1.54	-2.16	-4.46
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	*murA2,murA*	BN194_26780	K0NAR9	4.33	-2.16	-4.47
Folate transporter FolT	Unknown/uncharacterized	*folT*	BN194_23890	K0MXC9	3.88	-2.17	-4.49
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	3.73	-2.17	-4.51
Transcriptional repressor CcpN	Transcriptional regulation	*ccpN*	BN194_24740	K0MXH2	4.13	-2.18	-4.52

Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	Nucleic acid/nucleotide metabolism	*purD*	BN194_19290	K0MWC4	4.22	-2.19	-4.55
Cell division protein DivIB	Cytokinesis	*divIB*	BN194_14740	K0MV80	3.43	-2.19	-4.56
Uncharacterized protein			BN194_16060	K0N4Y8	1.86	-2.19	-4.58
Uncharacterized protein ysxB	Ribosomal proteins	*ysxB*	BN194_18280	K0N9A9	1.03	-2.21	-4.62
Threonylcarbamoyl-AMP synthase (TC-AMP synthase) (EC 2.7.7.87) (L-threonylcarbamoyladenylate synthase)	tRNA/Ribosome assembly/processing	*ywlC*	BN194_13530	K0N7S6	1.49	-2.24	-4.71
Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	*plsX*	BN194_17940	K0MW37	2.74	-2.24	-4.73
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	*act*	BN194_16090	K0MVI3	3.11	-2.25	-4.74
Uncharacterized protein	Unknown/uncharacterized		BN194_12200	K0N464	1.13	-2.25	-4.74
Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	*adk*	BN194_26010	K0N7F0	4.49	-2.25	-4.77
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	*iolS*	BN194_29680	K0NB94	5.91	-2.27	-4.82
Putative sporulation transcription regulator WhiA	Transcriptional regulation	*whiA*	BN194_10490	K0MU14	1.59	-2.29	-4.90
Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	0.87	-2.29	-4.90
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	*hmgCS1*	BN194_19680	K0N9K3	4.17	-2.32	-5.01
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB_2*	BN194_20630	K0N9S5	1.11	-2.36	-5.12
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	*ywpJ*	BN194_11320	K0N9U2	4.57	-2.37	-5.16
Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	4.66	-2.39	-5.23
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	*queA*	BN194_08370	K0N965	4.06	-2.39	-5.23
Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	*pyk*	BN194_15580	K0N8B6	5.12	-2.41	-5.32

Glycosyl transferase group 1	Cell wall biogenesis		BN194_09760	K0N3F8	2.73	-2.42	-5.34
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	Cell wall biogenesis	*glmS*	BN194_11560	K0N3V9	5.63	-2.42	-5.35
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_2*	BN194_04490	K0MSM9	4.82	-2.42	-5.37
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	*yhfP*	BN194_07740	K0MTE1	4.01	-2.44	-5.44
Phosphoesterase (EC 3.1.4.-)	General prediction only	*ysnB*	BN194_08650	K0N317	4.01	-2.44	-5.44
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	*ftsY*	BN194_17850	K0N5R8	4.77	-2.44	-5.44
Exopolyphosphatase	Membrane bioenergetics		BN194_27280	K0NAV4	1.29	-2.45	-5.46
Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.193)	tRNA/Ribosome assembly/processing	*rsmE*	BN194_17250	K0N5G8	1.53	-2.46	-5.50
FemAB family protein	General prediction only		BN194_22880	K0NA57	1.00	-2.47	-5.55
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	*rpoZ*	BN194_18100	K0N5T7	2.16	-2.48	-5.58
Ribosome biogenesis GTPase A	tRNA/Ribosome assembly/processing	*rbgA*	BN194_15940	K0MVH2	2.07	-2.49	-5.63
Ferredoxin--NADP reductase (FNR) (Fd-NADP(+) reductase) (EC 1.18.1.2)	Membrane bioenergetics		BN194_08950	K0N337	2.25	-2.49	-5.64
Uncharacterized protein	Unknown/uncharacterized		BN194_22290	K0MX11	2.46	-2.50	-5.67
GNAT family acetyltransferase	General prediction only		BN194_01510	K0N1L8	3.30	-2.51	-5.68
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacB*	BN194_07490	K0MTB7	2.94	-2.51	-5.70
Transcriptional regulator, xre family	Transcriptional regulation		BN194_05600	K0N260	1.61	-2.53	-5.76
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	*zwf*	BN194_08420	K0N966	5.39	-2.54	-5.84

Uncharacterized protein yslB	Unknown/uncharacterized	*yslB*	BN194_08630	K0N6L4	5.32	-2.55	-5.84
CCA-adding enzyme (EC 2.7.7.72) (CCA tRNA nucleotidyltransferase) (tRNA CCA-pyrophosphorylase) (tRNA adenylyl-/cytidylyl- transferase) (tRNA nucleotidyltransferase) (tRNA-NT)	tRNA/Ribosome assembly/processing	*cca*	BN194_15770	K0NAM4	1.05	-2.55	-5.85
GTPase HflX (GTP-binding protein HflX)	tRNA/Ribosome assembly/processing	*hflX*	BN194_21260	K0N689	1.89	-2.55	-5.86
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	*mhqD*	BN194_18770	K0NB71	2.23	-2.55	-5.86
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	*gltX*	BN194_24470	K0NC38	6.03	-2.56	-5.89
5-bromo-4-chloroindolyl phosphate hydrolysis protein	General prediction only		BN194_14860	K0N4M3	4.04	-2.57	-5.95
Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain)	Nucleic acid/nucleotide metabolism	*carA*	BN194_16460	K0N535	5.68	-2.57	-5.95
Probable copper-transporting P-type ATPase B (EC 3.6.3.-)	Other transporter proteins	*copB*	BN194_19280	K0N9H1	1.55	-2.58	-5.96
DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	5.04	-2.59	-6.04
Uncharacterized protein	Unknown/uncharacterized		BN194_19470	K0NBA0	2.89	-2.63	-6.18
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	5.26	-2.65	-6.28
Putative beta-phosphoglucomutase (EC 5.4.2.6)	Central glycolytic/intermediary pathways	*yvdM*	BN194_11170	K0N9S7	1.89	-2.65	-6.29
30S ribosomal protein S21	Ribosomal proteins	*rpsU*	BN194_17050	K0N5E5	0.97	-2.66	-6.34
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	*bkr4*	BN194_22550	K0N799	1.31	-2.68	-6.41
Uncharacterized protein	Unknown/uncharacterized		BN194_01150	K0N181	1.41	-2.69	-6.44
Putative RNA-binding protein ylmH	General prediction only	*ylmH*	BN194_14790	K0MV84	1.62	-2.71	-6.54
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA2,gpmA*	BN194_22740	K0MX58	3.69	-2.76	-6.76
Translation initiation factor IF-1	Protein translation (initiation)	*infA*	BN194_26000	K0N847	2.29	-2.77	-6.81
Uncharacterized protein	Prophage genome		BN194_09330	K0N6Q4	2.07	-2.77	-6.82

Uncharacterized protein	Unknown/uncharacterized		BN194_29850	K0N968	1.89	-2.80	-6.96
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	*apt*	BN194_17380	K0N902	5.68	-2.80	-6.96
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	*lplJ*	BN194_16640	K0MVN0	3.88	-2.81	-7.00
30S ribosomal protein S1 homolog	Ribosomal proteins	*ypfD*	BN194_15720	K0NAL9	6.88	-2.82	-7.07
Uncharacterized RNA methyltransferase lp_3226 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_19580	K0N9J4	2.75	-2.82	-7.07
Uncharacterized protein	Unknown/uncharacterized		BN194_21170	K0NBJ9	1.87	-2.83	-7.13
Hex regulon repressor	Transcriptional regulation		BN194_02320	K0N7J9	2.38	-2.84	-7.14
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		BN194_08960	K0N387	3.98	-2.86	-7.28
Replicative DNA helicase (EC 3.6.4.12)	DNA replication-related	*dnaC*	BN194_01140	K0MRW2	3.24	-2.86	-7.28
30S ribosomal protein S11	Ribosomal proteins	*rpsK*	BN194_25970	K0NCJ0	1.88	-2.87	-7.32
Cof protein	General prediction only		BN194_12010	K0N401	2.75	-2.87	-7.33
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	*ssdA*	BN194_24140	K0MXE0	5.86	-2.88	-7.38
DNA polymerase III subunit delta (EC 2.7.7.7)	DNA replication-related	*holB*	BN194_23930	K0NA93	2.47	-2.88	-7.39
Putative ribosome biogenesis GTPase RsgA (EC 3.6.1.-)	tRNA/Ribosome assembly/processing	*rsgA*	BN194_18010	K0N5J0	3.62	-2.89	-7.39
DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	DNA replication-related	*dnaX*	BN194_23990	K0MXD3	2.13	-2.90	-7.46
DNA translocase SftA	Cytokinesis	*sftA*	BN194_18960	K0N5Q1	3.82	-2.91	-7.51
Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase)	Cofactor-related metabolism	*coaA*	BN194_21080	K0N9V9	3.22	-2.94	-7.69
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	6.20	-2.95	-7.71
Manganese transport system ATP-binding protein MntB	ABC-type transporter systems	*mntB*	BN194_25460	K0N7A8	1.67	-2.98	-7.86
Elongation factor G (EF-G)	Protein translation (elongation)	*fusA*	BN194_26270	K0NCN8	4.30	-2.99	-7.92
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25570	K0NCD4	3.75	-3.00	-8.03
DNA replication protein dnaD	DNA replication-related	*dnaD*	BN194_16750	K0N5B1	1.94	-3.01	-8.07

GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*relA*	BN194_17230	K0N8Y0	3.52	-3.01	-8.07
Lactose phosphotransferase system repressor	Transcriptional regulation	*lacR*	BN194_07510	K0N2X5	2.15	-3.02	-8.12
DNA polymerase III PolC-type (PolIII) (EC 2.7.7.7)	DNA replication-related	*polC*	BN194_17600	K0N5L6	1.81	-3.03	-8.15
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	*fabH*	BN194_22600	K0N7B0	4.90	-3.04	-8.23
Thymidine kinase (EC 2.7.1.21)	Nucleic acid/nucleotide metabolism	*tdk*	BN194_13500	K0N4J4	1.70	-3.04	-8.25
ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease RexB)	DNA repair/recombination	*rexB*	BN194_16810	K0N573	0.78	-3.06	-8.32
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	*ycnE*	BN194_13230	K0N7R3	2.99	-3.06	-8.33
Uncharacterized protein	Cofactor-related metabolism		BN194_18720	K0NB69	3.31	-3.06	-8.34
Archaeal fructose-1,6-bisphosphatase related enzyme of inositol monophosphatase family	*Carbohydrate-related metabolism*		BN194_15140	K0MVB0	4.66	-3.07	-8.38
Uncharacterized protein yjbK	General prediction only	*yjbK*	BN194_09860	K0N3G6	1.48	-3.07	-8.39
Uncharacterized protein	Unknown/uncharacterized		BN194_19530	K0N9J0	3.49	-3.09	-8.50
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*manD*	BN194_02950	K0N1P4	5.34	-3.09	-8.52
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	*fabD*	BN194_22570	K0NBT1	4.30	-3.10	-8.55
Uncharacterized protein yloA	Cell surface proteins/internalins	*yloA*	BN194_16340	K0MVK5	2.40	-3.11	-8.62
Primosomal protein DnaI	DNA replication-related	*dnaI*	BN194_18880	K0N9E5	1.89	-3.12	-8.67
Uncharacterized protein	Unknown/uncharacterized		BN194_02900	K0N1P1	2.79	-3.12	-8.70
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB*	BN194_13410	K0N4C0	2.37	-3.16	-8.93
50S ribosomal protein L32	Ribosomal proteins	*rpmF*	BN194_15510	K0N4T0	0.68	-3.16	-8.95
HTH-type transcriptional repressor yvoA	Transcriptional regulation	*yvoA_2*	BN194_19880	K0N9L8	3.37	-3.16	-8.96

Ribosomal RNA small subunit methyltransferase H (EC 2.1.1.199) (16S rRNA m(4)C1402 methyltransferase) (rRNA (cytosine-N(4)-)-methyltransferase RsmH)	tRNA/Ribosome assembly/processing	*rsmH*	BN194_14680	K0N814	3.81	-3.17	-9.02
Putative RNA methyltransferase YpsC (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ypsC*	BN194_16670	K0NAU0	5.13	-3.17	-9.03
Uncharacterized protein	General prediction only		BN194_13850	K0N4L8	2.18	-3.18	-9.07
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	*yabR*	BN194_26500	K0N8A7	1.68	-3.19	-9.15
DNA-binding protein HU	DNA replication-related	*hup*	BN194_15740	K0MVF4	1.99	-3.20	-9.18
UPF0478 protein SAOUHSC_01855	Signal transduction		BN194_08710	K0N365	5.67	-3.23	-9.39
Probable tRNA sulfurtransferase (EC 2.8.1.4) (Sulfur carrier protein ThiS sulfurtransferase) (Thiamine biosynthesis protein ThiI) (tRNA 4-thiouridine synthase)	Cofactor-related metabolism	*thiI*	BN194_14480	K0N7Z7	4.38	-3.24	-9.43
DNA topoisomerase 4 subunit A (EC 5.99.1.-)		*parC*	BN194_16070	K0NAP8	3.26	-3.24	-9.45
Aspartate racemase (EC 5.1.1.13)	*Amino acid-related metabolism*		BN194_02170	K0N7H2	2.22	-3.25	-9.48
Uncharacterized protein	Unknown/uncharacterized		BN194_00400	K0N116	1.88	-3.25	-9.54
Uncharacterized protein yeaC		*yeaC*	BN194_29960	K0N8I6	1.76	-3.26	-9.55
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)	Nucleic acid/nucleotide metabolism	*ntd*	BN194_24240	K0MXE6	1.36	-3.27	-9.64
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	*pth*	BN194_26550	K0N8B3	1.99	-3.28	-9.69
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	*asnB*	BN194_22990	K0MX90	5.09	-3.28	-9.70
tRNA N6-adenosine threonylcarbamoyltransferase (EC 2.3.1.234) (N6-L-threonylcarbamoyladenine synthase) (t(6)A37 threonylcarbamoyladenosine biosynthesis protein TsaD) (tRNA threonylcarbamoyladenosine biosynthesis protein TsaD)	General prediction only	*tsaD,gcp*	BN194_23850	K0N7L3	4.29	-3.29	-9.80
tRNA pseudouridine synthase B (EC 5.4.99.25) (tRNA pseudouridine(55) synthase) (tRNA pseudouridylate synthase) (tRNA-uridine isomerase)	tRNA/Ribosome assembly/processing	*truB*	BN194_17520	K0NAZ5	1.90	-3.30	-9.86
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism		BN194_22460	K0N6M0	4.23	-3.32	-9.97

Protein dedA	Unknown/uncharacterized	*dedA*	BN194_08930	K0N6M9	1.56	-3.32	-9.97
Probable transcription repressor NiaR	Transcriptional regulation	*niaR*	BN194_08730	K0N6L8	1.94	-3.34	-10.14
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	*yqjQ*	BN194_15480	K0N8A1	4.90	-3.35	-10.21
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	*pyrH*	BN194_17660	K0N5E6	4.14	-3.36	-10.25
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF_2*	BN194_19090	K0MWB2	1.04	-3.36	-10.26
Uncharacterized protein	Unknown/uncharacterized		BN194_08190	K0MTK3	1.25	-3.37	-10.37
Uncharacterized oxidoreductase YcsN (EC 1.-.-.-)	General prediction only	*ycsN*	BN194_27290	K0MY45	2.88	-3.38	-10.42
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	*groL,groEL*	BN194_23750	K0N7K7	4.76	-3.39	-10.46
Cell division protein FtsA	Cytokinesis	*ftsA*	BN194_14750	K0N4T3	3.97	-3.40	-10.52
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	*yabO*	BN194_26520	K0NCR8	2.80	-3.40	-10.57
50S ribosomal protein L6	Ribosomal proteins	*rplF*	BN194_26070	K0NCK5	4.46	-3.40	-10.59
Putative transcriptional regulator (DtxR family)	Transcriptional regulation		BN194_08410	K0N354	4.92	-3.42	-10.72
Putative ADP-ribose pyrophosphatase yjhB (EC 3.6.1.-)	General prediction only	*yjhB*	BN194_25530	K0NAH4	2.19	-3.42	-10.73
Uncharacterized protein yuaG	Unknown/uncharacterized	*yuaG*	BN194_22920	K0NBV0	2.53	-3.45	-10.92
Oxidoreductase YdhF (EC 1.-.-.-)	General prediction only	*ydhF*	BN194_25320	K0NCA1	3.18	-3.45	-10.93
Uncharacterized protein	Transcriptional regulation		BN194_22670	K0NBT5	2.30	-3.45	-10.95
Maltose ABC transporter, periplasmic maltose-binding protein	*ABC-type transporter systems*		BN194_11200	K0N3U4	5.00	-3.46	-11.04
HTH-type transcriptional regulator iolR	Transcriptional regulation	*iolR*	BN194_02190	K0MS58	2.43	-3.47	-11.06
Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		BN194_20000	K0N684	7.13	-3.48	-11.18
30S ribosomal protein S3	Ribosomal proteins	*rpsC*	BN194_26160	K0N7G5	4.80	-3.49	-11.21
Uncharacterized protein	*Nucleic acid/nucleotide metabolism*		BN194_27260	K0N7R1	2.44	-3.50	-11.31
UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.3.1.98) (UDP-N-acetylmuramate dehydrogenase)	Cell wall biogenesis	*murB*	BN194_11400	K0N3X0	2.45	-3.51	-11.38

UPF0039 protein SAR1027	General prediction only		BN194_19510	K0N5U0	2.29	-3.52	-11.44
50S ribosomal protein L18	Ribosomal proteins	*rplR*	BN194_26060	K0N7F4	2.30	-3.54	-11.67
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	*murD*	BN194_14720	K0NAG5	5.55	-3.55	-11.68
Sensory transduction protein BceR	Signal transduction	*bceR_2*	BN194_19250	K0N630	4.62	-3.55	-11.71
Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*nrdD*	BN194_01250	K0N190	3.23	-3.56	-11.76
Diphosphomevalonate decarboxylase (EC 4.1.1.33)	Lipid-related metabolism	*mvd1*	BN194_16830	K0N8S2	2.95	-3.56	-11.80
Predicted hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	4.72	-3.57	-11.87
Uncharacterized protein	General prediction only		BN194_26820	K0NCV9	4.21	-3.58	-11.98
3-hydroxy-3-methylglutaryl coenzyme A reductase (HMG-CoA reductase) (EC 1.1.1.88)	Lipid-related metabolism	*mvaA*	BN194_19690	K0MWE8	3.45	-3.58	-11.98
Uncharacterized protein YdiC	General prediction only	*ydiC_3*	BN194_23870	K0NBZ8	4.08	-3.60	-12.13
Uncharacterized protein	Unknown/uncharacterized		BN194_12110	K0N410	2.51	-3.60	-12.15
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD(+)])	DNA replication-related	*ligA*	BN194_11930	K0N7A9	1.61	-3.61	-12.24
Uncharacterized protein YPL245W	Unknown/uncharacterized		BN194_25000	K0N7U3	0.90	-3.61	-12.25
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	*phoU*	BN194_10290	K0MTZ9	6.41	-3.64	-12.45
Transcriptional repressor NrdR	Transcriptional regulation	*nrdR*	BN194_18900	K0N5Z5	2.62	-3.64	-12.45
Uridine phosphorylase (EC 2.4.2.3)	Nucleic acid/nucleotide metabolism	*udp*	BN194_24830	K0NAD0	3.45	-3.64	-12.47
ABC-type uncharacterized transport system, ATPase component	*ABC-type transporter systems*		BN194_07730	K0N6C9	4.77	-3.65	-12.55
Uncharacterized protein in fgs 3'region	General prediction only		BN194_14530	K0N802	1.56	-3.67	-12.74
Type I restriction enzyme EcoR124II M protein (EC 2.1.1.72)	IS elements/foreign DNA defense	*hsdM*	BN194_22340	K0MX17	2.17	-3.68	-12.79

GTPase Era	tRNA/Ribosome assembly/processing	*era*	BN194_16990	K0MVQ8	3.17	-3.68	-12.80
DNA topoisomerase 4 subunit B (EC 5.99.1.3) (Topoisomerase IV subunit B)	DNA replication-related	*parE*	BN194_16050	K0N545	2.75	-3.70	-12.99
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	*dut*	BN194_24640	K0MXG3	1.34	-3.70	-13.01
FeS cluster assembly protein sufD	Cofactor-related metabolism	*sufD*	BN194_13780	K0N7U0	5.13	-3.71	-13.09
Transcription termination/antitermination protein NusG	Transcription-associated proteins	*nusG*	BN194_24260	K0N730	4.15	-3.71	-13.12
HTH-type transcriptional regulator yodB	Transcriptional regulation	*yodB*	BN194_18590	K0MW80	1.15	-3.72	-13.19
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	*ung*	BN194_11330	K0N758	1.31	-3.72	-13.19
Glucitol operon repressor	Transcriptional regulation	*srlR*	BN194_28690	K0MYG3	2.20	-3.73	-13.24
HTH-type transcriptional repressor glcR	Transcriptional regulation	*glcR*	BN194_02570	K0N7M8	4.08	-3.74	-13.32
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		BN194_11600	K0N3Z3	2.56	-3.74	-13.34
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	2.10	-3.74	-13.40
30S ribosomal protein S15	Ribosomal proteins	*rpsO*	BN194_15260	K0N4Q6	3.09	-3.75	-13.41
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	*grpE*	BN194_17470	K0NAZ2	5.21	-3.75	-13.46
Coenzyme A biosynthesis bifunctional protein CoaBC (EC 4.1.1.36) (EC 6.3.2.5)		*coaBC*	BN194_18090	K0MW49	2.67	-3.76	-13.58
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	*hslV*	BN194_16000	K0N542	3.57	-3.78	-13.72
Phosphatase YbjI (EC 3.1.3.-)	General prediction only	*ybjI*	BN194_30020	K0NDN5	2.71	-3.78	-13.73
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*yfmL*	BN194_12120	K0NA13	3.16	-3.78	-13.75
CBS domain-containing protein ykuL	Unknown/uncharacterized	*ykuL*	BN194_08670	K0N981	1.43	-3.79	-13.86
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh1,ldh*	BN194_06970	K0N8S5	3.16	-3.80	-13.93
Uncharacterized N-acetyltransferase ycf52-like (EC 2.3.1.-)	General prediction only	*speE1*	BN194_21490	K0MWT4	2.58	-3.81	-14.00

33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	*hslO*	BN194_26400	K0N893	2.76	-3.81	-14.01
tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	*dus1*	BN194_26390	K0MXV9	3.09	-3.81	-14.07
UvrABC system protein A	DNA repair/recombination	*uvrA_3*	BN194_27500	K0N8M1	3.80	-3.82	-14.15
tRNA (Adenine(22)-N(1))-methyltransferase (EC 2.1.1.217)	tRNA/Ribosome assembly/processing	*trmK*	BN194_16910	K0N584	2.39	-3.85	-14.38
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		BN194_13770	K0NAC0	3.88	-3.85	-14.41
DegV domain-containing protein SP_1112	Unknown/uncharacterized		BN194_15830	K0N8F3	6.46	-3.86	-14.48
Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (EC 2.7.7.12) (UDP-glucose--hexose-1-phosphate uridylyltransferase)		*galT*	BN194_07370	K0N8X1	3.68	-3.86	-14.48
Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)	Nucleic acid/nucleotide metabolism	*pdp*	BN194_23430	K0NA73	2.28	-3.86	-14.50
50S ribosomal protein L31 type B	Ribosomal proteins	*rpmE2*	BN194_26770	K0NCV4	3.13	-3.86	-14.51
50S ribosomal protein L23	Ribosomal proteins	*rplW*	BN194_26200	K0N869	1.69	-3.87	-14.62
Uncharacterized protein IRC4	Unknown/uncharacterized	*IRC4*	BN194_30110	K0N8K0	2.71	-3.88	-14.70
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	*clpP_2, clpP*	BN194_10510	K0N3M4	4.37	-3.89	-14.87
Uncharacterized protein	Unknown/uncharacterized		BN194_13840	K0MV29	2.77	-3.90	-14.89
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	*murI*	BN194_08640	K0MTN4	1.41	-3.92	-15.11
Glutathione peroxidase	Cell defense/detoxification	*gpo*	BN194_09780	K0N6T6	6.43	-3.92	-15.18
Probable L-serine dehydratase, beta chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAB*	BN194_13940	K0MV34	4.35	-3.93	-15.23
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	*frr*	BN194_17650	K0N5M3	5.28	-3.93	-15.25
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	*prfB*	BN194_10180	K0N6W9	2.77	-3.93	-15.29
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	*xpt*	BN194_12490	K0MUR6	5.53	-3.94	-15.36

Ribosomal RNA small subunit methyltransferase A (EC 2.1.1.182) (16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase) (16S rRNA dimethyladenosine transferase) (16S rRNA dimethylase) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase)	tRNA/Ribosome assembly/processing	*rsmA,ksgA*	BN194_27020	K0NCX3	4.40	-3.95	-15.46
Probable L-serine dehydratase, alpha chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAA*	BN194_13950	K0N4M4	4.73	-3.96	-15.56
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	*fabG*	BN194_22560	K0N6N3	2.12	-3.96	-15.57
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	*pfkA*	BN194_15570	K0NAK6	2.86	-3.96	-15.61
Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)	Nucleic acid/nucleotide metabolism	*pyrF*	BN194_16430	K0N8M7	2.87	-3.97	-15.65
tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA (guanine(46)-N(7))-methyltransferase) (tRNA(m7G46)-methyltransferase)	tRNA/Ribosome assembly/processing	*trmB*	BN194_19000	K0N606	3.75	-3.98	-15.74
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*argS*	BN194_19120	K0NB86	7.35	-3.99	-15.88
UvrABC system protein B (Protein UvrB) (Excinuclease ABC subunit B)	DNA repair/recombination	*uvrB*	BN194_10440	K0MU09	3.09	-3.99	-15.91
Uncharacterized protein ytoI	Transcriptional regulation	*ytoI*	BN194_08440	K0MTM0	4.30	-4.00	-15.95
50S ribosomal protein L24	Ribosomal proteins	*rplX*	BN194_26110	K0N7F9	3.01	-4.00	-16.03
Uncharacterized ABC transporter ATP-binding protein YdiF	General prediction only	*ydiF*	BN194_23830	K0NA88	4.80	-4.01	-16.13
Polyphosphate kinase (EC 2.7.4.1) (ATP-polyphosphate phosphotransferase) (Polyphosphoric acid kinase)	Membrane bioenergetics	*ppk*	BN194_27270	K0ND10	2.87	-4.02	-16.23
Uncharacterized protein	General prediction only		BN194_14990	K0MV99	2.24	-4.02	-16.24
Uncharacterized protein	Unknown/uncharacterized		BN194_19810	K0N5W5	5.74	-4.03	-16.32
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox*	BN194_01780	K0N4U4	3.84	-4.03	-16.35
Transcriptional regulator	Transcriptional regulation		BN194_08230	K0N6I4	2.65	-4.03	-16.36
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB*	BN194_19860	K0N5X0	4.43	-4.04	-16.47
30S ribosomal protein S12	Ribosomal proteins	*rpsL*	BN194_26290	K0MXV0	6.01	-4.05	-16.54

Uncharacterized protein			BN194_07360	K0N2W3	4.65	-4.05	-16.57
Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	*fba_2*	BN194_05060	K0N2C9	4.24	-4.06	-16.70
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	*fabZ*	BN194_22520	K0NBS8	4.29	-4.06	-16.72
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	*der*	BN194_15730	K0N8E1	4.72	-4.08	-16.96
50S ribosomal protein L16	Ribosomal proteins	*rplP*	BN194_26150	K0N863	3.23	-4.09	-17.07
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	*guaB*	BN194_02100	K0N1G3	5.06	-4.09	-17.08
Phosphatase YidA (EC 3.1.3.-)	General prediction only	*yidA*	BN194_28520	K0NDD5	5.71	-4.10	-17.17
50S ribosomal protein L3	Ribosomal proteins	*rplC*	BN194_26220	K0NCN1	2.62	-4.11	-17.24
50S ribosomal protein L11	Ribosomal proteins	*rplK*	BN194_24160	K0N724	4.47	-4.11	-17.26
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	*pdhD*	BN194_15110	K0N4P1	3.63	-4.12	-17.38
Recombination protein RecR	DNA repair/recombination	*recR*	BN194_23970	K0NC03	3.05	-4.13	-17.48
Chromosome partition protein Smc	Cytokinesis	*smc*	BN194_17860	K0N5H9	2.68	-4.13	-17.56
Uncharacterized protein HI_0912	General prediction only	*thiF3*	BN194_05090	K0MSS8	4.13	-4.15	-17.77
Bifunctional protein FolD	Cofactor-related metabolism	*folD*	BN194_18210	K0N5K0	4.77	-4.16	-17.83
Uncharacterized protein ylxR	General prediction only	*ylxR*	BN194_17570	K0NAZ6	2.81	-4.16	-17.90
Ribosomal RNA small subunit methyltransferase G (EC 2.1.1.-) (16S rRNA 7-methylguanosine methyltransferase)	tRNA/Ribosome assembly/processing	*rsmG*	BN194_02020	K0N7F1	2.75	-4.17	-18.06
Transcription termination/antitermination protein NusA	Transcription-associated proteins	*nusA*	BN194_17580	K0N927	3.51	-4.18	-18.15
50S ribosomal protein L22	Ribosomal proteins	*rplV*	BN194_26170	K0NCM1	3.75	-4.19	-18.31
DNA mismatch repair protein MutL	DNA repair/recombination	*mutL*	BN194_23710	K0N6Z8	2.79	-4.21	-18.54

50S ribosomal protein L30	Ribosomal proteins	*rpmD*	BN194_26040	K0MXS6	1.87	-4.23	-18.83
ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	DNA repair/recombination	*addA*	BN194_16800	K0N5B6	2.39	-4.25	-19.00
50S ribosomal protein L10	Ribosomal proteins	*rplJ*	BN194_24090	K0MXD8	5.14	-4.26	-19.21
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	*thyA*	BN194_15800	K0N522	2.32	-4.27	-19.29
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA_2,ackA*	BN194_23060	K0N6W4	4.35	-4.27	-19.31
Uncharacterized protein YxeH	General prediction only	*yxeH*	BN194_04750	K0N1Y7	1.81	-4.29	-19.51
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_2*	BN194_20600	K0N6C6	2.88	-4.31	-19.77
Uncharacterized protein ybxB	tRNA/Ribosome assembly/processing	*ybxB*	BN194_24020	K0NC08	2.44	-4.31	-19.87
MFS permease-like protein	Other transporter proteins		BN194_06910	K0N2S6	2.83	-4.32	-19.92
Heat-inducible transcription repressor HrcA	Transcriptional regulation	*hrcA*	BN194_17480	K0N915	5.59	-4.35	-20.36
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	*glgD*	BN194_21590	K0MWU4	3.01	-4.35	-20.40
Holo-[acyl-carrier-protein] synthase (Holo-ACP synthase) (EC 2.7.8.7) (4'-phosphopantetheinyl transferase AcpS)	Cofactor-related metabolism	*acpS*	BN194_26690	K0MXY2	4.25	-4.36	-20.57
GTP pyrophosphokinase yjbM (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*yjbM*	BN194_09870	K0N9G5	3.01	-4.36	-20.60
Adenosylcobalamin-dependent ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*rtpR*	BN194_24230	K0NAA3	3.31	-4.37	-20.67
50S ribosomal protein L14	Ribosomal proteins	*rplN*	BN194_26120	K0NCL3	4.24	-4.37	-20.69
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	*gmk*	BN194_18110	K0N5J6	2.60	-4.38	-20.83
30S ribosomal protein S6	Ribosomal proteins	*rpsF*	BN194_00100	K0N0Z1	6.13	-4.38	-20.88
Transcriptional regulator, xre family	Transcriptional regulation		BN194_13860	K0N4E8	2.95	-4.41	-21.29

Peptide chain release factor 3 (RF-3)	Protein translation (peptide release)	*prfC*	BN194_19480	K0N9I7	3.26	-4.42	-21.36
30S ribosomal protein S20	Ribosomal proteins	*rpsT*	BN194_15250	K0N4X9	4.98	-4.42	-21.38
Transcriptional regulator, XRE family	Transcriptional regulation		BN194_30170	K0NDP4	3.08	-4.42	-21.48
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	5.98	-4.43	-21.51
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	*pycB*	BN194_20290	K0MWI8	4.82	-4.45	-21.91
30S ribosomal protein S10	Ribosomal proteins	*rpsJ*	BN194_26230	K0NAM5	5.12	-4.47	-22.10
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	*cap4C*	BN194_12280	K0N7E3	5.12	-4.47	-22.19
30S ribosomal protein S17	Ribosomal proteins	*rpsQ*	BN194_26130	K0NAL6	6.25	-4.47	-22.20
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	*map*	BN194_12230	K0N7E0	1.63	-4.48	-22.32
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhB*	BN194_15090	K0MVA7	3.53	-4.49	-22.54
30S ribosomal protein S13	Ribosomal proteins	*rpsM*	BN194_25980	K0NAK3	3.98	-4.51	-22.78
50S ribosomal protein L13	Ribosomal proteins	*rplM*	BN194_25850	K0N828	5.36	-4.52	-22.95
UvrABC system protein A	DNA repair/recombination	*uvrA_2*	BN194_14920	K0NAH3	2.46	-4.53	-23.06
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	*ohrR*	BN194_10500	K0N3J7	1.91	-4.53	-23.07
50S ribosomal protein L4	Ribosomal proteins	*rplD*	BN194_26210	K0N7H0	5.15	-4.53	-23.10
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA*	BN194_01620	K0N7B1	2.59	-4.53	-23.11
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	*yclJ*	BN194_11790	K0MUE5	2.21	-4.53	-23.18
Alternansucrase	Cell wall biogenesis		BN194_02430	K0N547	4.88	-4.56	-23.67
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	*rpoB*	BN194_26340	K0MXV4	2.36	-4.57	-23.77

50S ribosomal protein L1	Ribosomal proteins	*rplA*	BN194_24150	K0N7M7	4.24	-4.57	-23.82
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*pcrA*	BN194_11920	K0N9Z6	3.24	-4.58	-23.86
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	*pyrG*	BN194_26790	K0MXZ1	5.40	-4.58	-23.87
Chromosomal replication initiator protein DnaA	DNA replication-related	*dnaA*	BN194_00010	K0N1B5	4.21	-4.58	-23.91
Glutamate--cysteine ligase/gamma-glutamylcysteine synthetase	Cofactor-related metabolism	*gshAB*	BN194_13910	K0N4F0	3.52	-4.63	-24.72
PhoH-like protein	General prediction only	*phoH*	BN194_17020	K0NAW2	3.62	-4.67	-25.41
Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase)	Nucleic acid/nucleotide metabolism	*purM*	BN194_19320	K0NB95	5.74	-4.69	-25.78
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	*prs1,prs*	BN194_26930	K0NAT2	4.85	-4.69	-25.80
Glutathione reductase, chloroplastic (EC 1.8.1.7)	Cofactor-related metabolism	*GOR*	BN194_23200	K0N7H3	3.88	-4.70	-26.07
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	*yqeL,rsfS*	BN194_18710	K0N5N6	2.27	-4.71	-26.10
50S ribosomal protein L17	Ribosomal proteins	*rplQ*	BN194_25950	K0N841	1.29	-4.71	-26.16
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA_2*	BN194_22950	K0N7F8	2.68	-4.72	-26.43
50S ribosomal protein L15	Ribosomal proteins	*rplO*	BN194_26030	K0NAK7	5.21	-4.73	-26.52
30S ribosomal protein S16	Ribosomal proteins	*rpsP*	BN194_17810	K0N5H1	4.88	-4.73	-26.54
SMC domain protein	DNA repair/recombination		BN194_07540	K0MTC3	2.98	-4.74	-26.66
Sporulation initiation inhibitor protein soj	Cytokinesis	*soj*	BN194_02040	K0MS45	2.46	-4.74	-26.70
Bifunctional protein GlmU	Cell wall biogenesis	*glmU*	BN194_26940	K0MY10	4.06	-4.75	-26.86
30S ribosomal protein S5	Ribosomal proteins	*rpsE*	BN194_26050	K0N853	5.01	-4.75	-26.87
30S ribosomal protein S7	Ribosomal proteins	*rpsG*	BN194_26280	K0NAM9	5.50	-4.77	-27.22
DNA mismatch repair protein MutS	DNA repair/recombination	*mutS*	BN194_23720	K0NBY9	3.35	-4.77	-27.32

Ribosome maturation factor RimM	tRNA/Ribosome assembly/processing	*rimM*	BN194_17790	K0MVZ6	3.51	-4.78	-27.46
Uncharacterized protein			BN194_22500	K0N788	3.30	-4.79	-27.69
Translation initiation factor IF-2	Protein translation (initiation)	*infB*	BN194_17550	K0N5K7	2.56	-4.80	-27.92
Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	*upp*	BN194_13550	K0N4J8	6.75	-4.81	-28.08
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	*prfA*	BN194_13510	K0N4C6	5.06	-4.82	-28.25
Uncharacterized protein yieF	General prediction only	*yieF_2*	BN194_06540	K0MT25	3.62	-4.83	-28.36
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	*clpE*	BN194_19450	K0N644	5.47	-4.86	-29.14
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA1,gpmA*	BN194_24750	K0N7R7	2.68	-4.88	-29.43
Transcriptional regulator, TetR family	Transcriptional regulation		BN194_12190	K0MUM1	1.45	-4.89	-29.73
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	*prs1_2*	BN194_30370	K0NDQ5	3.47	-4.90	-29.87
Uncharacterized protein	Lipid-related metabolism		BN194_11980	K0N7B3	6.11	-4.90	-29.96
Uncharacterized protein	Unknown/uncharacterized		BN194_27210	K0N7Q6	2.85	-4.92	-30.19
3'-5' exoribonuclease yhaM (EC 3.1.-.-)	RNA degradation	*yhaM*	BN194_19070	K0NB84	3.98	-4.93	-30.57
30S ribosomal protein S2	Ribosomal proteins	*rpsB*	BN194_17680	K0N936	6.28	-4.94	-30.74
30S ribosomal protein S8	Ribosomal proteins	*rpsH*	BN194_26080	K0NAL1	4.03	-4.97	-31.39
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB_2*	BN194_21970	K0NBP6	2.83	-5.01	-32.16
50S ribosomal protein L5	Ribosomal proteins	*rplE*	BN194_26100	K0N859	4.65	-5.01	-32.16
Elongation factor P	Protein translation (elongation)	*efp_2*	BN194_22050	K0N712	2.33	-5.02	-32.39
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*yacO*	BN194_24420	K0NC34	3.41	-5.06	-33.33

50S ribosomal protein L33	Ribosomal proteins	*rpmG*	BN194_20200	K0N697	1.17	-5.08	-33.83
FeS cluster assembly protein sufB	Cofactor-related metabolism	*sufB*	BN194_13810	K0N4E5	3.07	-5.09	-34.09
Uncharacterized protein	Signal transduction		BN194_18490	K0MW74	1.49	-5.10	-34.25
Mevalonate kinase (EC 2.7.1.36)	Lipid-related metabolism	*mvk*	BN194_12270	K0NA23	3.80	-5.11	-34.65
Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		BN194_08520	K0N972	2.72	-5.12	-34.79
Manganese ABC transporter substrate-binding lipoprotein	ABC-type transporter systems	*fimA*	BN194_25450	K0N7Y2	3.49	-5.14	-35.24
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	*thrS*	BN194_18860	K0N5P5	4.31	-5.16	-35.72
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	*typA*	BN194_15150	K0N4W9	3.98	-5.16	-35.75
Phosphoribosylformylglycinamidine synthase subunit PurS (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit III) (Phosphoribosylformylglycinamidine synthase subunit III)	Nucleic acid/nucleotide metabolism	*yexA,purS*	BN194_19350	K0N638	2.96	-5.19	-36.52
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	*fabZ_2*	BN194_22620	K0NBT3	2.70	-5.19	-36.54
30S ribosomal protein S14 type Z	Ribosomal proteins	*rpsZ,rpsN*	BN194_26090	K0MXS9	5.77	-5.24	-37.78
30S ribosomal protein S4	Ribosomal proteins	*rpsD*	BN194_14440	K0MV63	4.14	-5.24	-37.80
Protein RecA (Recombinase A)	DNA repair/recombination	*recA_2,recA*	BN194_27650	K0N8P0	2.66	-5.25	-38.01
30S ribosomal protein S9	Ribosomal proteins	*rpsI*	BN194_25840	K0MXR0	0.90	-5.26	-38.20
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	*rnc*	BN194_17870	K0NB31	4.90	-5.26	-38.45
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	*guaA*	BN194_21070	K0NBJ2	6.62	-5.28	-38.91
50S ribosomal protein L2	Ribosomal proteins	*rplB*	BN194_26190	K0MXU1	5.10	-5.29	-39.12
Cadmium efflux system accessory protein	Other transporter proteins	*cadC*	BN194_21540	K0MWU0	6.12	-5.31	-39.76
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	*rpoE*	BN194_26810	K0N7L4	1.39	-5.32	-39.96

Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	*phoP*	BN194_10220	K0N9J6	3.14	-5.35	-40.66
Uncharacterized protein yutG	Lipid-related metabolism	*yutG*	BN194_08940	K0MTQ3	4.83	-5.35	-40.73
Elongation factor 4 (EF-4) (EC 3.6.5.n1) (Ribosomal back-translocase LepA)	Protein translation (elongation)	*lepA*	BN194_17440	K0MVU5	4.91	-5.36	-40.97
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	2.99	-5.36	-41.07
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	*coaD*	BN194_15200	K0N4X3	3.55	-5.38	-41.51
RNA polymerase sigma factor SigA	RNA polymerase	*rpoD,sigA*	BN194_16920	K0NAV6	3.45	-5.40	-42.23
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	*rpe*	BN194_18000	K0N5T1	3.35	-5.41	-42.48
Transcriptional regulator, xre family	Transcriptional regulation		BN194_23510	K0N6Y7	2.38	-5.43	-43.02
Uncharacterized RNA methyltransferase lp_1151 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_11990	K0MUI2	4.28	-5.44	-43.36
Uncharacterized protein YqhY	Unknown/uncharacterized	*yqhY*	BN194_18230	K0N9A7	3.61	-5.44	-43.37
Nucleotide-binding protein BN194_10470	General prediction only		BN194_10470	K0N9L7	2.43	-5.44	-43.41
50S ribosomal protein L35	Ribosomal proteins	*rpmI*	BN194_18810	K0N5P1	2.70	-5.45	-43.80
50S ribosomal protein L29	Ribosomal proteins	*rpmC*	BN194_26140	K0MXT6	5.80	-5.46	-43.89
30S ribosomal protein S19	Ribosomal proteins	*rpsS*	BN194_26180	K0NAM1	2.94	-5.46	-44.17
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	*ndk*	BN194_08160	K0N340	5.57	-5.49	-44.79
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	*yqeH*	BN194_18740	K0MW90	3.48	-5.52	-45.86
Uncharacterized protein SE_0534	*tRNA/Ribosome assembly/processing*		BN194_10150	K0N3F2	3.08	-5.52	-45.93
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	*rnjA*	BN194_15020	K0NAH6	3.36	-5.53	-46.29
Regulatory protein vanR	Signal transduction	*vanR*	BN194_02120	K0N7G4	3.11	-5.53	-46.29

DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	*gyrB*	BN194_00060	K0N1B8	1.71	-5.53	-46.31
D-ribose-binding protein	ABC-type transporter systems	*rbsB*	BN194_03290	K0MSF6	3.09	-5.54	-46.43
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshB*	BN194_08460	K0N356	3.99	-5.54	-46.61
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	*glyA*	BN194_13540	K0MV12	3.87	-5.56	-47.16
Uncharacterized ABC transporter ATP-binding protein YfmR (EC 3.6.3.-)	ABC-type transporter systems	*yfmR*	BN194_15790	K0MVF8	3.74	-5.58	-47.79
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	*obg*	BN194_15440	K0MVD3	3.08	-5.58	-47.96
50S ribosomal protein L20	Ribosomal proteins	*rplT*	BN194_18800	K0N5Y4	4.25	-5.61	-48.99
Uncharacterized protein ypgQ	General prediction only	*ypgQ*	BN194_27480	K0NAX0	3.48	-5.64	-49.74
ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	*clpX*	BN194_15340	K0MVC6	2.51	-5.74	-53.32
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	*uvrA*	BN194_10450	K0N3J2	5.43	-5.77	-54.68
Signal recognition particle protein (Fifty-four homolog)	Protein export	*ffh*	BN194_17820	K0NB27	3.88	-5.80	-55.85
50S ribosomal protein L27	Ribosomal proteins	*rpmA*	BN194_18270	K0NB51	2.79	-5.87	-58.32
Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	*ADH2*	BN194_08400	K0N307	5.99	-5.88	-58.98
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	*hslU*	BN194_16010	K0N4Y1	3.12	-5.88	-59.02
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	*hprK*	BN194_10330	K0N6Y3	3.56	-5.90	-59.56
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	*pyrC*	BN194_16470	K0NAS6	4.43	-5.90	-59.85
GMP reductase (EC 1.7.1.7) (Guanosine 5'-monophosphate oxidoreductase)	Nucleic acid/nucleotide metabolism	*guaC*	BN194_09960	K0N3H4	4.49	-5.92	-60.47
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	*ykpA*	BN194_07220	K0N8V6	2.90	-5.93	-61.10
DNA topoisomerase 1 (EC 5.99.1.2) (DNA topoisomerase I)	DNA replication-related	*topA*	BN194_15970	K0NAP0	4.81	-5.95	-61.78

Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	*rpiA_2, ripA*	BN194_28600	K0N8W9	2.66	-5.95	-61.90
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	4.35	-6.00	-63.99
Response regulator ArlR	Signal transduction	*arlR*	BN194_18650	K0N5X3	3.39	-6.05	-66.06
PspC domain-containing protein	Unknown/uncharacterized	*ythC*	BN194_10300	K0N3H5	6.13	-6.05	-66.38
Translation initiation factor IF-3	Protein translation (initiation)	*infC*	BN194_18820	K0NB73	3.39	-6.05	-66.41
1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157)	Cell wall biogenesis		BN194_09040	K0MTQ9	4.31	-6.09	-68.07
Chaperone protein ClpB	Protein folding/turnover	*clpB*	BN194_15500	K0N4Z8	4.57	-6.11	-69.01
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	4.19	-6.13	-69.85
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF_2*	BN194_20590	K0MWL1	5.23	-6.22	-74.60
Stage 0 sporulation protein J	Cytokinesis	*spo0J*	BN194_02050	K0N1F9	4.15	-6.25	-76.31
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	*apbE_3*	BN194_21550	K0N6S8	3.02	-6.34	-80.94
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	*gpsA*	BN194_10350	K0N3I2	4.99	-6.36	-82.20
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhA*	BN194_15080	K0N860	2.19	-6.45	-87.21
Transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	4.01	-6.46	-87.80
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA_2*	BN194_18340	K0MW64	5.76	-6.52	-92.03
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	4.25	-6.54	-93.30
Phosphoribosylformylglycinamidine synthase subunit PurQ (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit I) (Glutaminase PurQ) (Phosphoribosylformylglycinamidine synthase subunit I)	Nucleic acid/nucleotide metabolism	*purQ*	BN194_19340	K0MWC7	4.74	-6.56	-94.12
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	*polA*	BN194_18930	K0N9E7	3.34	-6.56	-94.61
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	*rnr*	BN194_11100	K0N3S4	3.73	-6.58	-95.68

50S ribosomal protein L9	Ribosomal proteins	*rplI*	BN194_01130	K0N4K3	6.26	-6.68	-102.75
Uncharacterized protein	Unknown/uncharacterized		BN194_20160	K0N5Z4	3.28	-6.97	-125.35
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	*rex_2,rex*	BN194_23820	K0NBZ5	3.62	-7.00	-127.91
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshA*	BN194_26700	K0N8C7	5.47	-7.01	-128.50
Uncharacterized protein	Unknown/uncharacterized		BN194_01760	K0N1N3	3.62	-7.05	-132.14
Uncharacterized protein	General prediction only		BN194_21200	K0N6M8	4.53	-7.05	-132.67
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	*gyrA*	BN194_00070	K0N6S7	2.12	-7.12	-139.32
Chaperone protein ClpB	Protein folding/turnover	*clpB_2*	BN194_26350	K0N887	3.69	-7.22	-148.71
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	*murE*	BN194_02160	K0N1S5	3.76	-7.24	-151.21
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	*pyc*	BN194_15170	K0NAI2	4.26	-7.25	-152.71
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*helD*	BN194_21130	K0N9W3	3.49	-7.28	-155.17
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	*rpoC*	BN194_26330	K0NAN3	4.50	-7.41	-170.53
Pur operon repressor	Transcriptional regulation	*purR_2*	BN194_26960	K0N7M9	3.83	-7.46	-176.61
Bifunctional purine biosynthesis protein PurH	Nucleic acid/nucleotide metabolism	*purH*	BN194_19300	K0N634	2.35	-7.57	-189.69
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	*rpoA*	BN194_25960	K0N7E5	5.41	-7.60	-194.50
N5-carboxyaminoimidazole ribonucleotide synthase (N5-CAIR synthase) (EC 6.3.4.18) (5-(carboxyamino)imidazole ribonucleotide synthetase)	Nucleic acid/nucleotide metabolism	*purK_2, purK*	BN194_19370	K0NB96	4.43	-8.25	-303.98
Phosphoribosylformylglycinamidine synthase subunit PurL (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit II) (Glutamine amidotransferase PurL) (Phosphoribosylformylglycinamidine synthase subunit II)	Nucleic acid/nucleotide metabolism	*purL*	BN194_19330	K0N9H6	2.12	-8.32	-319.21

Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	*purB*	BN194_12520	K0NA41	3.76	-8.38	-333.24
Probable catabolite control protein A	Transcriptional regulation	*ccpA*	BN194_08750	K0N323	3.52	-8.51	-363.89
Alpha-galactosidase 2 (EC 3.2.1.22)	Carbohydrate-related metabolism	*agaS_2*	BN194_22160	K0N6I2	4.40	-8.55	-375.32
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_07700	K0N2V5	7.50	-8.59	-385.39
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	*pflB*	BN194_16080	K0N8I5	4.77	-8.85	-460.27
Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)	Nucleic acid/nucleotide metabolism	*purC*	BN194_19360	K0N5S8	4.95	-9.36	-655.75

(7c)Protein FC UC pH Vs CFE 4.5

Protein names	Functional Class	Gene	Gene locus	Protein IDs	-Log t-test p-value	t-test difference	Fold change
UPF0337 protein yhjA	General prediction only	*yhjA*	BN194_24800	K0N7S1	3.70	8.35	326.62
Uncharacterized protein	Unknown/uncharacterized		BN194_07550	K0N2T9	3.26	5.08	33.83
UPF0346 protein BN194_15870	Unknown/uncharacterized		BN194_15870	K0NAN2	3.46	4.74	26.78
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA_2*	BN194_20640	K0MWL6	8.19	4.63	24.78
Malolactic enzyme (EC 1.-.-.-)	Tricarboxylic acid pathway	*mleA*	BN194_08070	K0N949	7.67	4.38	20.83
Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	*pox5*	BN194_19670	K0NBB6	4.65	4.22	18.64
Uncharacterized isochorismatase family protein pncA (EC 3.-.-.-)	General prediction only	*pncA*	BN194_29120	K0NDH8	2.52	4.18	18.11
UPF0337 protein lp_1708	General prediction only		BN194_05810	K0N2J8	3.07	3.96	15.52
6-phospho-beta-galactosidase (EC 3.2.1.85) (Beta-D-phosphogalactoside galactohydrolase) (P-beta-Gal)	Carbohydrate-related metabolism	*lacG*	BN194_07320	K0N8W7	4.35	3.95	15.45

ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_07710	K0N2Z3	6.50	3.57	11.92
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	*mtlD_3mtlD*	BN194_30400	K0N9C8	7.26	3.53	11.54
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	*nagB*	BN194_30440	K0MYW0	6.96	3.43	10.78
3-keto-L-gulonate-6-phosphate decarboxylase sgbH (EC 4.1.1.85)	Carbohydrate-related metabolism	*sgbH*	BN194_28550	K0N8W6	3.26	3.39	10.49
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_23190	K0MXA1	4.65	3.31	9.92
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	*HBN1*	BN194_16550	K0N597	6.97	3.26	9.56
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2,lacD*	BN194_07480	K0N6A8	6.72	3.25	9.54
UPF0342 protein yheA	Unknown/uncharacterized	*yheA*	BN194_19080	K0N9F7	3.20	3.24	9.43
Uncharacterized protein	Phosphotransferase systems		BN194_04820	K0N885	4.74	3.24	9.42
Uncharacterized protein	General prediction only		BN194_28370	K0NDC5	4.68	3.17	9.02
Probable flavodoxin-1	General prediction only	*ykuN*	BN194_01860	K0N1P2	3.69	3.01	8.07
Putative 2-hydroxyacid dehydrogenase SH0752 (EC 1.1.1.-)	General prediction only		BN194_01890	K0MS33	5.48	3.00	8.02
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP*	BN194_17930	K0N988	2.68	2.99	7.93
18 kDa heat shock protein	Protein folding/turnover	*hsp18*	BN194_07570	K0N8Z3	2.89	2.94	7.68
Oligo-1,6-glucosidase (EC 3.2.1.10)	Carbohydrate-related metabolism	*malL*	BN194_04830	K0N5P4	5.67	2.94	7.68
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	*pepS*	BN194_12180	K0N7D5	5.45	2.94	7.68
Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	Nucleic acid/nucleotide metabolism	*purN*	BN194_19310	K0N5S4	1.75	2.89	7.42
Microcin C7 self-immunity protein mccF			BN194_01360	K0N1K5	5.87	2.87	7.29
Cell wall surface anchor family protein	*Cell surface proteins/internalins*		BN194_05290	K0MSU3	3.26	2.86	7.25
Uncharacterized protein yueI	Unknown/uncharacterized	*yueI*	BN194_13920	K0NAC7	5.45	2.84	7.18
ABC-type uncharacterized transport system, ATPase component	*ABC-type transporter systems*		BN194_07730	K0N6C9	2.44	2.79	6.93
Maf-like protein maf	General prediction only	*maf*	BN194_23700	K0N7K3	2.31	2.78	6.89
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	*galK*	BN194_07340	K0MTA3	4.18	2.74	6.68
Uncharacterized protein	Unknown/uncharacterized		BN194_15370	K0NAJ2	3.21	2.71	6.56
Putative carboxypeptidase SCO6489 (EC 3.4.16.-)			BN194_01370	K0N787	4.52	2.69	6.46

Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC_2,deoC*	BN194_02790	K0MSB5	3.49	2.68	6.43
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	*luxS*	BN194_08330	K0N6J0	5.18	2.68	6.39
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citE*	BN194_20320	K0NBF4	3.54	2.63	6.21
Beta-galactosidase 17 (EC 3.2.1.23)	Carbohydrate-related metabolism	*BGAL17*	BN194_02960	K0N204	5.38	2.62	6.17
Uncharacterized protein ycaC	General prediction only	*ycaC*	BN194_29650	K0N948	5.64	2.62	6.13
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citF*	BN194_20310	K0N607	5.22	2.58	5.96
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox_2*	BN194_02850	K0N1N9	4.97	2.55	5.85
UPF0659 protein YMR090W	General prediction only	*ylbE*	BN194_07030	K0N671	5.65	2.53	5.77
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	*galE*	BN194_07350	K0N2R3	4.84	2.52	5.74
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		BN194_03130	K0N5D9	4.34	2.52	5.73
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_13380	K0N7S0	5.77	2.50	5.67
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI*	BN194_07860	K0N327	2.61	2.49	5.61
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	*mco*	BN194_25410	K0N7A4	5.46	2.46	5.52
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA*	BN194_08450	K0N309	5.76	2.46	5.51
Uncharacterized protein YwcC	Carbohydrate-related metabolism	*ywcC*	BN194_09930	K0N6V0	5.69	2.45	5.46
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	*BN194_21350*	BN194_21780	K0N6Q5	5.70	2.43	5.40
Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	Nucleic acid/nucleotide metabolism	*add*	BN194_23440	K0MXB1	5.92	2.38	5.22
Multifunctional protein: 5-nucleotidase 2,3-cyclic-nucleotide 2-phosphodiesterase	Nucleic acid/nucleotide metabolism	*ushA*	BN194_15530	K0N8A9	4.72	2.37	5.18
NAD-dependent epimerase/dehydratase:3-beta hydroxysteroid dehydrogenase/isomerase:NmrA-like	General prediction only		BN194_25520	K0NCC8	4.91	2.36	5.12
Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Phosphoglucose isomerase) (Phosphohexose isomerase)	Central glycolytic/intermediary pathways	*pgi*	BN194_12580	K0N7I6	6.00	2.36	5.12
Acetyltransferase	General prediction only		BN194_08200	K0N2Z8	3.25	2.35	5.11
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	*tpiA*	BN194_11030	K0N736	5.35	2.32	5.01
Cytidine deaminase (EC 3.5.4.5)	Nucleic acid/nucleotide metabolism	*cdd*	BN194_17000	K0N5D8	3.03	2.32	5.00
Glucose-1-phosphate thymidylyltransferase		*rmlA*		K0N699;K0MWW4	6.90	2.31	4.95

Uncharacterized protein	Unknown/uncharacterized		BN194_20240	K0MWI3	4.43	2.30	4.94
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO_2*	BN194_16630	K0N8Q0	5.48	2.30	4.92
Glycine cleavage system H protein	Amino acid-related metabolism	*gcvH*	BN194_13700	K0N4K8	3.58	2.30	4.92
Aldose 1-epimerase (EC 5.1.3.3)	*Central glycolytic/intermediary pathways*		BN194_07390	K0MTA8	4.57	2.27	4.84
Uncharacterized protein MJ1651	General prediction only		BN194_04410	K0N281	5.04	2.27	4.83
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrDA, pyrD*	BN194_19150	K0N623	5.32	2.27	4.81
Protein lacX, plasmid	Carbohydrate-related metabolism	*lacX*	BN194_27070	K0NCY0	5.56	2.27	4.81
Spore coat polysaccharide biosynthesis protein spsK				K0N9X8;K0N6D6	4.93	2.25	4.77
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	*treA*	BN194_06930	K0N662	3.32	2.24	4.74
L-asparaginase (EC 3.5.1.1)	Amino acid-related metabolism	*ansA*	BN194_23900	K0N7L6	4.96	2.24	4.73
Uncharacterized protein MJ0282	Cofactor-related metabolism		BN194_03700	K0N1T2	4.66	2.23	4.70
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	*glpK_2,glpK*	BN194_27720	K0ND65	2.84	2.22	4.66
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	5.68	2.22	4.64
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	*nadE*	BN194_19840	K0MWF6	4.89	2.19	4.56
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	*deoD*	BN194_02810	K0N1Z0	5.42	2.18	4.54
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	*dnaK*	BN194_17460	K0N5C7	4.63	2.15	4.44
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	*pcp*	BN194_01980	K0N4Y4	3.66	2.14	4.40
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		BN194_21400	K0N6R1	5.34	2.13	4.38
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	*deoB*	BN194_02800	K0N1N0	6.79	2.13	4.37
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	*serS*	BN194_20080	K0N9N4	5.32	2.13	4.37
GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	5.95	2.12	4.35
D-alanine--poly(phosphoribitol) ligase subunit 2 (EC 6.1.1.13) (D-alanyl carrier protein)	Cell wall biogenesis	*dltC*	BN194_08610	K0N361	2.38	2.11	4.32
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC_2*	BN194_24680	K0NAC2	6.91	2.11	4.32
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*glyS*	BN194_16950	K0N5D3	6.20	2.11	4.31

Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	*pgcA*	BN194_10370	K0N9K8	5.58	2.05	4.15
Uncharacterized protein	Unknown/uncharacterized		BN194_25890	K0MXR4	2.89	2.05	4.13
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_01410	K0N1L0	6.15	2.04	4.10
Penicillin acylase (EC 3.5.1.11)	Cell defense/detoxification		BN194_04910	K0N2B8	5.45	2.03	4.08
Uncharacterized protein	*Central glycolytic/intermediary pathways*		BN194_04970	K0N8A3	7.00	2.03	4.08
Probable phosphoketolase (EC 4.1.2.-)	*Central glycolytic/intermediary pathways*		BN194_28700	K0N8X7	3.81	2.02	4.06
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	*pepV*	BN194_08800	K0N324	5.07	2.01	4.04
Uncharacterized protein ynbB	Cell defense/detoxification	*ynbB*	BN194_18380	K0N9B7	5.91	1.98	3.95
Glycolate oxidase subunit glcD	General prediction only	*glcD*	BN194_24440	K0MXF3	2.06	1.95	3.87
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	*ppaC*	BN194_16110	K0N4Z4	5.98	1.94	3.84
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification		BN194_25280	K0NAG2	3.39	1.94	3.83
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatB*	BN194_11970	K0NA01	5.55	1.94	3.83
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	*eno*	BN194_11040	K0MU67	6.05	1.93	3.82
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	*gatA*	BN194_11960	K0N3Z6	6.26	1.92	3.78
Protein hit	tRNA aminoacyl synthesis	*hit*	BN194_19040	K0MWA8	5.07	1.92	3.77
Uncharacterized aminotransferase SSO0104 (EC 2.6.1.-)	*Amino acid-related metabolism*		BN194_27600	K0N8N4	6.43	1.91	3.76
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	*proC*	BN194_19900	K0N677	3.14	1.88	3.69
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	*pmi*	BN194_02920	K0N7U2	5.59	1.88	3.67
Predicted Zn-dependent peptidase	*Amino acid-related metabolism*		BN194_10020	K0N9H8	5.58	1.86	3.63
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatC*	BN194_11950	K0N436	4.64	1.86	3.63
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrD*	BN194_16440	K0MVL3	4.19	1.84	3.58
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	*pepDB*	BN194_21110	K0N678	5.95	1.84	3.58
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	5.97	1.83	3.55
Manganese transport system ATP-binding protein MntB	ABC-type transporter systems	*mntB*	BN194_25460	K0N7A8	1.05	1.78	3.44
Uncharacterized protein	Unknown/uncharacterized		BN194_29560	K0N8E9	1.87	1.76	3.38

Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	*iscS1*	BN194_14900	K0N4U8	4.98	1.72	3.29
Dihydrofolate reductase (EC 1.5.1.3)	Cofactor-related metabolism	*folA*	BN194_15810	K0N4W0	3.00	1.71	3.28
Uncharacterized protein	Unknown/uncharacterized		BN194_28350	K0N8V3	4.45	1.71	3.26
Uncharacterized zinc protease ymfH (EC 3.4.24.-)	Amino acid-related metabolism	*ymfH*	BN194_10030	K0N6V9	2.98	1.70	3.25
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	*yfeX*	BN194_07170	K0N8U9	3.97	1.69	3.23
GNAT family acetyltransferase	General prediction only		BN194_29620	K0NDL0	1.05	1.69	3.22
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	*hpt*	BN194_26470	K0NCR2	4.12	1.68	3.21
Histidinol-phosphatase	General prediction only		BN194_14010	K0N4F8	3.10	1.68	3.21
Putative tRNA-binding protein ytpR	General prediction only	*ytpR*	BN194_18970	K0NB80	5.13	1.68	3.20
Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	*fhs*	BN194_16520	K0NAT0	4.23	1.66	3.16
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	*asd*	BN194_01060	K0N1I5	4.69	1.63	3.10
Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	*rbsK*	BN194_03300	K0N1R2	4.72	1.63	3.09
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	*agaS*	BN194_02940	K0MSD9	5.58	1.62	3.08
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	*pepN*	BN194_05410	K0N2F5	5.68	1.62	3.07
Bifunctional protein BirA (EC 6.3.4.15)	Lipid-related metabolism	*birA*	BN194_08790	K0MTP3	4.01	1.61	3.04
Uncharacterized protein ybfG	General prediction only	*ybfG*	BN194_00330	K0N4B3	4.59	1.60	3.04
Zinc-transporting ATPase (EC 3.6.3.5)	Other transporter proteins	*zosA_2*	BN194_29430	K0NB79	4.41	1.60	3.04
L-sorbose 1-phosphate reductase (EC 1.1.1.-)	Carbohydrate-related metabolism	*sorE*	BN194_04300	K0N1W2	1.77	1.60	3.03
Uncharacterized protein	Unknown/uncharacterized		BN194_01870	K0N7D4	4.76	1.60	3.02
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*pip_2*	BN194_27140	K0MY30	4.42	1.58	3.00
LPXTG-motif cell wall anchor domain protein			BN194_26300	K0N883	1.22	1.58	2.99
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB_2*	BN194_29110	K0N8A4	4.56	1.58	2.98
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	*aldB*	BN194_20140	K0MWH5	3.47	1.56	2.95
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	2.95	1.56	2.95
Uncharacterized protein yaaQ	Unknown/uncharacterized	*yaaQ*	BN194_23940	K0MXD1	3.02	1.56	2.95

Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2_2,lacD*	BN194_27060	K0N7P0	5.85	1.55	2.94
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	Central glycolytic/intermediary pathways	*gap*	BN194_11010	K0N3R3	4.93	1.55	2.93
Uncharacterized protein yxkA	General prediction only	*yxkA*	BN194_27230	K0NAV1	4.75	1.53	2.90
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	*pta*	BN194_11340	K0MU95	5.80	1.52	2.88
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	*alsS*	BN194_20150	K0N695	3.97	1.52	2.86
Thioredoxin-like protein ytpP	Posttranslational modification	*ytpP*	BN194_18980	K0N9F1	3.58	1.49	2.81
Probable flavodoxin-1	Membrane bioenergetics	*ykuN_2*	BN194_12220	K0NA19	3.76	1.49	2.81
Putative secreted protein	cell wall biogenesis		BN194_02820	K0N7S8	2.66	1.49	2.81
tRNA pseudouridine synthase A (EC 5.4.99.12) (tRNA pseudouridine(38-40) synthase) (tRNA pseudouridylate synthase I) (tRNA-uridine isomerase I)	tRNA/Ribosome assembly/processing	*truA*	BN194_25910	K0N7E2	1.58	1.48	2.79
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	4.31	1.47	2.78
Uncharacterized protein yhfI	General prediction only	*yhfI*	BN194_19200	K0N627	4.43	1.47	2.77
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC*	BN194_00080	K0N486	4.79	1.47	2.77
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1_2*	BN194_12550	K0N496	3.22	1.46	2.75
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP_2, acpP*	BN194_22590	K0MX45	3.09	1.46	2.75
Uncharacterized protein	Unknown/uncharacterized		BN194_07460	K0N2W9	1.92	1.45	2.73
Uncharacterized protein ACIAD3023	Cell defense/detoxification		BN194_07010	K0N2T5	1.89	1.44	2.72
Uncharacterized protein	RNA degradation		BN194_11250	K0N3V2	2.86	1.42	2.67
Uncharacterized protein yghZ	General prediction only	*yghZ*	BN194_27510	K0N7U8	5.20	1.39	2.62
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	*proS*	BN194_17610	K0N5E2	6.17	1.38	2.60
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	*pycB*	BN194_20290	K0MWI8	1.04	1.38	2.60
Uncharacterized protein	Unknown/uncharacterized		BN194_01600	K0N1B9	2.25	1.37	2.59
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	*citD*	BN194_20330	K0N9Q5	3.23	1.37	2.59
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	*dhaK_2*	BN194_04980	K0N5Q3	3.88	1.35	2.55
Uncharacterized protein	Unknown/uncharacterized	*yvcC*	BN194_05260	K0N2E5	2.94	1.34	2.54
Uncharacterized protein YneR	General prediction only	*yneR*	BN194_18480	K0N9C1	2.13	1.34	2.54

NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	*npr*	BN194_04740	K0MSP8	3.65	1.34	2.53
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_07700	K0N2V5	1.33	1.34	2.53
Uncharacterized protein ykuJ	Unknown/uncharacterized	*ykuJ*	BN194_09100	K0N348	2.44	1.33	2.52
Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Phosphotransferase system, enzyme I)		*ptsI*	BN194_19410	K0N5T2	3.24	1.32	2.50
Probable phosphoketolase (EC 4.1.2.-)	Central glycolytic/intermediary pathways	*xpkA*	BN194_01710	K0N1M9	4.72	1.31	2.48
Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*leuS*	BN194_09210	K0N3A9	4.37	1.31	2.47
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC*	BN194_24670	K0NC50	4.58	1.29	2.45
Uncharacterized protein			BN194_19420	K0NB98	4.58	1.27	2.42
Esterase/lipase	General prediction only	*yneB*	BN194_20230	K0N9P7	3.75	1.27	2.41
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB*	BN194_21340	K0MWS0	3.45	1.26	2.40
Possible TrsG protein	Unknown/uncharacterized		BN194_00240	K0MRM8	3.92	1.26	2.39
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E_2,P100*	BN194_05160	K0N2D7	3.04	1.24	2.36
D-2-hydroxyacid dehydrogenase (EC 1.1.1.-)	General prediction only	*ddh*	BN194_16660	K0N557	2.79	1.24	2.36
UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	2.73	1.22	2.34
Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-)	Nucleic acid/nucleotide metabolism	*purK*	BN194_12510	K0N441	6.08	1.22	2.33
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	*ptsH*	BN194_19430	K0N9I2	4.66	1.21	2.32
Sorbose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*sorB_2*	BN194_29180	K0NB63	0.67	1.20	2.30
Zinc-type alcohol dehydrogenase-like protein SE_1777	General prediction only		BN194_07910	K0N329	3.48	1.15	2.23
Uncharacterized protein				K0N2Q1;K0MXJ1	3.55	1.14	2.20
Peptidase T (EC 3.-.-.-) (EC 3.4.11.-) (EC 3.4.11.4)	Amino acid-related metabolism	*pepT*	BN194_03110	K0N213	3.08	1.13	2.18
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	*glmM*	BN194_11550	K0N3Y7	4.64	1.12	2.17
Hydroxyacid oxidase (EC 1.1.3.15)	Central glycolytic/intermediary pathways	*haox*	BN194_24790	K0MXH5	5.42	1.11	2.16
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	*cysS*	BN194_24430	K0NAB2	3.76	1.11	2.15
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	*tpx*	BN194_08090	K0MTJ5	3.05	1.10	2.15
Sorbitol PTS, EIIA	Phosphotransferase systems		BN194_09940	K0MTX4	2.24	1.10	2.14
Cysteine desulfurase (EC 2.8.1.7)	Cofactor-related metabolism	*csd*	BN194_13790	K0MV25	5.14	1.08	2.11

Predicted hydrolase of the HAD superfamily	General prediction only	*mtlD*	BN194_30450	K0N9D4	2.61	1.07	2.10
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	*purA*	BN194_01160	K0N1J0	4.96	1.07	2.10
Mannose permease IID component	Phosphotransferase systems	*manZ_4*	BN194_04510	K0N287	1.55	1.06	2.09
Diaminopimelate decarboxylase (DAP decarboxylase) (DAPDC) (EC 4.1.1.20)	Amino acid-related metabolism	*lysA*	BN194_01030	K0N4I7	1.50	1.06	2.08
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	*pgk*	BN194_11020	K0N9R1	4.42	1.06	2.08
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB_2*	BN194_21770	K0NBN4	2.83	1.05	2.07
Oligoendopeptidase, pepF/M3 family	*Amino acid-related metabolism*		BN194_11580	K0N779	4.35	1.03	2.05
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	*ddl*	BN194_01390	K0MRY4	4.20	1.03	2.04
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E,P100*	BN194_02180	K0N513	4.51	0.99	1.98
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA_2*	BN194_29210	K0N8B2	4.42	0.98	1.97
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	*groS,grES*	BN194_23760	K0N700	3.55	0.97	1.96
Glutamate dehydrogenase	Amino acid-related metabolism	*gdh*	BN194_06980	K0N666	5.03	0.97	1.96
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*asnS*	BN194_16760	K0N569	4.56	0.96	1.95
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*yqeC*	BN194_02330	K0N532	0.65	0.95	1.93
Uncharacterized protein yqeY	Unknown/uncharacterized	*yqeY*	BN194_17040	K0MVR2	3.25	0.94	1.92
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	*tsf*	BN194_17670	K0NB01	3.39	0.93	1.91
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	*glyr1*	BN194_30100	K0N992	3.77	0.92	1.90
Alkyl hydroperoxide reductase subunit C (EC 1.11.1.15)	Cell defense/detoxification	*ahpC*	BN194_26250	K0N876	2.48	0.90	1.87
ABC-type phosphate/phosphonate transport system,periplasmic component	*ABC-type transporter systems*		BN194_25680	K0NAI1	5.29	0.89	1.85
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_2*	BN194_04490	K0MSM9	0.71	0.88	1.85
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE*	BN194_13710	K0N4D8	1.81	0.88	1.85
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		BN194_18780	K0N9E0	2.16	0.87	1.82
Thioredoxin	Posttranslational modification	*trxA_2*	BN194_08570	K0N975	3.36	0.83	1.78
Pyridoxine 5'-phosphate oxidase V related favin-nucleotide-binding protein	Cofactor-related metabolism		BN194_01900	K0N1E7	3.74	0.82	1.77

Dehydrogenase	General prediction only		BN194_24480	K0NAB4	1.78	0.81	1.75
Uncharacterized protein	Unknown/uncharacterized		BN194_23650	K0N7J8	3.07	0.80	1.74
Phosphonates import ATP-binding protein PhnC (EC 3.6.3.28)	ABC-type transporter systems	*phnC_2,phnC*	BN194_25690	K0MXP5	2.31	0.78	1.72
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	*glcK*	BN194_18420	K0NB57	3.98	0.78	1.72
Cold shock-like protein CspLA	Transcription-associated proteins	*cspLA*	BN194_12460	K0N438	1.14	0.75	1.68
Single-stranded DNA-binding protein (SSB)	DNA replication-related	*ssb*	BN194_00110	K0N1C2	2.08	0.73	1.66
Uncharacterized protein yjdJ	General prediction only	*yjdJ*	BN194_24650	K0N7R2	3.55	0.73	1.66
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	*yhaA*	BN194_30550	K0N9E4	2.71	0.72	1.65
Aldose 1-epimerase	*Central glycolytic/intermediary pathways*		BN194_16020	K0NAP4	2.91	0.69	1.61
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	*pepQ*	BN194_08740	K0MTP0	3.06	0.68	1.60
Xre-like DNA-binding protein	Transcriptional regulation		BN194_10050	K0N3E1	0.18	0.66	1.58
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	*htrA*	BN194_29460	K0N8D9	2.92	0.66	1.58
Methionyl-tRNA formyltransferase (EC 2.1.2.9)	Protein translation (initiation)	*fmt*	BN194_18060	K0N5J2	2.37	0.65	1.57
Transcriptional regulator lytR	Transcriptional regulation	*lytR*	BN194_02540	K0MS94	3.98	0.64	1.56
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	*ilvE*	BN194_21620	K0NBM4	5.10	0.63	1.55
Queuosine transporter QueT	General prediction only	*queT*	BN194_21930	K0NA07	0.14	0.60	1.51
Cold shock protein 1	Transcription-associated proteins	*csp*	BN194_06990	K0MT67	1.09	0.59	1.51
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	*cysK*	BN194_05520	K0N8E6	2.28	0.56	1.47
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA*	BN194_18520	K0NB62	2.79	0.55	1.46
UPF0237 protein BN194_09820	Unknown/uncharacterized		BN194_09820	K0N9F9	0.19	0.54	1.46
Uncharacterized protein	Unknown/uncharacterized		BN194_08270	K0N959	0.34	0.54	1.46
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*lacC*	BN194_07470	K0N8Y4	2.33	0.54	1.45
Uncharacterized protein ypuA	Unknown/uncharacterized	*ypuA*	BN194_27250	K0N8I3	1.80	0.54	1.45
Uncharacterized protein	Unknown/uncharacterized		BN194_05660	K0N2I2	0.84	0.52	1.44
tRNA-specific adenosine deaminase (EC 3.5.4.33)	tRNA/Ribosome assembly/processing	*tadA*	BN194_24000	K0N7M1	2.34	0.52	1.43
4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase) (EC 1.17.1.8)	Amino acid-related metabolism	*dapB*	BN194_01000	K0N166	0.26	0.51	1.42

Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ*	BN194_14610	K0N4K4	0.21	0.48	1.39
Uncharacterized protein	*ABC-type transporter systems*		BN194_21220	K0NBK2	1.59	0.48	1.39
Transcriptional regulator	*Posttranslational modification*		BN194_29310	K0N8C2	2.09	0.48	1.39
Guanine deaminase (EC 3.5.4.3)	Nucleic acid/nucleotide metabolism	*guaD*	BN194_13320	K0NA96	2.98	0.44	1.36
FMN-binding domain protein	General prediction only		BN194_24320	K0NC29	3.63	0.44	1.35
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO*	BN194_12030	K0N7B7	1.13	0.43	1.35
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*pheT*	BN194_18560	K0N5M4	2.48	0.43	1.34
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_3*	BN194_04780	K0N5N9	1.09	0.42	1.34
Uncharacterized protein yeaE	General prediction only	*yeaE*	BN194_07040	K0MT72	2.78	0.41	1.33
Uncharacterized protein	Unknown/uncharacterized		BN194_29450	K0N932	2.89	0.41	1.32
Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	*gntK*	BN194_02340	K0MS76	1.05	0.40	1.32
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_27170	K0NCZ6	1.97	0.38	1.30
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	*pheS*	BN194_18570	K0NB64	2.26	0.38	1.30
Alanine racemase (EC 5.1.1.1)	Amino acid-related metabolism	*alr*	BN194_26680	K0NAR1	2.73	0.37	1.29
Nod factor export ATP-binding protein I (EC 3.6.3.-)	ABC-type transporter systems	*nodI*	BN194_06850	K0N2J7	1.84	0.36	1.28
Endonuclease MutS2 (EC 3.1.-.-)	DNA repair/recombination	*mutS2*	BN194_08560	K0N359	0.11	0.36	1.28
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	*hisS*	BN194_17110	K0N5A0	4.09	0.36	1.28
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		BN194_24180	K0NAA2	1.81	0.35	1.28
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	*dnaN*	BN194_00020	K0N6S3	3.10	0.35	1.27
N5-carboxyaminoimidazole ribonucleotide mutase (N5-CAIR mutase) (EC 5.4.99.18) (5-(carboxyamino)imidazole ribonucleotide mutase)	Nucleic acid/nucleotide metabolism	*purE*	BN194_19380	K0N9H9	2.49	0.34	1.26
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_3*	BN194_29920	K0NDN0	1.18	0.31	1.24
Uncharacterized protein yitL	General prediction only	*yitL*	BN194_15600	K0N505	0.07	0.30	1.23
NADH-dependent butanol dehydrogenase A (EC 1.1.1.-)	Carbohydrate-related metabolism	*bdhA*	BN194_22640	K0MX50	1.65	0.29	1.22
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	*dacA*	BN194_02140	K0MS53	1.45	0.29	1.22
Cytochrome d ubiquinol oxidase subunit 1 (EC 1.10.3.-)	Membrane bioenergetics	*cydA_2*	BN194_23410	K0N6Y2	1.05	0.29	1.22

Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	0.85	0.28	1.21
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	*trpS*	BN194_27360	K0N7S4	1.93	0.27	1.21
Dumpy	Cell surface proteins/internalins	*dp*	BN194_05390	K0MSV0	0.91	0.27	1.21
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	1.71	0.26	1.20
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh*	BN194_26560	K0N7J5	1.20	0.25	1.19
Monooxygenase	General prediction only		BN194_07600	K0N2U5	1.54	0.25	1.19
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	1.01	0.25	1.19
Coenzyme A biosynthesis bifunctional protein CoaBC (EC 4.1.1.36) (EC 6.3.2.5)		*coaBC*	BN194_18090	K0MW49	0.18	0.25	1.19
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_2*	BN194_29910	K0N8I1	0.90	0.23	1.18
Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	*bceA_2*	BN194_21230	K0N9X1	2.16	0.23	1.17
Oligoendopeptidase F	Amino acid-related metabolism	*yjbG_2*	BN194_08130	K0N6H7	2.07	0.23	1.17
Uncharacterized protein			BN194_02080	K0N4Z7	0.27	0.22	1.17
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	*murF*	BN194_26720	K0NCU5	0.44	0.21	1.16
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	*agl*	BN194_27950	K0N8T1	1.73	0.21	1.16
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	2.00	0.21	1.16
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	1.85	0.20	1.15
Hydrolase of the alpha/beta superfamily	General prediction only		BN194_08240	K0MTK6	0.65	0.19	1.14
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	0.96	0.18	1.14
Putative HAD-hydrolase yfnB (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yfnB*	BN194_08780	K0N6M1	0.05	0.18	1.13
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	*fabF*	BN194_22540	K0MX40	0.51	0.18	1.13
Surface antigen	Cell wall biogenesis		BN194_21500	K0N6S2	0.53	0.18	1.13
Xanthine permease	Other transporter proteins	*pbuX*	BN194_12500	K0N490	0.08	0.18	1.13
Signal peptidase I (EC 3.4.21.89)	Protein export	*lepB*	BN194_02610	K0N1V9	1.69	0.18	1.13
Uncharacterized oxidoreductase YbdH (EC 1.1.-.-)	Carbohydrate-related metabolism	*ybdH*	BN194_30540	K0MYX0	1.26	0.17	1.12
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*nagA*	BN194_19890	K0MWF9	1.21	0.17	1.12
ABC transporter, ATP-binding protein	*Cell surface proteins/internalins*		BN194_15700	K0N514	0.09	0.16	1.12

Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	*mtlF*	BN194_30410	K0N8N0	0.51	0.15	1.11
Uncharacterized amino acid permease YfnA	Other transporter proteins	*yfnA*	BN194_06960	K0N2T0	0.12	0.15	1.11
Zinc metalloprotease (EC 3.4.24.-)	General prediction only	*eep*	BN194_17620	K0NAZ9	0.54	0.14	1.10
4-hydroxy-tetrahydrodipicolinate synthase (HTPA synthase) (EC 4.3.3.7)	Amino acid-related metabolism	*dapA*	BN194_01010	K0N1I2	0.37	0.12	1.09
ABC-type antimicrobial peptide transport system,ATPase component	*ABC-type transporter systems*		BN194_19940	K0MWG2	0.56	0.12	1.09
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	*yjlD*	BN194_24330	K0NAA7	1.72	0.12	1.09
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	*mnmA*	BN194_14930	K0N844	0.55	0.12	1.09
Transcriptional regulator lytR	Transcriptional regulation	*lytR_4*	BN194_23780	K0NA85	0.35	0.10	1.07
Uncharacterized protein	Unknown/uncharacterized		BN194_20190	K0MWI0	0.76	0.10	1.07
Uncharacterized ABC transporter ATP-binding protein TM_0288	*ABC-type transporter systems*		BN194_06900	K0N2K4	0.05	0.08	1.06
Uncharacterized protein	Unknown/uncharacterized		BN194_19210	K0N5R7	0.22	0.07	1.05
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	*atpA*	BN194_13600	K0N4K1	1.45	0.06	1.04
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	0.31	0.05	1.03
Sorbose permease IIC component	Phosphotransferase systems	*sorA_4*	BN194_29710	K0N8G4	0.13	0.04	1.03
UPF0039 protein SAR1027	General prediction only		BN194_19510	K0N5U0	0.02	0.03	1.02
Uncharacterized protein ywfO	General prediction only	*ywfO*	BN194_26840	K0MXZ5	0.12	0.02	1.01
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE*	BN194_02970	K0N7U7	0.05	0.02	1.01
Uncharacterized protein	Unknown/uncharacterized		BN194_02470	K0N7L7	0.02	0.01	1.01
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ*	BN194_11360	K0N3U2	0.02	0.01	1.01
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*fruK*	BN194_15420	K0NAJ6	0.01	0.00	1.00
Hypothetical lipoprotein	Unknown/uncharacterized		BN194_12440	K0MUR1	0.00	-0.01	-1.01
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	*ykwC*	BN194_02520	K0N7M3	0.04	-0.01	-1.01
Xanthine/uracil/vitamin C permease	Other transporter proteins		BN194_01470	K0N796	0.10	-0.03	-1.02
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	*yhfP*	BN194_07740	K0MTE1	0.09	-0.03	-1.02
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	*patB_2*	BN194_09790	K0MTW3	0.24	-0.04	-1.03
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA*	BN194_09090	K0MTR3	0.11	-0.04	-1.03

Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*gmuB*	BN194_23840	K0MXC7	0.17	-0.06	-1.04
Transcriptional regulator lytR	Transcriptional regulation	*lytR_3*	BN194_21700	K0N6U3	2.42	-0.06	-1.04
Nucleoid-associated protein BN194_23980	General prediction only		BN194_23980	K0NA95	0.15	-0.07	-1.05
Uncharacterized MscS family protein YkuT	Other transporter proteins	*ykuT*	BN194_08700	K0N322	0.05	-0.07	-1.05
Uncharacterized protein yaaA	General prediction only	*yaaA*	BN194_00040	K0MRL5	0.03	-0.07	-1.05
Arginine repressor	Transcriptional regulation	*argR1,argR*	BN194_19110	K0N5R1	0.02	-0.07	-1.05
Probable calcium-transporting ATPase (EC 3.6.3.8)	Other transporter proteins	*pacL*	BN194_11490	K0MUB1	0.10	-0.08	-1.05
Mannose permease IID component	Phosphotransferase systems	*manZ_9*	BN194_29700	K0N954	0.78	-0.08	-1.06
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA*	BN194_05120	K0N8B5	0.30	-0.08	-1.06
Mannose permease IID component	Phosphotransferase systems	*manZ*	BN194_02990	K0MSE1	0.62	-0.09	-1.06
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	*aspS*	BN194_17100	K0N5F3	0.54	-0.09	-1.06
SPFH/Band 7/PHB domain protein	Unknown/uncharacterized		BN194_29820	K0NDM1	0.06	-0.10	-1.07
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	*rny*	BN194_10100	K0N3E5	0.06	-0.10	-1.07
Uncharacterized protein	Unknown/uncharacterized		BN194_01790	K0MS25	0.02	-0.11	-1.08
ABC transporter glutamine-binding protein glnH	ABC-type transporter systems	*glnH*	BN194_21430	K0N9Y4	0.64	-0.11	-1.08
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_19800	K0N670	0.05	-0.11	-1.08
Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	*ADH2*	BN194_08400	K0N307	0.18	-0.11	-1.08
Cell division protein FtsX	Cytokinesis	*ftsX*	BN194_10200	K0N3G0	0.85	-0.12	-1.09
Membrane protein	Unknown/uncharacterized		BN194_22700	K0N7C6	0.08	-0.12	-1.09
Uncharacterized ABC transporter ATP-binding protein YfiB	ABC-type transporter systems	*yfiB*	BN194_06890	K0MT56	0.64	-0.13	-1.10
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	*atpD*	BN194_13620	K0NAB3	1.64	-0.13	-1.10
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	*rbfA*	BN194_17540	K0MVV7	0.57	-0.13	-1.10
Cell division ATP-binding protein FtsE	Cytokinesis	*ftsE*	BN194_10190	K0MTZ2	0.60	-0.15	-1.11
Manganese ABC transporter substrate-binding lipoprotein	ABC-type transporter systems	*fimA*	BN194_25450	K0N7Y2	0.13	-0.16	-1.11
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdE2*	BN194_16600	K0N5A1	1.41	-0.16	-1.12
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	*garB*	BN194_27400	K0N8K3	0.99	-0.16	-1.12
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdF*	BN194_16610	K0N552	2.47	-0.16	-1.12

Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	*accB*	BN194_22530	K0NA35	0.23	-0.17	-1.12
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	*rpe*	BN194_18000	K0N5T1	0.07	-0.17	-1.12
Uncharacterized ABC transporter ATP-binding protein YdbJ	ABC-type transporter systems	*ydbJ*	BN194_24600	K0N7Q8	0.94	-0.17	-1.13
Uncharacterized protein	Unknown/uncharacterized		BN194_15850	K0N527	0.71	-0.18	-1.13
Inner membrane amino-acid ABC transporter permease protein yecS	ABC-type transporter systems	*yecS_3*	BN194_29780	K0NB99	0.14	-0.20	-1.15
Protein LemA	Unknown/uncharacterized	*lemA*	BN194_27350	K0N8J7	2.19	-0.20	-1.15
Penicillin-binding protein 1A	Cell wall biogenesis	*ponA*	BN194_16720	K0NAU3	2.07	-0.20	-1.15
Uridine kinase (EC 2.7.1.48)		*udk*	BN194_18540	K0MW76	0.55	-0.21	-1.15
Maltose ABC transporter, periplasmic maltose-binding protein	*ABC-type transporter systems*		BN194_11200	K0N3U4	1.15	-0.22	-1.17
Uncharacterized protein	General prediction only		BN194_30000	K0N979	0.81	-0.23	-1.17
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1*	BN194_09110	K0N399	3.47	-0.24	-1.18
PTS family mannose/fructose/sorbose porter component IIC	Phosphotransferase systems		BN194_02980	K0N5D0	1.42	-0.25	-1.19
Predicted ORF			BN194_P0560	K0MZ29	0.09	-0.25	-1.19
HTH-type transcriptional regulator galR	Transcriptional regulation	*galR*	BN194_03780	K0N5G9	0.22	-0.26	-1.19
Penicillin-binding protein 3	Cell wall biogenesis	*pbpC*	BN194_03320	K0N7W9	0.68	-0.26	-1.19
Uncharacterized protein	Unknown/uncharacterized		BN194_23630	K0NA78	0.37	-0.26	-1.20
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.-)	Lipid-related metabolism	*plsC*	BN194_17710	K0N5F1	0.10	-0.27	-1.20
Uncharacterized protein yuaG	Unknown/uncharacterized	*yuaG*	BN194_22920	K0NBV0	0.66	-0.27	-1.20
Putative N-acetylmuramoyl-L-alanine amidase YrvJ (EC 3.5.1.28)	Cytokinesis	*yrvJ*	BN194_17200	K0N5G4	0.12	-0.28	-1.22
DltD protein	Cell wall biogenesis		BN194_08620	K0N978	2.30	-0.29	-1.22
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	Nucleic acid/nucleotide metabolism	*tmk*	BN194_23950	K0N7L9	1.50	-0.29	-1.22
Phosphohydrolase (MutT/nudix family protein)	General prediction only		BN194_27160	K0N7P9	0.13	-0.30	-1.23
Uncharacterized lipoprotein yerH	General prediction only	*yerH*	BN194_11940	K0MUH2	1.97	-0.30	-1.23
Calcium-transporting ATPase lmo0841 (EC 3.6.3.8)	Other transporter proteins		BN194_19820	K0NBC5	3.11	-0.31	-1.24
Uncharacterized glycosyltransferase HI_0868 (EC 2.4.-.-)	Cell wall biogenesis		BN194_02410	K0N1U3	0.69	-0.32	-1.25
Uncharacterized protein	Unknown/uncharacterized		BN194_23540	K0MXB4	0.74	-0.33	-1.25
UPF0092 membrane protein yrbF	Protein export	*yrbF*	BN194_08390	K0MTL6	0.66	-0.33	-1.26

Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_4*	BN194_29900	K0N971	0.82	-0.34	-1.26
Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase)	Cofactor-related metabolism	*coaE*	BN194_18910	K0N5P8	1.26	-0.34	-1.27
Uncharacterized protein	Unknown/uncharacterized		BN194_27530	K0NAX5	0.69	-0.34	-1.27
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	0.19	-0.37	-1.29
Uncharacterized protein	Unknown/uncharacterized		BN194_12100	K0N456	0.53	-0.37	-1.29
Protein QmcA	Unknown/uncharacterized	*qmcA*	BN194_12070	K0NA10	1.58	-0.37	-1.30
Integral membrane protein	Unknown/uncharacterized		BN194_02590	K0MS97	0.51	-0.39	-1.31
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	*act*	BN194_16090	K0MVI3	0.56	-0.39	-1.31
Elongation factor P	Protein translation (elongation)	*efp*	BN194_18240	K0MW57	0.81	-0.39	-1.31
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	*tuf*	BN194_15310	K0N4R1	1.35	-0.40	-1.32
ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	*atpF*	BN194_13580	K0N7S9	1.12	-0.40	-1.32
Ribonuclease H (EC 3.1.26.4)	DNA repair/recombination	*rnhA*	BN194_27580	K0NAX8	0.54	-0.40	-1.32
Uncharacterized protein	Unknown/uncharacterized		BN194_20070	K0NBE0	3.15	-0.40	-1.32
D-ribose-binding protein	ABC-type transporter systems	*rbsB*	BN194_03290	K0MSF6	0.14	-0.40	-1.32
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	*coaD*	BN194_15200	K0N4X3	0.38	-0.41	-1.32
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03940	K0MSJ3	0.33	-0.41	-1.33
Nuclease sbcCD subunit D	DNA repair/recombination	*sbcD*	BN194_07530	K0N6B1	0.14	-0.43	-1.34
Transcription-repair-coupling factor (TRCF) (EC 3.6.4.-)	DNA repair/recombination	*mfd*	BN194_26540	K0MXW9	0.17	-0.44	-1.36
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25510	K0N7B2	2.76	-0.45	-1.36
Uncharacterized protein	Unknown/uncharacterized		BN194_01760	K0N1N3	0.42	-0.45	-1.36
Protein translocase subunit SecY	Protein export	*secY*	BN194_26020	K0NCJ6	0.78	-0.47	-1.39
Serine/threonine-protein kinase PrkC (EC 2.7.11.1)	Posttranslational modification	*prkC*	BN194_18020	K0NB40	0.42	-0.47	-1.39
Putative transcriptional regulator, MarR family	Transcriptional regulation		BN194_27490	K0MY64	0.40	-0.48	-1.39
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	*msrA_2,msrA*	BN194_15860	K0N4W6	0.67	-0.48	-1.40
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase 2 (EC 5.4.2.1)	Central glycolytic/intermediary pathways	*gpmA2_2*	BN194_27560	K0N7W0	1.59	-0.50	-1.41

Putative tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207) (tRNA (cytidine/uridine-2'-O-)-methyltransferase)	*tRNA/Ribosome assembly/processing*		BN194_09990	K0MTX9	1.94	-0.50	-1.42
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB1,pstB*	BN194_10270	K0N9K1	0.91	-0.50	-1.42
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	1.62	-0.50	-1.42
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_3*	BN194_21440	K0MWS9	1.92	-0.51	-1.42
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	*def*	BN194_15060	K0N4N6	2.56	-0.51	-1.42
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF*	BN194_08770	K0N987	1.65	-0.51	-1.43
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	*ftsH*	BN194_26460	K0N7I8	4.26	-0.51	-1.43
Uncharacterized protein ypmR	General prediction only	*ypmR*	BN194_15840	K0MVG3	0.92	-0.52	-1.43
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	3.10	-0.52	-1.43
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	*trxB*	BN194_10360	K0N3L1	1.84	-0.54	-1.45
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	*maa*	BN194_30010	K0N8I9	2.47	-0.54	-1.46
Glycine betaine/carnitine/choline-binding protein OpuCC	ABC-type transporter systems	*opuCC*	BN194_00670	K0N6Z3	2.76	-0.55	-1.46
Uncharacterized protein ytxK	DNA repair/recombination	*ytxK*	BN194_11680	K0N791	2.49	-0.55	-1.46
Uncharacterized protein	Unknown/uncharacterized		BN194_11890	K0MUG0	3.28	-0.55	-1.47
Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	*Steap4*	BN194_01990	K0MS41	2.21	-0.56	-1.47
Lipopolysaccharide synthesis sugar transferase	Cell wall biogenesis		BN194_21390	K0MWS4	1.87	-0.56	-1.48
50S ribosomal protein L32	Ribosomal proteins	*rpmF*	BN194_15510	K0N4T0	0.30	-0.56	-1.48
Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	0.23	-0.58	-1.49
Uncharacterized protein RP368	*ABC-type transporter systems*		BN194_07720	K0N914	0.21	-0.58	-1.50
Glycosyltransferase	Cell wall biogenesis		BN194_09050	K0N346	0.29	-0.58	-1.50
Probable cation-transporting ATPase exp7 (EC 3.6.3.-)	Other transporter proteins	*exp7*	BN194_08170	K0N955	1.39	-0.59	-1.50
Guanylate kinase (EC 2.7.4.8)	Nucleic acid/nucleotide metabolism	*gmk_2*	BN194_21480	K0N9Y7	1.34	-0.59	-1.51
Probable dipeptidase A (EC 3.4.-.-)	Amino acid-related metabolism	*pepDA*	BN194_00410	K0N1E0	2.42	-0.59	-1.51
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_2*	BN194_20600	K0N6C6	0.44	-0.60	-1.52
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	*mhqA_3*	BN194_18760	K0N5N7	2.29	-0.61	-1.53
ABC-type Na+ efflux pump permease component-like protein	*ABC-type transporter systems*		BN194_11370	K0N9U5	0.32	-0.61	-1.53

Transcriptional repressor smtB homolog	Transcriptional regulation	*ziaR*	BN194_01180	K0N4L0	0.35	-0.61	-1.53
Penicillin-binding protein 2B	Cytokinesis	*pbpB*	BN194_14700	K0N4S9	1.58	-0.62	-1.53
Sortase	Cell wall biogenesis		BN194_22780	K0NA48	2.50	-0.62	-1.53
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*ileS*	BN194_14810	K0N4L9	3.61	-0.62	-1.53
Putative nrdI-like protein	*Nucleic acid/nucleotide metabolism*		BN194_08250	K0N300	2.16	-0.62	-1.54
MarR family transcriptional regulator	Transcriptional regulation		BN194_22610	K0N6N9	0.27	-0.63	-1.55
Uncharacterized RNA pseudouridine synthase YhcT (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*yhcT_2*	BN194_20220	K0NBE7	0.51	-0.64	-1.55
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP*	BN194_08180	K0N6I0	3.05	-0.64	-1.55
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	*msmK*	BN194_11180	K0N747	0.39	-0.64	-1.56
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	2.96	-0.64	-1.56
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_29810	K0N8H4	2.96	-0.64	-1.56
Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		BN194_20000	K0N684	4.72	-0.65	-1.57
Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (EC 5.3.3.2) (Isopentenyl diphosphate:dimethylallyl diphosphate isomerase) (Isopentenyl pyrophosphate isomerase) (Type 2 isopentenyl diphosphate isomerase)	Lipid-related metabolism	*fni*	BN194_16840	K0MVP7	0.50	-0.66	-1.58
UPF0755 protein yrrL	Unknown/uncharacterized	*yrrL*	BN194_18550	K0N5W7	2.19	-0.66	-1.58
Ribosome-binding ATPase YchF	Protein translation (peptide release)	*engD,ychF*	BN194_02070	K0N7F7	2.01	-0.68	-1.60
Predicted pyrophosphatase	General prediction only		BN194_15360	K0N4R6	2.12	-0.68	-1.60
Uncharacterized protein	Unknown/uncharacterized		BN194_12200	K0N464	0.41	-0.68	-1.60
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*manX_5*	BN194_29720	K0NDL4	2.32	-0.69	-1.61
TPR repeat-containing protein ypiA	Unknown/uncharacterized	*ypiA*	BN194_15750	K0N517	3.12	-0.70	-1.63
Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	*ptp3*	BN194_23520	K0NBX6	4.16	-0.71	-1.64
Glycosyl transferase family 2	Cell wall biogenesis		BN194_02460	K0N1U7	0.33	-0.72	-1.65
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF*	BN194_17910	K0N5I3	3.07	-0.73	-1.65
Uncharacterized protein			BN194_07360	K0N2W3	1.78	-0.73	-1.66
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA*	BN194_11290	K0MU90	3.03	-0.74	-1.67

Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	*fbp*	BN194_21660	K0N6C3	0.79	-0.76	-1.69
Uncharacterized protein	Unknown/uncharacterized		BN194_08020	K0N947	2.27	-0.76	-1.70
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	*valS*	BN194_14510	K0N4J6	5.00	-0.77	-1.70
Acid shock protein	Protein folding/turnover		BN194_29440	K0MYM2	2.78	-0.77	-1.70
Septum site-determining protein DivIVA	Cytokinesis	*divIVA*	BN194_14800	K0N4T8	3.41	-0.77	-1.70
Phosphate-binding protein pstS 1	ABC-type transporter systems	*pstS1*	BN194_10240	K0MTZ5	0.38	-0.77	-1.71
Ribosomal protein L11 methyltransferase (L11 Mtase) (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*prmA*	BN194_17260	K0N5B0	1.07	-0.77	-1.71
D-lactate dehydrogenase (EC 1.1.1.28)	Carbohydrate-related metabolism	*dld*	BN194_06590	K0MT28	1.87	-0.77	-1.71
Glycerol-3-phosphate ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_11260	K0N3T6	4.18	-0.77	-1.71
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI_2*	BN194_16210	K0N508	4.00	-0.78	-1.72
Predicted acetyltransferase			BN194_11820	K0N9Y9	3.49	-0.79	-1.72
41 kDa protein		*repA*	BN194_P0550	K0NBI6	1.53	-0.79	-1.73
Glucose 1-dehydrogenase 2 (EC 1.1.1.47)	Central glycolytic/intermediary pathways	*gdhII*	BN194_23130	K0NA64	3.47	-0.79	-1.73
Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	General prediction only	*yqiG*	BN194_25330	K0NAG4	2.48	-0.80	-1.74
Uncharacterized protein yqgF	Cell wall biogenesis	*yqgF*	BN194_18440	K0MW71	3.92	-0.80	-1.74
NifU-like protein	Cofactor-related metabolism	*nifU*	BN194_13800	K0N4L4	0.51	-0.81	-1.75
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	2.35	-0.81	-1.75
Putative beta-phosphoglucomutase (EC 5.4.2.6)	Central glycolytic/intermediary pathways	*yvdM*	BN194_11170	K0N9S7	0.53	-0.81	-1.75
UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	4.42	-0.81	-1.76
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*rluB*	BN194_15650	K0N509	0.53	-0.82	-1.76
Cell shape-determining protein MreC (Cell shape protein MreC)	Cytokinesis	*mreC*	BN194_14560	K0N4K0	3.93	-0.82	-1.76
Transaldolase (EC 2.2.1.2)	Central glycolytic/intermediary pathways	*fsa*	BN194_28440	K0MYF0	1.09	-0.82	-1.76
Acylphosphatase	Carbohydrate-related metabolism	*acyP*	BN194_18620	K0NB65	2.95	-0.82	-1.76
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*gnd*	BN194_18660	K0N5N2	4.48	-0.83	-1.78

Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD*	BN194_17920	K0NB35	3.65	-0.87	-1.82
Uncharacterized protein	General prediction only		BN194_21910	K0N6F1	2.99	-0.88	-1.84
Transport protein	Other transporter proteins		BN194_00630	K0N4D9	1.51	-0.88	-1.84
Glycosyl transferase family protein	Cell wall biogenesis		BN194_02420	K0N7L2	2.21	-0.88	-1.84
Folate transporter FolT	Unknown/uncharacterized	*folT*	BN194_23890	K0MXC9	1.93	-0.90	-1.87
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB*	BN194_17900	K0N5S3	0.63	-0.90	-1.87
Uncharacterized protein yqhL	General prediction only	*yqhL*	BN194_18410	K0N5L5	3.31	-0.91	-1.87
Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	Nucleic acid/nucleotide metabolism	*purD*	BN194_19290	K0MWC4	3.77	-0.91	-1.88
Uncharacterized protein	General prediction only		BN194_17420	K0NAY8	1.74	-0.91	-1.88
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	*thiD_2*	BN194_07650	K0N2U9	3.37	-0.91	-1.88
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	*atpG*	BN194_13610	K0N4D3	3.30	-0.91	-1.88
Hex regulon repressor	Transcriptional regulation		BN194_02320	K0N7J9	1.21	-0.92	-1.89
Exopolyphosphatase	Membrane bioenergetics		BN194_27280	K0NAV4	0.85	-0.93	-1.90
Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	Carbohydrate-related metabolism	*scrB*	BN194_22440	K0MX27	0.56	-0.93	-1.90
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	*hmgCS1*	BN194_19680	K0N9K3	2.26	-0.93	-1.90
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC_2*	BN194_20620	K0NBH0	0.66	-0.93	-1.91
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ_2*	BN194_20470	K0NBG3	1.02	-0.94	-1.92
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA1,gpmA*	BN194_24750	K0N7R7	0.50	-0.94	-1.92
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	*pflB*	BN194_16080	K0N8I5	1.07	-0.95	-1.93
Glycine betaine/carnitine/choline transport ATP-binding protein OpuCA	ABC-type transporter systems	*opuCA*	BN194_00680	K0N4E4	3.77	-0.96	-1.94
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	3.56	-0.96	-1.94
Uncharacterized protein	Unknown/uncharacterized		BN194_15540	K0MVD8	1.52	-0.96	-1.95
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_02890	K0MSD4	2.25	-0.96	-1.95
Double-stranded beta-helix related protein	Transcriptional regulation		BN194_11420	K0N9U8	0.67	-0.96	-1.95
Putative integral membrane protein	Unknown/uncharacterized		BN194_01660	K0N1M7	0.16	-0.97	-1.96

S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	*metK*	BN194_09150	K0N352	4.93	-0.98	-1.97
Kinase, putative	General prediction only		BN194_29890	K0MYR0	2.45	-0.98	-1.97
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	*glgC*	BN194_21600	K0N6T3	0.72	-0.98	-1.97
Septum formation inhibitor MinC, C-terminal domain family	Cytokinesis	*minC*	BN194_14580	K0N805	4.12	-0.98	-1.97
Uncharacterized protein	Cell wall biogenesis		BN194_21890	K0MWX1	1.93	-1.00	-2.00
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	*dltA*	BN194_08590	K0MTN0	3.08	-1.00	-2.00
tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA (guanine(46)-N(7))-methyltransferase) (tRNA(m7G46)-methyltransferase)	tRNA/Ribosome assembly/processing	*trmB*	BN194_19000	K0N606	1.01	-1.01	-2.01
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC*	BN194_17890	K0MW34	2.99	-1.02	-2.02
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA_2,ackA*	BN194_23060	K0N6W4	1.94	-1.02	-2.03
Uncharacterized peptidase yqhT (EC 3.4.-.-)	Amino acid-related metabolism	*yqhT*	BN194_18260	K0N5K4	3.87	-1.03	-2.04
Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (EC 2.7.7.12) (UDP-glucose--hexose-1-phosphate uridylyltransferase)		*galT*	BN194_07370	K0N8X1	1.55	-1.03	-2.05
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA_2, potA*	BN194_11430	K0N765	2.96	-1.04	-2.06
Oligoendopeptidase F homolog (EC 3.4.24.-)	Amino acid-related metabolism	*yjbG*	BN194_02530	K0N560	4.64	-1.05	-2.07
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ysgA*	BN194_18610	K0N5M8	1.43	-1.05	-2.07
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	*dkgB*	BN194_08260	K0N347	2.88	-1.06	-2.09
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	*metG*	BN194_27130	K0NAU5	4.61	-1.06	-2.09
Uncharacterized protein MJ1445	General prediction only		BN194_08880	K0N6M7	0.69	-1.07	-2.10
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	*atpH*	BN194_13590	K0MV16	3.08	-1.08	-2.11
Anaerobic ribonucleoside-triphosphate reductase-activating protein (EC 1.97.1.-)	Nucleic acid/nucleotide metabolism	*nrdG*	BN194_19270	K0NB93	0.65	-1.08	-2.12
Fructoselysine kinase (EC 2.7.1.-)	Carbohydrate-related metabolism	*frlD*	BN194_22240	K0MX05	3.23	-1.08	-2.12
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA*	BN194_17880	K0N983	3.52	-1.09	-2.12
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE*	BN194_01720	K0N7C1	1.83	-1.09	-2.13
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	1.66	-1.09	-2.13
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_3*	BN194_14020	K0NAD1	1.04	-1.09	-2.13

NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	4.98	-1.11	-2.16
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	*pdhC*	BN194_15100	K0N4W5	3.87	-1.12	-2.17
Membrane protein insertase YidC 1	Protein export	*yidC1*	BN194_18630	K0N9D1	0.98	-1.12	-2.17
Exodeoxyribonuclease 7 small subunit (EC 3.1.11.6) (Exodeoxyribonuclease VII small subunit)	DNA repair/recombination	*xseB*	BN194_18190	K0MW55	2.96	-1.12	-2.17
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)		*accC*	BN194_22510	K0N6M5	0.42	-1.13	-2.18
Acyl-ACP thioesterase	Lipid-related metabolism		BN194_23910	K0N709	3.69	-1.13	-2.19
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	*cmk*	BN194_15710	K0N4V1	4.40	-1.14	-2.21
NAD kinase (EC 2.7.1.23) (ATP-dependent NAD kinase)		*nadK*	ppnK	K0N6U5	0.38	-1.15	-2.22
Transcriptional regulator, PadR-like family	Transcriptional regulation		BN194_26580	K0NAQ3	0.69	-1.15	-2.22
Gluconate 5-dehydrogenase (EC 1.1.1.69)	General prediction only	*idnO*	BN194_08150	K0N2Z5	0.85	-1.16	-2.23
Spermidine/putrescine-binding periplasmic protein	ABC-type transporter systems	*potD*	BN194_11460	K0N3U9	1.34	-1.16	-2.24
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB_2*	BN194_20630	K0N9S5	0.76	-1.17	-2.25
YbbR-like domain-containing protein ybbR	Unknown/uncharacterized	*ybbR*	BN194_11540	K0MUB6	1.39	-1.18	-2.27
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF_2*	BN194_20590	K0MWL1	2.10	-1.19	-2.28
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	*ispA*	BN194_18180	K0N9A2	1.15	-1.22	-2.32
Uncharacterized protein	General prediction only	*gpm1*	BN194_13960	K0N4F5	2.41	-1.22	-2.33
Uncharacterized protein	Unknown/uncharacterized		BN194_16650	K0N5A4	0.43	-1.25	-2.38
Uncharacterized protein	Unknown/uncharacterized		BN194_20720	K0NBH5	3.75	-1.25	-2.38
Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	DNA repair/recombination	*recJ*	BN194_17390	K0MVT7	0.68	-1.25	-2.38
GCN5-related N-acetyltransferase	General prediction only		BN194_19760	K0N5W1	1.70	-1.25	-2.38
Large-conductance mechanosensitive channel	Other transporter proteins	*mscL*	BN194_26890	K0MY02	2.71	-1.26	-2.39
Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	*aspC*	BN194_16770	K0NAU6	4.23	-1.26	-2.40
50S ribosomal protein L7/L12	Ribosomal proteins	*rplL*	BN194_24080	K0NA98	3.48	-1.27	-2.42
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	*prsA*	BN194_19060	K0N5Q8	4.27	-1.27	-2.42
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*fruA_3*	BN194_15410	K0N4S1	0.57	-1.28	-2.43
Uncharacterized protein	Unknown/uncharacterized		BN194_21450	K0N6R7	4.12	-1.29	-2.44
Transcriptional regulator GltC	Transcriptional regulation	*nac*	BN194_16620	K0NAT7	1.78	-1.29	-2.45

Uncharacterized metallophosphoesterase yunD	Nucleic acid/nucleotide metabolism	*yunD*	BN194_08890	K0MTQ0	2.99	-1.30	-2.46
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	*citX*	BN194_20300	K0N6A3	4.19	-1.31	-2.48
Cof protein	General prediction only		BN194_12010	K0N401	0.68	-1.32	-2.49
Carboxy-terminal processing protease CtpA (EC 3.4.21.102)	Protein folding/turnover	*ctpA*	BN194_15880	K0N8G1	3.29	-1.32	-2.49
Lactose phosphotransferase system repressor	Transcriptional regulation	*lacR*	BN194_07510	K0N2X5	0.70	-1.32	-2.50
Cell growth regulatory protein	*IS elements/foreign DNA defense*		BN194_00940	K0MRU4	1.07	-1.32	-2.50
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	*nusB*	BN194_18220	K0NB49	3.63	-1.33	-2.51
Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	*adk*	BN194_26010	K0N7F0	3.58	-1.33	-2.52
Putative RNA-binding protein ylmH	General prediction only	*ylmH*	BN194_14790	K0MV84	0.64	-1.33	-2.52
Uncharacterized protein	Unknown/uncharacterized		BN194_05550	K0N257	0.80	-1.34	-2.53
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	*sph*	BN194_04930	K0N5Q0	4.30	-1.34	-2.53
Ribosomal RNA small subunit methyltransferase F (EC 2.1.1.178)	tRNA/Ribosome assembly/processing	*rsmF*	BN194_16850	K0N5C0	1.07	-1.37	-2.58
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yutF*	BN194_08910	K0N383	5.49	-1.37	-2.59
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_4*	BN194_22020	K0NBQ1	4.69	-1.38	-2.60
Nucleoid occlusion protein	Cytokinesis	*noc*	BN194_02030	K0N4Z1	1.01	-1.40	-2.63
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25570	K0NCD4	2.04	-1.40	-2.63
Thymidine kinase (EC 2.7.1.21)	Nucleic acid/nucleotide metabolism	*tdk*	BN194_13500	K0N4J4	0.63	-1.41	-2.66
Probable transcription repressor NiaR	Transcriptional regulation	*niaR*	BN194_08730	K0N6L8	0.87	-1.41	-2.66
Aspartate racemase (EC 5.1.1.13)	*Amino acid-related metabolism*		BN194_02170	K0N7H2	1.08	-1.44	-2.71
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	4.06	-1.44	-2.72
Protein ytsP	Signal transduction	*ytsP*	BN194_14450	K0N4Q9	2.27	-1.45	-2.73
Cell division protein DivIB	Cytokinesis	*divIB*	BN194_14740	K0MV80	1.10	-1.46	-2.74
Uncharacterized protein ywnB	General prediction only	*ywnB_2*	BN194_20050	K0N687	2.87	-1.47	-2.77
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	*gpsB*	BN194_16690	K0MVN5	7.10	-1.48	-2.79
Putative ADP-ribose pyrophosphatase yjhB (EC 3.6.1.-)	General prediction only	*yjhB*	BN194_25530	K0NAH4	1.41	-1.49	-2.80
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_3*	BN194_21990	K0MWY0	2.10	-1.49	-2.80
Uncharacterized protein	Cofactor-related metabolism		BN194_18720	K0NB69	1.45	-1.49	-2.81

Uncharacterized protein yeaC		*yeaC*	BN194_29960	K0N8I6	0.73	-1.50	-2.84
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB2,pstB*	BN194_10280	K0N6X8	0.79	-1.52	-2.86
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	*tig*	BN194_15330	K0N884	3.82	-1.54	-2.91
UbiE/COQ5 family methyltransferase	General prediction only		BN194_23620	K0NBY4	1.59	-1.55	-2.92
50S ribosomal protein L21	Ribosomal proteins	*rplU*	BN194_18290	K0MW61	1.30	-1.56	-2.95
Uncharacterized protein yloA	Cell surface proteins/internalins	*yloA*	BN194_16340	K0MVK5	1.41	-1.56	-2.95
Isoprenyl transferase (EC 2.5.1.-)	Lipid-related metabolism	*uppS*	BN194_17640	K0MVX1	0.90	-1.56	-2.95
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*bglP*	BN194_06940	K0MT60	1.36	-1.56	-2.96
TPR repeats containing protein	Unknown/uncharacterized		BN194_14960	K0N4M8	3.65	-1.56	-2.96
Uncharacterized protein	Posttranslational modification	*pp2C*	BN194_18030	K0N993	0.89	-1.57	-2.97
Putative ribosome biogenesis GTPase RsgA (EC 3.6.1.-)	tRNA/Ribosome assembly/processing	*rsgA*	BN194_18010	K0N5J0	1.05	-1.57	-2.98
Methionine import ATP-binding protein MetN (EC 3.6.3.-)	ABC-type transporter systems	*metN*	BN194_13750	K0N4L1	2.80	-1.59	-3.00
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB*	BN194_13410	K0N4C0	1.66	-1.59	-3.01
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	*lysS*	BN194_26380	K0NAN7	4.89	-1.61	-3.05
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	*mtnN*	BN194_14890	K0MV90	3.93	-1.61	-3.06
Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.193)	tRNA/Ribosome assembly/processing	*rsmE*	BN194_17250	K0N5G8	1.07	-1.62	-3.06
GNAT family acetyltransferase	General prediction only		BN194_01510	K0N1L8	3.47	-1.62	-3.07
Cell division protein FtsZ	Cytokinesis	*ftsZ*	BN194_14760	K0N4L6	5.11	-1.63	-3.09
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE_2*	BN194_19740	K0MWF1	3.67	-1.63	-3.09
Putative sporulation transcription regulator WhiA	Transcriptional regulation	*whiA*	BN194_10490	K0MU14	1.21	-1.63	-3.09
Uncharacterized protein	*Cell surface proteins/internalins*		BN194_20060	K0N5Y7	3.09	-1.63	-3.09
Uncharacterized protein	Unknown/uncharacterized		BN194_19050	K0N613	2.32	-1.63	-3.10
Lipoprotein	ABC-type transporter systems	*metQ_2*	BN194_13740	K0MV23	6.31	-1.64	-3.13
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	*ybeY*	BN194_17010	K0N594	2.49	-1.65	-3.13

Acyltransferase 3			BN194_15460	K0N4S6	1.54	-1.66	-3.16
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	*bkr4*	BN194_22550	K0N799	0.82	-1.67	-3.19
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	*phoU*	BN194_10290	K0MTZ9	2.72	-1.68	-3.20
Uncharacterized protein	Unknown/uncharacterized	*FNV1452*	BN194_18830	K0N9E3	1.09	-1.68	-3.20
MFS permease-like protein	Other transporter proteins		BN194_06910	K0N2S6	1.24	-1.68	-3.21
Rod shape-determining protein MreB	Cytokinesis	*mreB*	BN194_14550	K0N4R7	4.84	-1.68	-3.21
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*ytzG*	BN194_09230	K0N6P7	0.70	-1.68	-3.21
Uncharacterized protein in fgs 3'region	General prediction only		BN194_14530	K0N8O2	0.63	-1.69	-3.22
3-hydroxy-3-methylglutaryl coenzyme A reductase (HMG-CoA reductase) (EC 1.1.1.88)	Lipid-related metabolism	*mvaA*	BN194_19690	K0MWE8	2.72	-1.70	-3.25
50S ribosomal protein L19	Ribosomal proteins	*rplS*	BN194_17770	K0NB12	3.18	-1.70	-3.25
Protein dedA	Unknown/uncharacterized	*dedA*	BN194_08930	K0N6M9	0.46	-1.72	-3.28
Bifunctional protein FolD	Cofactor-related metabolism	*folD*	BN194_18210	K0N5K0	0.76	-1.72	-3.30
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227) (Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase)	Cell wall biogenesis	*murG*	BN194_14730	K0N819	0.84	-1.72	-3.30
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	*dhaM*	BN194_04960	K0N2C2	4.52	-1.73	-3.31
Probable copper-transporting P-type ATPase B (EC 3.6.3.-)	Other transporter proteins	*copB*	BN194_19280	K0N9H1	1.04	-1.73	-3.31
Putative competence-damage inducible protein	General prediction only	*cinA*	BN194_10070	K0N9I3	2.69	-1.73	-3.32
Probable glutamine ABC transporter permease protein glnP	ABC-type transporter systems	*glnP*	BN194_21410	K0N6A4	1.17	-1.74	-3.33
Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	0.62	-1.75	-3.36
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	*pfkA*	BN194_15570	K0NAK6	1.63	-1.75	-3.36
Uncharacterized protein	Cell wall biogenesis		BN194_02360	K0N1U1	0.63	-1.76	-3.39
Oxidoreductase YdhF (EC 1.-.-.-)	General prediction only	*ydhF*	BN194_25320	K0NCA1	1.04	-1.76	-3.39
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	*alaS*	BN194_08480	K0N6K2	5.10	-1.77	-3.42
Uncharacterized N-acetyltransferase ycf52-like (EC 2.3.1.-)	General prediction only	*speE1*	BN194_21490	K0MWT4	1.47	-1.78	-3.42
Uncharacterized protein	Unknown/uncharacterized		BN194_16570	K0NAT3	2.46	-1.78	-3.43
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	*ywpJ*	BN194_11320	K0N9U2	4.02	-1.78	-3.43
Tyrosine--tRNA ligase (EC 6.1.1.1)		*tyrS*	BN194_21510	K0N6A9	4.50	-1.79	-3.45

Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	*plsX*	BN194_17940	K0MW37	2.31	-1.79	-3.46
Uncharacterized protein			BN194_16060	K0N4Y8	2.54	-1.80	-3.47
Uncharacterized ABC transporter ATP-binding protein YdiF	General prediction only	*ydiF*	BN194_23830	K0NA88	3.46	-1.81	-3.50
Diphosphomevalonate decarboxylase (EC 4.1.1.33)	Lipid-related metabolism	*mvd1*	BN194_16830	K0N8S2	1.81	-1.81	-3.50
30S ribosomal protein S18	Ribosomal proteins	*rpsR*	BN194_00120	K0N6T2	1.55	-1.81	-3.51
Uncharacterized protein yslB	Unknown/uncharacterized	*yslB*	BN194_08630	K0N6L4	3.10	-1.81	-3.52
Protein translocase subunit SecA	Protein export	*secA*	BN194_10170	K0N9J2	5.47	-1.82	-3.52
Uncharacterized protein	Unknown/uncharacterized		BN194_24220	K0NC21	1.30	-1.82	-3.53
Phosphoenolpyruvate-dependent sugar phosphotransferase system EIIA, galactitol/fructose specific	Phosphotransferase systems		BN194_27050	K0N8F9	1.14	-1.82	-3.53
Uncharacterized protein	Unknown/uncharacterized		BN194_24010	K0N715	4.69	-1.82	-3.53
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	2.86	-1.83	-3.56
Septation ring formation regulator EzrA	Cytokinesis	*ezrA*	BN194_14460	K0N4J2	4.99	-1.84	-3.57
HTH-type transcriptional regulator iolR	Transcriptional regulation	*iolR*	BN194_02190	K0MS58	1.08	-1.84	-3.59
Phosphatase YbjI (EC 3.1.3.-)	General prediction only	*ybjI*	BN194_30020	K0NDN5	2.17	-1.86	-3.63
Protein RibT (EC 2.3.1.-)	Cofactor-related metabolism	*ribT*	BN194_15620	K0NAL0	2.92	-1.87	-3.65
Alternansucrase	Cell wall biogenesis		BN194_02430	K0N547	3.43	-1.87	-3.66
Uncharacterized protein HI_0912	General prediction only	*thiF3*	BN194_05090	K0MSS8	1.59	-1.88	-3.67
Uncharacterized protein	Unknown/uncharacterized		BN194_13400	K0N4I9	2.29	-1.88	-3.69
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	*apt*	BN194_17380	K0N902	4.75	-1.88	-3.69
SsrA-binding protein (Small protein B)	Posttranslational modification	*smpB*	BN194_11110	K0N3S3	0.66	-1.89	-3.71
50S ribosomal protein L33	Ribosomal proteins	*rpmG2,rpmG*	BN194_24280	K0NAA5	1.79	-1.90	-3.73
DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	4.34	-1.92	-3.78
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	*glgD*	BN194_21590	K0MWU4	1.44	-1.93	-3.81
5'-nucleotidase (EC 3.1.3.5)	General prediction only		BN194_08220	K0N957	5.43	-1.93	-3.81
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	*hslV*	BN194_16000	K0N542	2.49	-1.94	-3.83
Virulence factor mviM	General prediction only	*mviM*	BN194_13310	K0N4B2	5.40	-1.94	-3.84
Segregation and condensation protein B	Cytokinesis	*scpB*	BN194_15640	K0MVE6	2.46	-1.94	-3.84

Uncharacterized protein	Unknown/uncharacterized		BN194_11770	K0N9Y6	1.03	-1.97	-3.91
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	*murA2,murA*	BN194_26780	K0NAR9	5.31	-1.97	-3.91
ErfK family protein	Cell wall biogenesis		BN194_26570	K0NCS1	0.97	-1.98	-3.93
Recombination protein RecR	DNA repair/recombination	*recR*	BN194_23970	K0NC03	1.38	-1.98	-3.95
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox*	BN194_01780	K0N4U4	2.61	-1.98	-3.95
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	*murC*	BN194_18950	K0N600	4.09	-1.99	-3.98
Transcriptional repressor CcpN	Transcriptional regulation	*ccpN*	BN194_24740	K0MXH2	4.18	-2.00	-3.99
UPF0473 protein BN194_08530	Unknown/uncharacterized		BN194_08530	K0N6K6	3.03	-2.02	-4.05
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	*xpt*	BN194_12490	K0MUR6	4.07	-2.03	-4.08
Putative gluconeogenesis factor	General prediction only	*yjiF*	BN194_10480	K0N6Z4	1.76	-2.03	-4.08
5-bromo-4-chloroindolyl phosphate hydrolysis protein	General prediction only		BN194_14860	K0N4M3	3.57	-2.04	-4.10
Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	ABC-type transporter systems	*ecfA2, ecfA*	BN194_25920	K0NCI4	0.91	-2.04	-4.10
DegV domain-containing protein CPE0026	Unknown/uncharacterized		BN194_12060	K0N405	4.26	-2.04	-4.11
Uncharacterized protein	Unknown/uncharacterized		BN194_21380	K0N9Y1	5.07	-2.04	-4.12
Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	4.42	-2.05	-4.15
Fumarate hydratase class II (Fumarase C) (EC 4.2.1.2)	Tricarboxylic acid pathway	*fumC*	BN194_25340	K0MXL5	3.53	-2.05	-4.15
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	*ndk*	BN194_08160	K0N340	3.62	-2.06	-4.17
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	*murI*	BN194_08640	K0MTN4	0.73	-2.06	-4.17
Phosphatase YidA (EC 3.1.3.-)	General prediction only	*yidA*	BN194_28520	K0NDD5	4.54	-2.07	-4.19
Uncharacterized protein	General prediction only		BN194_14990	K0MV99	1.32	-2.07	-4.19
Exodeoxyribonuclease (EC 3.1.11.2)	DNA repair/recombination	*exoA*	BN194_11390	K0MUA0	2.48	-2.08	-4.21
Uncharacterized protein ybbP	Unknown/uncharacterized	*ybbP*	BN194_11530	K0N776	0.65	-2.08	-4.22
Protein veg	Unknown/uncharacterized	*veg*	BN194_27010	K0N7N4	1.56	-2.09	-4.25
Uncharacterized protein	*Nucleic acid/nucleotide metabolism*		BN194_27260	K0N7R1	1.59	-2.09	-4.26
Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	*pyk*	BN194_15580	K0N8B6	4.92	-2.10	-4.28
Uncharacterized protein	Unknown/uncharacterized		BN194_30140	K0MYT6	2.58	-2.11	-4.30

Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	*mhqD*	BN194_18770	K0NB71	2.02	-2.11	-4.32
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	*iolS*	BN194_29680	K0NB94	6.31	-2.11	-4.33
Glycosyl transferase family 8	Cell wall biogenesis		BN194_11730	K0N795	1.35	-2.14	-4.39
Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) (Peptide-methionine (R)-S-oxide reductase)	Posttranslational modification	*msrB*	BN194_17090	K0MVR6	1.48	-2.14	-4.41
Uncharacterized protein	Unknown/uncharacterized		BN194_21170	K0NBJ9	1.50	-2.14	-4.42
Uncharacterized protein	Unknown/uncharacterized		BN194_12110	K0N410	1.08	-2.15	-4.44
Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase)	Cofactor-related metabolism	*coaA*	BN194_21080	K0N9V9	2.69	-2.16	-4.46
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	*lplJ*	BN194_16640	K0MVN0	2.73	-2.16	-4.48
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	*yuxL*	BN194_19910	K0N5X4	3.80	-2.18	-4.53
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	*yabO*	BN194_26520	K0NCR8	1.89	-2.19	-4.56
Uncharacterized oxidoreductase YcsN (EC 1.-.-.-)	General prediction only	*ycsN*	BN194_27290	K0MY45	3.05	-2.20	-4.58
ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136) (ADP-dependent NAD(P)HX dehydratase)	Cofactor-related metabolism	*nnrD*	BN194_09250	K0N360	2.82	-2.20	-4.59
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	5.01	-2.20	-4.59
MreB-like protein	Cytokinesis	*mbl*	BN194_13650	K0N4K5	3.05	-2.21	-4.61
Uncharacterized protein ysxB	Ribosomal proteins	*ysxB*	BN194_18280	K0N9A9	1.03	-2.21	-4.62
Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)	Nucleic acid/nucleotide metabolism	*pyrF*	BN194_16430	K0N8M7	2.02	-2.22	-4.66
tRNA pseudouridine synthase B (EC 5.4.99.25) (tRNA pseudouridine(55) synthase) (tRNA pseudouridylate synthase) (tRNA-uridine isomerase)	tRNA/Ribosome assembly/processing	*truB*	BN194_17520	K0NAZ5	1.67	-2.23	-4.69
Threonylcarbamoyl-AMP synthase (TC-AMP synthase) (EC 2.7.7.87) (L-threonylcarbamoyladenylate synthase)	tRNA/Ribosome assembly/processing	*ywlC*	BN194_13530	K0N7S6	1.55	-2.24	-4.73
Uncharacterized protein YdiC	General prediction only	*ydiC_3*	BN194_23870	K0NBZ8	3.26	-2.25	-4.75
Glycosyl transferase group 1	Cell wall biogenesis		BN194_09760	K0N3F8	2.25	-2.25	-4.77
Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-)		*rsmB*	BN194_18040	K0MW45	1.40	-2.26	-4.79
Uncharacterized protein ydcI	General prediction only	*ydcI*	BN194_14310	K0N4I1	0.96	-2.28	-4.85
tRNA N6-adenosine threonylcarbamoyltransferase (EC 2.3.1.234) (N6-L-threonylcarbamoyladenine synthase) (t(6)A37 threonylcarbamoyladenosine biosynthesis protein TsaD) (tRNA threonylcarbamoyladenosine biosynthesis protein TsaD)	General prediction only	*tsaD,gcp*	BN194_23850	K0N7L3	4.14	-2.28	-4.86

DegV domain-containing protein SP_1112	Unknown/uncharacterized		BN194_15830	K0N8F3	5.28	-2.31	-4.96
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	*zwf*	BN194_08420	K0N966	5.13	-2.32	-4.99
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacA*	BN194_07500	K0N2T4	2.69	-2.35	-5.10
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	*clpP_2, clpP*	BN194_10510	K0N3M4	3.43	-2.35	-5.11
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_2*	BN194_15390	K0MVD0	1.02	-2.35	-5.12
DNA polymerase III subunit delta (EC 2.7.7.7)	DNA replication-related	*holB*	BN194_23930	K0NA93	2.33	-2.37	-5.16
Uncharacterized protein			BN194_21520	K0NBL8	3.50	-2.38	-5.19
ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease RexB)	DNA repair/recombination	*rexB*	BN194_16810	K0N573	0.59	-2.38	-5.22
Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		BN194_08520	K0N972	1.55	-2.39	-5.23
Uncharacterized protein	Unknown/uncharacterized		BN194_01150	K0N181	1.24	-2.39	-5.24
Uncharacterized protein	Unknown/uncharacterized		BN194_25820	K0NCG9	0.61	-2.39	-5.26
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	Cell wall biogenesis	*glmS*	BN194_11560	K0N3V9	5.81	-2.40	-5.29
Elongation factor G (EF-G)	Protein translation (elongation)	*fusA*	BN194_26270	K0NCN8	4.01	-2.42	-5.34
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	4.50	-2.43	-5.37
Replicative DNA helicase (EC 3.6.4.12)	DNA replication-related	*dnaC*	BN194_01140	K0MRW2	3.20	-2.44	-5.42
Uncharacterized protein	Prophage genome		BN194_09330	K0N6Q4	1.90	-2.45	-5.46
Primosomal protein DnaI	DNA replication-related	*dnaI*	BN194_18880	K0N9E5	1.48	-2.45	-5.46
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP_3*	BN194_21160	K0N682	4.06	-2.45	-5.48
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	*carB*	BN194_16450	K0N587	6.67	-2.46	-5.49
Site-determining protein	Cytokinesis	*minD*	BN194_14590	K0MV70	4.95	-2.46	-5.50
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	*gltX*	BN194_24470	K0NC38	5.44	-2.46	-5.52
Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase)	Nucleic acid/nucleotide metabolism	*pyrB*	BN194_16480	K0N8N2	8.79	-2.50	-5.65
NAD-dependent protein deacetylase (EC 3.5.1.-)	General prediction only	*cobB*	BN194_27190	K0MY36	1.83	-2.51	-5.70

Ribosome maturation factor RimP	tRNA/Ribosome assembly/processing	*rimP*	BN194_17590	K0MVW3	1.55	-2.52	-5.74
Uncharacterized protein YxeH	General prediction only	*yxeH*	BN194_04750	K0N1Y7	1.11	-2.52	-5.75
Ribosomal RNA small subunit methyltransferase H (EC 2.1.1.199) (16S rRNA m(4)C1402 methyltransferase) (rRNA (cytosine-N(4)-)-methyltransferase RsmH)	tRNA/Ribosome assembly/processing	*rsmH*	BN194_14680	K0N814	2.78	-2.52	-5.75
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	*ftsY*	BN194_17850	K0N5R8	4.88	-2.52	-5.75
Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	*rp2*	BN194_17060	K0N598	1.62	-2.53	-5.77
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	*dut*	BN194_24640	K0MXG3	0.92	-2.53	-5.78
DNA topoisomerase 4 subunit A (EC 5.99.1.-)		*parC*	BN194_16070	K0NAP8	2.82	-2.53	-5.79
SMC domain protein	DNA repair/recombination		BN194_07540	K0MTC3	1.05	-2.54	-5.81
Translation initiation factor IF-1	Protein translation (initiation)	*infA*	BN194_26000	K0N847	2.18	-2.54	-5.82
UPF0478 protein SAOUHSC_01855	Signal transduction		BN194_08710	K0N365	5.88	-2.55	-5.84
DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	DNA replication-related	*dnaX*	BN194_23990	K0MXD3	1.95	-2.55	-5.84
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	*gmk*	BN194_18110	K0N5J6	1.77	-2.55	-5.88
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA1, greA*	BN194_02150	K0N1G7	2.23	-2.57	-5.93
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB_2*	BN194_21970	K0NBP6	2.08	-2.58	-5.98
Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	*fba_2*	BN194_05060	K0N2C9	3.43	-2.59	-6.01
Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	4.95	-2.59	-6.02
Uncharacterized protein	General prediction only		BN194_13850	K0N4L8	1.89	-2.60	-6.06
tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	tRNA/Ribosome assembly/processing	*mnmG,gidA*	BN194_30590	K0MYX4	2.68	-2.62	-6.14
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	*ycnE*	BN194_13230	K0N7R3	2.78	-2.62	-6.17
Archaeal fructose-1,6-bisphosphatase related enzyme of inositol monophosphatase family	*Carbohydrate-related metabolism*		BN194_15140	K0MVB0	4.78	-2.62	-6.17
tRNA (Adenine(22)-N(1))-methyltransferase (EC 2.1.1.217)	tRNA/Ribosome assembly/processing	*trmK*	BN194_16910	K0N584	1.83	-2.63	-6.17
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	*fabZ*	BN194_22520	K0NBS8	3.57	-2.63	-6.21
Uncharacterized protein	Unknown/uncharacterized		BN194_01080	K0N4J7	1.73	-2.64	-6.25
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	*frr*	BN194_17650	K0N5M3	5.35	-2.65	-6.26

Uncharacterized protein	Unknown/uncharacterized		BN194_17360	K0N5B9	3.78	-2.66	-6.31
Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase (EC 4.2.-.-)	*tRNA/Ribosome assembly/processing*		BN194_17370	K0NAY4	2.88	-2.66	-6.32
DNA translocase SftA	Cytokinesis	*sftA*	BN194_18960	K0N5Q1	4.06	-2.67	-6.35
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA*	BN194_01620	K0N7B1	1.63	-2.68	-6.40
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	*ssdA*	BN194_24140	K0MXE0	5.84	-2.68	-6.42
tRNA modification GTPase MnmE (EC 3.6.-.-)	tRNA/Ribosome assembly/processing	*mnmE,trmE*	BN194_30600	K0N9F0	3.73	-2.68	-6.42
DNA replication protein dnaD	DNA replication-related	*dnaD*	BN194_16750	K0N5B1	1.88	-2.70	-6.51
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	*fabD*	BN194_22570	K0NBT1	4.33	-2.71	-6.53
Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	6.08	-2.71	-6.54
Holo-[acyl-carrier-protein] synthase (Holo-ACP synthase) (EC 2.7.8.7) (4'-phosphopantetheinyl transferase AcpS)	Cofactor-related metabolism	*acpS*	BN194_26690	K0MXY2	3.44	-2.71	-6.56
Phosphoesterase (EC 3.1.4.-)	General prediction only	*ysnB*	BN194_08650	K0N317	4.10	-2.72	-6.57
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA_2*	BN194_22950	K0N7F8	1.84	-2.74	-6.69
Ribosome biogenesis GTPase A	tRNA/Ribosome assembly/processing	*rbgA*	BN194_15940	K0MVH2	2.23	-2.74	-6.70
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	1.67	-2.75	-6.71
Uncharacterized protein IRC4	Unknown/uncharacterized	*IRC4*	BN194_30110	K0N8K0	2.29	-2.76	-6.79
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD(+)])	DNA replication-related	*ligA*	BN194_11930	K0N7A9	1.28	-2.77	-6.82
Phosphoribosylformylglycinamidine synthase subunit PurS (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit III) (Phosphoribosylformylglycinamidine synthase subunit III)	Nucleic acid/nucleotide metabolism	*yexA,purS*	BN194_19350	K0N638	1.90	-2.77	-6.83
Transcriptional repressor NrdR	Transcriptional regulation	*nrdR*	BN194_18900	K0N5Z5	2.14	-2.78	-6.88
Polyphosphate kinase (EC 2.7.4.1) (ATP-polyphosphate phosphotransferase) (Polyphosphoric acid kinase)	Membrane bioenergetics	*ppk*	BN194_27270	K0ND10	2.42	-2.80	-6.96
Ribosomal RNA small subunit methyltransferase A (EC 2.1.1.182) (16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase) (16S rRNA dimethyladenosine transferase) (16S rRNA dimethylase) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase)	tRNA/Ribosome assembly/processing	*rsmA,ksgA*	BN194_27020	K0NCX3	3.84	-2.80	-6.97
30S ribosomal protein S11	Ribosomal proteins	*rpsK*	BN194_25970	K0NCJ0	1.83	-2.80	-6.98
DNA topoisomerase 4 subunit B (EC 5.99.1.3) (Topoisomerase IV subunit B)	DNA replication-related	*parE*	BN194_16050	K0N545	2.31	-2.81	-7.02

Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	*nfo*	BN194_17070	K0NAW5	1.91	-2.84	-7.14
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF_2*	BN194_19090	K0MWB2	0.88	-2.85	-7.20
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	*fabG*	BN194_22560	K0N6N3	1.65	-2.85	-7.23
Transcriptional regulator, xre family	Transcriptional regulation		BN194_05600	K0N260	1.77	-2.86	-7.28
Uncharacterized protein	General prediction only		BN194_01300	K0N194	1.63	-2.87	-7.30
HTH-type transcriptional regulator yodB	Transcriptional regulation	*yodB*	BN194_18590	K0MW80	0.78	-2.87	-7.30
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	*asnB*	BN194_22990	K0MX90	4.89	-2.88	-7.36
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	5.39	-2.89	-7.39
Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase)	Nucleic acid/nucleotide metabolism	*purM*	BN194_19320	K0NB95	5.63	-2.90	-7.46
Uncharacterized RNA methyltransferase lp_3226 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_19580	K0N9J4	2.78	-2.90	-7.47
DNA topoisomerase 1 (EC 5.99.1.2) (DNA topoisomerase I)	DNA replication-related	*topA*	BN194_15970	K0NAP0	1.06	-2.92	-7.58
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh1,ldh*	BN194_06970	K0N8S5	2.70	-2.93	-7.61
Probable GTP-binding protein EngB	tRNA/Ribosome assembly/processing	*engB*	BN194_15350	K0N4Y5	2.39	-2.93	-7.63
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	*hslO*	BN194_26400	K0N893	2.25	-2.93	-7.64
Ribonuclease Z (RNase Z) (EC 3.1.26.11) (tRNA 3 endonuclease) (tRNase Z)	tRNA/Ribosome assembly/processing	*rnz*	BN194_15470	K0NAK0	1.93	-2.94	-7.67
Glutathione reductase, chloroplastic (EC 1.8.1.7)	Cofactor-related metabolism	*GOR*	BN194_23200	K0N7H3	3.08	-2.97	-7.83
GTP pyrophosphokinase yjbM (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*yjbM*	BN194_09870	K0N9G5	2.39	-2.98	-7.91
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*argS*	BN194_19120	K0NB86	6.85	-2.99	-7.95
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*yfmL*	BN194_12120	K0NA13	2.78	-3.00	-7.98
Phage capsid protein	Prophage genome		BN194_30330	K0NBD3	2.54	-3.00	-8.00
Elongation factor P	Protein translation (elongation)	*efp_2*	BN194_22050	K0N712	1.57	-3.02	-8.08
Transcriptional regulatory protein YycF	Signal transduction	*yycF_2*	BN194_29510	K0N8E4	2.54	-3.02	-8.09
Adapter protein MecA	Competence (DNA uptake)	*mecA*	BN194_19170	K0NB89	1.36	-3.02	-8.09
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	*clpC*	BN194_21680	K0N9Z7	5.25	-3.02	-8.11
Protein RecA (Recombinase A)	DNA repair/recombination	*recA_2,recA*	BN194_27650	K0N8P0	1.94	-3.03	-8.16

CCA-adding enzyme (EC 2.7.7.72) (CCA tRNA nucleotidyltransferase) (tRNA CCA-pyrophosphorylase) (tRNA adenylyl-/cytidylyl- transferase) (tRNA nucleotidyltransferase) (tRNA-NT)	tRNA/Ribosome assembly/processing	*cca*	BN194_15770	K0NAM4	1.48	-3.03	-8.16
Glucitol operon repressor	Transcriptional regulation	*srlR*	BN194_28690	K0MYG3	1.90	-3.05	-8.31
Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*nrdD*	BN194_01250	K0N190	2.99	-3.06	-8.33
Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain)	Nucleic acid/nucleotide metabolism	*carA*	BN194_16460	K0N535	7.33	-3.07	-8.38
Esterase/lipase	General prediction only		BN194_30390	K0MYV7	5.84	-3.07	-8.41
Uncharacterized protein	Unknown/uncharacterized		BN194_22290	K0MX11	2.82	-3.07	-8.42
Uncharacterized protein	Unknown/uncharacterized		BN194_25540	K0MXN3	2.13	-3.10	-8.59
Probable amino-acid ABC transporter-binding protein HI_1080	*ABC-type transporter systems*		BN194_06710	K0N2R6	5.16	-3.10	-8.59
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	*yqjQ*	BN194_15480	K0N8A1	2.82	-3.11	-8.61
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	*pyrH*	BN194_17660	K0N5E6	3.85	-3.11	-8.66
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*pcrA*	BN194_11920	K0N9Z6	2.72	-3.12	-8.69
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacB*	BN194_07490	K0MTB7	3.57	-3.14	-8.80
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	*pyc*	BN194_15170	K0NAI2	2.86	-3.14	-8.83
HTH-type transcriptional repressor glcR	Transcriptional regulation	*glcR*	BN194_02570	K0N7M8	3.95	-3.15	-8.86
DNA polymerase III PolC-type (PolIII) (EC 2.7.7.7)	DNA replication-related	*polC*	BN194_17600	K0N5L6	1.88	-3.17	-9.00
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA2,gpmA*	BN194_22740	K0MX58	4.18	-3.20	-9.18
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	*fabK*	BN194_22580	K0NA38	2.68	-3.21	-9.26
30S ribosomal protein S15	Ribosomal proteins	*rpsO*	BN194_15260	K0N4Q6	3.05	-3.22	-9.31
30S ribosomal protein S21	Ribosomal proteins	*rpsU*	BN194_17050	K0N5E5	1.22	-3.22	-9.34
30S ribosomal protein S1 homolog	Ribosomal proteins	*ypfD*	BN194_15720	K0NAL9	6.12	-3.24	-9.45
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	*guaB*	BN194_02100	K0N1G3	4.95	-3.24	-9.47
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	*apbE_3*	BN194_21550	K0N6S8	1.94	-3.25	-9.52
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	*der*	BN194_15730	K0N8E1	4.29	-3.26	-9.59
GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*relA*	BN194_17230	K0N8Y0	3.72	-3.27	-9.65

Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_2*	BN194_03120	K0N7V6	4.38	-3.31	-9.90
CBS domain-containing protein ykuL	Unknown/uncharacterized	*ykuL*	BN194_08670	K0N981	1.26	-3.32	-9.96
ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	DNA repair/recombination	*addA*	BN194_16800	K0N5B6	2.00	-3.33	-10.05
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	*prs1,prs*	BN194_26930	K0NAT2	4.53	-3.34	-10.10
Probable tRNA sulfurtransferase (EC 2.8.1.4) (Sulfur carrier protein ThiS sulfurtransferase) (Thiamine biosynthesis protein ThiI) (tRNA 4-thiouridine synthase)	Cofactor-related metabolism	*thiI*	BN194_14480	K0N7Z7	4.58	-3.34	-10.16
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	*rnc*	BN194_17870	K0NB31	2.57	-3.35	-10.17
Chromosome partition protein Smc	Cytokinesis	*smc*	BN194_17860	K0N5H9	2.37	-3.35	-10.22
Sensory transduction protein BceR	Signal transduction	*bceR_2*	BN194_19250	K0N630	5.17	-3.36	-10.28
Uncharacterized protein	Unknown/uncharacterized		BN194_00400	K0N116	1.93	-3.38	-10.38
Uncharacterized protein	Unknown/uncharacterized		BN194_29850	K0N968	2.15	-3.39	-10.47
GTPase Era	tRNA/Ribosome assembly/processing	*era*	BN194_16990	K0MVQ8	3.07	-3.39	-10.51
Uncharacterized protein	Unknown/uncharacterized		BN194_02900	K0N1P1	2.92	-3.39	-10.52
Uncharacterized protein ytoI	Transcriptional regulation	*ytoI*	BN194_08440	K0MTM0	5.25	-3.41	-10.65
30S ribosomal protein S3	Ribosomal proteins	*rpsC*	BN194_26160	K0N7G5	4.77	-3.41	-10.66
Uncharacterized protein	Unknown/uncharacterized		BN194_15520	K0NAK2	2.49	-3.43	-10.75
FemAB family protein	General prediction only		BN194_22880	K0NA57	1.37	-3.44	-10.86
Cell division protein FtsA	Cytokinesis	*ftsA*	BN194_14750	K0N4T3	4.11	-3.44	-10.89
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		BN194_11600	K0N3Z3	2.46	-3.46	-10.99
Uncharacterized protein	Unknown/uncharacterized		BN194_08190	K0MTK3	1.09	-3.47	-11.06
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	*rpoZ*	BN194_18100	K0N5T7	7.24	-3.47	-11.06
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	*thyA*	BN194_15800	K0N522	1.99	-3.47	-11.09
CBS domain-containing protein	Unknown/uncharacterized		BN194_26610	K0N7J7	5.25	-3.47	-11.11
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	*cap4C*	BN194_12280	K0N7E3	4.73	-3.48	-11.14
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB*	BN194_19860	K0N5X0	4.21	-3.48	-11.14

DNA mismatch repair protein MutL	DNA repair/recombination	*mutL*	BN194_23710	K0N6Z8	2.49	-3.49	-11.23
Uncharacterized protein	Unknown/uncharacterized		BN194_13840	K0MV29	3.18	-3.51	-11.41
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	*gpsA*	BN194_10350	K0N3I2	4.04	-3.52	-11.47
Uncharacterized protein	Unknown/uncharacterized		BN194_19470	K0NBA0	5.13	-3.52	-11.48
Integral membrane protein	Unknown/uncharacterized		BN194_07890	K0MTI0	3.05	-3.53	-11.54
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	*grpE*	BN194_17470	K0NAZ2	5.03	-3.54	-11.66
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)	Nucleic acid/nucleotide metabolism	*ntd*	BN194_24240	K0MXE6	1.47	-3.56	-11.78
Probable L-serine dehydratase, beta chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAB*	BN194_13940	K0MV34	4.62	-3.57	-11.87
UvrABC system protein B (Protein UvrB) (Excinuclease ABC subunit B)	DNA repair/recombination	*uvrB*	BN194_10440	K0MU09	2.93	-3.58	-11.97
Uncharacterized protein	Unknown/uncharacterized		BN194_19530	K0N9J0	3.64	-3.61	-12.21
50S ribosomal protein L6	Ribosomal proteins	*rplF*	BN194_26070	K0NCK5	4.60	-3.64	-12.43
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	*yclJ*	BN194_11790	K0MUE5	1.83	-3.66	-12.66
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	*pyrG*	BN194_26790	K0MXZ1	6.87	-3.68	-12.78
Transcriptional regulator	Transcriptional regulation		BN194_08230	K0N6I4	2.52	-3.70	-12.99
Putative transcriptional regulator (DtxR family)	Transcriptional regulation		BN194_08410	K0N354	5.03	-3.71	-13.11
Uncharacterized protein yutG	Lipid-related metabolism	*yutG*	BN194_08940	K0MTQ3	4.31	-3.72	-13.17
Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)	Nucleic acid/nucleotide metabolism	*pdp*	BN194_23430	K0NA73	2.23	-3.73	-13.30
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	*hprK*	BN194_10330	K0N6Y3	2.79	-3.75	-13.45
50S ribosomal protein L18	Ribosomal proteins	*rplR*	BN194_26060	K0N7F4	2.43	-3.75	-13.45
FeS cluster assembly protein sufD	Cofactor-related metabolism	*sufD*	BN194_13780	K0N7U0	5.70	-3.76	-13.58
Uncharacterized protein	Transcriptional regulation		BN194_22670	K0NBT5	2.48	-3.78	-13.77
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (ACCase subunit beta) (Acetyl-CoA carboxylase carboxyltransferase subunit beta) (EC 6.4.1.2)	Lipid-related metabolism	*accD*	BN194_22480	K0NA32	2.23	-3.79	-13.80
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	*pth*	BN194_26550	K0N8B3	2.24	-3.79	-13.82
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	*fabH*	BN194_22600	K0N7B0	5.75	-3.79	-13.84

Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	*prs1_2*	BN194_30370	K0NDQ5	3.35	-3.80	-13.91
50S ribosomal protein L11	Ribosomal proteins	*rplK*	BN194_24160	K0N724	5.18	-3.81	-14.02
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	*fabZ_2*	BN194_22620	K0NBT3	2.22	-3.83	-14.21
HTH-type transcriptional repressor yvoA	Transcriptional regulation	*yvoA_2*	BN194_19880	K0N9L8	3.68	-3.84	-14.34
Transcription termination/antitermination protein NusG	Transcription-associated proteins	*nusG*	BN194_24260	K0N730	4.98	-3.85	-14.44
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		BN194_13770	K0NAC0	4.17	-3.85	-14.46
DNA-binding protein HU	DNA replication-related	*hup*	BN194_15740	K0MVF4	2.27	-3.85	-14.46
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	*murD*	BN194_14720	K0NAG5	5.71	-3.86	-14.48
Uncharacterized protein ybxB	tRNA/Ribosome assembly/processing	*ybxB*	BN194_24020	K0NC08	2.27	-3.86	-14.56
Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	*upp*	BN194_13550	K0N4J8	6.33	-3.88	-14.72
DNA mismatch repair protein MutS	DNA repair/recombination	*mutS*	BN194_23720	K0NBY9	2.95	-3.88	-14.72
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	*queA*	BN194_08370	K0N965	4.91	-3.88	-14.73
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	*guaA*	BN194_21070	K0NBJ2	6.39	-3.88	-14.76
Uncharacterized protein yeaO	Unknown/uncharacterized	*yeaO*	BN194_08040	K0MTJ2	2.30	-3.91	-15.01
Uncharacterized protein yieF	General prediction only	*yieF_2*	BN194_06540	K0MT25	3.01	-3.92	-15.11
UvrABC system protein A	DNA repair/recombination	*uvrA_3*	BN194_27500	K0N8M1	4.01	-3.95	-15.40
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	*pyrC*	BN194_16470	K0NAS6	4.09	-4.01	-16.07
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	5.80	-4.02	-16.17
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	*groL,groEL*	BN194_23750	K0N7K7	4.91	-4.03	-16.38
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	*prfB*	BN194_10180	K0N6W9	2.82	-4.05	-16.57
50S ribosomal protein L22	Ribosomal proteins	*rplV*	BN194_26170	K0NCM1	3.77	-4.07	-16.74
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		BN194_08960	K0N387	4.96	-4.07	-16.85
50S ribosomal protein L10	Ribosomal proteins	*rplJ*	BN194_24090	K0MXD8	5.36	-4.08	-16.91
50S ribosomal protein L31 type B	Ribosomal proteins	*rpmE2*	BN194_26770	K0NCV4	3.23	-4.09	-16.98
Putative RNA methyltransferase YpsC (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ypsC*	BN194_16670	K0NAU0	6.04	-4.09	-17.02

Probable L-serine dehydratase, alpha chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAA*	BN194_13950	K0N4M4	4.61	-4.09	-17.09
50S ribosomal protein L23	Ribosomal proteins	*rplW*	BN194_26200	K0N869	1.77	-4.11	-17.25
Transcriptional regulator, xre family	Transcriptional regulation		BN194_13860	K0N4E8	2.65	-4.11	-17.32
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshB*	BN194_08460	K0N356	3.52	-4.12	-17.40
Bifunctional purine biosynthesis protein PurH	Nucleic acid/nucleotide metabolism	*purH*	BN194_19300	K0N634	1.42	-4.12	-17.42
N5-carboxyaminoimidazole ribonucleotide synthase (N5-CAIR synthase) (EC 6.3.4.18) (5-(carboxyamino)imidazole ribonucleotide synthetase)	Nucleic acid/nucleotide metabolism	*purK_2, purK*	BN194_19370	K0NB96	3.26	-4.14	-17.61
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	2.58	-4.14	-17.64
Ferredoxin--NADP reductase (FNR) (Fd-NADP(+) reductase) (EC 1.18.1.2)	Membrane bioenergetics		BN194_08950	K0N337	3.03	-4.15	-17.71
tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	*dus1*	BN194_26390	K0MXV9	3.22	-4.15	-17.73
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	*purB*	BN194_12520	K0NA41	2.55	-4.17	-18.02
Bifunctional protein GlmU	Cell wall biogenesis	*glmU*	BN194_26940	K0MY10	3.84	-4.18	-18.10
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	*ohrR*	BN194_10500	K0N3J7	1.84	-4.18	-18.11
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA_2*	BN194_18340	K0MW64	4.97	-4.18	-18.13
Uncharacterized protein yjbK	General prediction only	*yjbK*	BN194_09860	K0N3G6	1.93	-4.19	-18.20
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	*yqeH*	BN194_18740	K0MW90	3.01	-4.20	-18.35
Glutathione peroxidase	Cell defense/detoxification	*gpo*	BN194_09780	K0N6T6	7.11	-4.20	-18.42
50S ribosomal protein L3	Ribosomal proteins	*rplC*	BN194_26220	K0NCN1	2.68	-4.21	-18.49
Transcriptional regulator, XRE family	Transcriptional regulation		BN194_30170	K0NDP4	2.99	-4.21	-18.53
Transcription termination/antitermination protein NusA	Transcription-associated proteins	*nusA*	BN194_17580	K0N927	3.52	-4.21	-18.54
Mevalonate kinase (EC 2.7.1.36)	Lipid-related metabolism	*mvk*	BN194_12270	K0NA23	3.46	-4.23	-18.82
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	*accA*	BN194_22470	K0NBS6	2.82	-4.24	-18.88
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	*pdhD*	BN194_15110	K0N4P1	3.14	-4.24	-18.91
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	*yabR*	BN194_26500	K0N8A7	2.14	-4.25	-19.06
Chaperone protein DnaJ	Protein folding/turnover	*dnaJ*	BN194_17450	K0N5J4	3.69	-4.26	-19.11

ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	*hslU*	BN194_16010	K0N4Y1	2.56	-4.26	-19.20
50S ribosomal protein L14	Ribosomal proteins	*rplN*	BN194_26120	K0NCL3	4.01	-4.27	-19.24
50S ribosomal protein L16	Ribosomal proteins	*rplP*	BN194_26150	K0N863	3.55	-4.28	-19.37
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	*yqeL,rsfS*	BN194_18710	K0N5N6	2.11	-4.28	-19.37
Predicted hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	5.10	-4.29	-19.56
30S ribosomal protein S12	Ribosomal proteins	*rpsL*	BN194_26290	K0MXV0	6.97	-4.29	-19.57
Transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	3.34	-4.30	-19.71
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	*glyA*	BN194_13540	K0MV12	3.43	-4.31	-19.80
50S ribosomal protein L24	Ribosomal proteins	*rplX*	BN194_26110	K0N7F9	3.25	-4.33	-20.11
30S ribosomal protein S17	Ribosomal proteins	*rpsQ*	BN194_26130	K0NAL6	5.45	-4.33	-20.12
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	*ung*	BN194_11330	K0N758	1.51	-4.33	-20.14
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	*prfA*	BN194_13510	K0N4C6	5.32	-4.33	-20.14
50S ribosomal protein L30	Ribosomal proteins	*rpmD*	BN194_26040	K0MXS6	1.92	-4.36	-20.47
Chromosomal replication initiator protein DnaA	DNA replication-related	*dnaA*	BN194_00010	K0N1B5	4.06	-4.36	-20.50
Ribonuclease P protein component (RNase P protein) (RNaseP protein) (EC 3.1.26.5) (Protein C5)	tRNA/Ribosome assembly/processing	*rnpA*	BN194_30620	K0NDS2	2.44	-4.36	-20.51
30S ribosomal protein S6	Ribosomal proteins	*rpsF*	BN194_00100	K0N0Z1	5.76	-4.40	-21.09
Uncharacterized protein	General prediction only		BN194_26820	K0NCV9	4.80	-4.42	-21.46
Uncharacterized protein yxjH	Amino acid-related metabolism	*yxjH*	BN194_08320	K0N962	2.69	-4.44	-21.78
30S ribosomal protein S10	Ribosomal proteins	*rpsJ*	BN194_26230	K0NAM5	4.84	-4.46	-21.98
GMP reductase (EC 1.7.1.7) (Guanosine 5'-monophosphate oxidoreductase)	Nucleic acid/nucleotide metabolism	*guaC*	BN194_09960	K0N3H4	4.01	-4.47	-22.17
Adenosylcobalamin-dependent ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*rtpR*	BN194_24230	K0NAA3	3.30	-4.48	-22.39
Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	*phoP*	BN194_10220	K0N9J6	2.84	-4.51	-22.76
3'-5' exoribonuclease yhaM (EC 3.1.-.-)	RNA degradation	*yhaM*	BN194_19070	K0NB84	3.75	-4.51	-22.83
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*manD*	BN194_02950	K0N1P4	5.97	-4.53	-23.03
Deoxyguanosine kinase (EC 2.7.1.113)	*Nucleic acid/nucleotide metabolism*		BN194_14000	K0N4M7	4.83	-4.55	-23.43
UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.3.1.98) (UDP-N-acetylmuramate dehydrogenase)	Cell wall biogenesis	*murB*	BN194_11400	K0N3X0	2.89	-4.56	-23.60

30S ribosomal protein S20	Ribosomal proteins	*rpsT*	BN194_15250	K0N4X9	4.75	-4.56	-23.61
Sporulation initiation inhibitor protein soj	Cytokinesis	*soj*	BN194_02040	K0MS45	2.40	-4.57	-23.70
Ribosomal RNA small subunit methyltransferase G (EC 2.1.1.-) (16S rRNA 7-methylguanosine methyltransferase)	tRNA/Ribosome assembly/processing	*rsmG*	BN194_02020	K0N7F1	2.91	-4.57	-23.70
Uncharacterized protein ylxR	General prediction only	*ylxR*	BN194_17570	K0NAZ6	2.95	-4.57	-23.72
LexA repressor (EC 3.4.21.-) (EC 3.4.21.88)	DNA repair/recombination	*lexA*	BN194_07970	K0N944	4.09	-4.58	-23.87
Peptide chain release factor 3 (RF-3)	Protein translation (peptide release)	*prfC*	BN194_19480	K0N9I7	3.30	-4.62	-24.56
Uncharacterized ABC transporter ATP-binding protein YfmR (EC 3.6.3.-)	ABC-type transporter systems	*yfmR*	BN194_15790	K0MVF8	3.43	-4.63	-24.81
PhoH-like protein	General prediction only	*phoH*	BN194_17020	K0NAW2	3.63	-4.64	-24.88
Uncharacterized protein	Signal transduction		BN194_18490	K0MW74	1.35	-4.64	-24.90
50S ribosomal protein L1	Ribosomal proteins	*rplA*	BN194_24150	K0N7M7	4.27	-4.64	-24.93
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	*murE*	BN194_02160	K0N1S5	3.01	-4.64	-24.93
Heat-inducible transcription repressor HrcA	Transcriptional regulation	*hrcA*	BN194_17480	K0N915	5.23	-4.65	-25.12
50S ribosomal protein L13	Ribosomal proteins	*rplM*	BN194_25850	K0N828	5.41	-4.66	-25.23
50S ribosomal protein L4	Ribosomal proteins	*rplD*	BN194_26210	K0N7H0	5.28	-4.66	-25.36
DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	*gyrB*	BN194_00060	K0N1B8	1.49	-4.69	-25.87
Uncharacterized protein	Unknown/uncharacterized		BN194_19810	K0N5W5	5.19	-4.72	-26.30
Uridine phosphorylase (EC 2.4.2.3)	Nucleic acid/nucleotide metabolism	*udp*	BN194_24830	K0NAD0	3.90	-4.72	-26.38
30S ribosomal protein S16	Ribosomal proteins	*rpsP*	BN194_17810	K0N5H1	4.47	-4.73	-26.45
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	*rpoB*	BN194_26340	K0MXV4	2.40	-4.73	-26.54
Putative thiamine pyrophosphate-containing protein ydaP	Carbohydrate-related metabolism	*ydaP*	BN194_05070	K0N8B1	5.14	-4.76	-27.18
Transcriptional regulator, TetR family	Transcriptional regulation		BN194_12190	K0MUM1	1.44	-4.77	-27.36
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*yacO*	BN194_24420	K0NC34	3.38	-4.78	-27.45
Uncharacterized protein SE_0534	*tRNA/Ribosome assembly/processing*		BN194_10150	K0N3F2	2.83	-4.78	-27.50
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	*thrS*	BN194_18860	K0N5P5	4.18	-4.79	-27.64
Elongation factor 4 (EF-4) (EC 3.6.5.n1) (Ribosomal back-translocase LepA)	Protein translation (elongation)	*lepA*	BN194_17440	K0MVU5	4.49	-4.80	-27.83

30S ribosomal protein S5	Ribosomal proteins	*rpsE*	BN194_26050	K0N853	5.09	-4.81	-28.13
30S ribosomal protein S14 type Z	Ribosomal proteins	*rpsZ,rpsN*	BN194_26090	K0MXS9	4.79	-4.82	-28.24
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism		BN194_22460	K0N6M0	4.64	-4.82	-28.27
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	*ykpA*	BN194_07220	K0N8V6	2.56	-4.84	-28.66
Translation initiation factor IF-2	Protein translation (initiation)	*infB*	BN194_17550	K0N5K7	2.49	-4.85	-28.88
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	*clpE*	BN194_19450	K0N644	5.46	-4.86	-28.98
50S ribosomal protein L15	Ribosomal proteins	*rplO*	BN194_26030	K0NAK7	5.54	-4.88	-29.39
PspC domain-containing protein	Unknown/uncharacterized	*ythC*	BN194_10300	K0N3H5	6.03	-4.89	-29.56
30S ribosomal protein S7	Ribosomal proteins	*rpsG*	BN194_26280	K0NAM9	5.37	-4.91	-29.97
Type I restriction enzyme EcoR124II M protein (EC 2.1.1.72)	IS elements/foreign DNA defense	*hsdM*	BN194_22340	K0MX17	2.64	-4.93	-30.55
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhB*	BN194_15090	K0MVA7	3.68	-4.95	-30.93
FeS cluster assembly protein sufB	Cofactor-related metabolism	*sufB*	BN194_13810	K0N4E5	2.92	-4.95	-30.99
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Cobalamin-independent methionine synthase) (Methionine synthase, vitamin-B12 independent isozyme)	Amino acid-related metabolism	*metE*	BN194_06880	K0N658	4.94	-5.02	-32.38
30S ribosomal protein S2	Ribosomal proteins	*rpsB*	BN194_17680	K0N936	6.24	-5.02	-32.39
50S ribosomal protein L5	Ribosomal proteins	*rplE*	BN194_26100	K0N859	4.61	-5.02	-32.52
30S ribosomal protein S13	Ribosomal proteins	*rpsM*	BN194_25980	K0NAK3	5.55	-5.03	-32.78
GTPase HflX (GTP-binding protein HflX)	tRNA/Ribosome assembly/processing	*hflX*	BN194_21260	K0N689	2.97	-5.05	-33.20
Uncharacterized protein			BN194_22500	K0N788	3.39	-5.06	-33.28
Uncharacterized protein	Lipid-related metabolism		BN194_11980	K0N7B3	5.88	-5.06	-33.31
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	*obg*	BN194_15440	K0MVD3	2.91	-5.08	-33.79
50S ribosomal protein L2	Ribosomal proteins	*rplB*	BN194_26190	K0MXU1	4.95	-5.09	-34.00
30S ribosomal protein S8	Ribosomal proteins	*rpsH*	BN194_26080	K0NAL1	4.07	-5.09	-34.08
50S ribosomal protein L17	Ribosomal proteins	*rplQ*	BN194_25950	K0N841	1.39	-5.10	-34.29
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	*rpoE*	BN194_26810	K0N7L4	1.34	-5.10	-34.39
Nucleotide-binding protein BN194_10470	General prediction only		BN194_10470	K0N9L7	2.34	-5.15	-35.42
Uncharacterized protein ypgQ	General prediction only	*ypgQ*	BN194_27480	K0NAX0	3.71	-5.16	-35.80

Phosphoribosylformylglycinamidine synthase subunit PurQ (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit I) (Glutaminase PurQ) (Phosphoribosylformylglycinamidine synthase subunit I)	Nucleic acid/nucleotide metabolism	*purQ*	BN194_19340	K0MWC7	4.33	-5.17	-36.04
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	4.03	-5.18	-36.14
30S ribosomal protein S4	Ribosomal proteins	*rpsD*	BN194_14440	K0MV63	4.14	-5.22	-37.22
Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	*rpiA_2, ripA*	BN194_28600	K0N8W9	2.46	-5.23	-37.52
30S ribosomal protein S14	Ribosomal proteins	*rpsN*	BN194_09950	K0N3D1	3.33	-5.24	-37.80
Cadmium efflux system accessory protein	Other transporter proteins	*cadC*	BN194_21540	K0MWU0	6.53	-5.29	-39.00
UvrABC system protein A	DNA repair/recombination	*uvrA_2*	BN194_14920	K0NAH3	2.73	-5.34	-40.60
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	*uvrA*	BN194_10450	K0N3J2	5.22	-5.35	-40.78
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshA*	BN194_26700	K0N8C7	4.67	-5.38	-41.77
Uncharacterized protein YqhY	Unknown/uncharacterized	*yqhY*	BN194_18230	K0N9A7	4.21	-5.41	-42.39
Uncharacterized protein YPL245W	Unknown/uncharacterized		BN194_25000	K0N7U3	1.35	-5.41	-42.42
1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157)	Cell wall biogenesis		BN194_09040	K0MTQ9	4.07	-5.42	-42.85
ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	*clpX*	BN194_15340	K0MVC6	2.43	-5.45	-43.84
Regulatory protein vanR	Signal transduction	*vanR*	BN194_02120	K0N7G4	3.09	-5.47	-44.32
Ribosome maturation factor RimM	tRNA/Ribosome assembly/processing	*rimM*	BN194_17790	K0MVZ6	3.74	-5.49	-44.84
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	*rnjA*	BN194_15020	K0NAH6	3.38	-5.55	-46.76
Uncharacterized protein	General prediction only		BN194_21200	K0N6M8	4.14	-5.58	-47.93
50S ribosomal protein L29	Ribosomal proteins	*rpmC*	BN194_26140	K0MXT6	5.76	-5.61	-48.71
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	*typA*	BN194_15150	K0N4W9	4.05	-5.61	-48.93
50S ribosomal protein L35	Ribosomal proteins	*rpmI*	BN194_18810	K0N5P1	2.79	-5.62	-49.29
Transcriptional regulator, xre family	Transcriptional regulation		BN194_23510	K0N6Y7	2.44	-5.64	-49.90
Glutamate--cysteine ligase/gamma-glutamylcysteine synthetase	Cofactor-related metabolism	*gshAB*	BN194_13910	K0N4F0	3.85	-5.67	-50.89
Signal recognition particle protein (Fifty-four homolog)	Protein export	*ffh*	BN194_17820	K0NB27	3.71	-5.70	-51.86
Uncharacterized RNA methyltransferase lp_1151 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_11990	K0MUI2	4.36	-5.75	-53.80
Chaperone protein ClpB	Protein folding/turnover	*clpB*	BN194_15500	K0N4Z8	4.33	-5.75	-53.99

50S ribosomal protein L27	Ribosomal proteins	*rpmA*	BN194_18270	K0NB51	2.78	-5.76	-54.38
Stage 0 sporulation protein J	Cytokinesis	*spo0J*	BN194_02050	K0N1F9	4.05	-5.87	-58.65
30S ribosomal protein S19	Ribosomal proteins	*rpsS*	BN194_26180	K0NAM1	3.04	-5.90	-59.67
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*helD*	BN194_21130	K0N9W3	3.13	-5.92	-60.42
RNA polymerase sigma factor SigA	RNA polymerase	*rpoD,sigA*	BN194_16920	K0NAV6	3.66	-5.92	-60.62
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	4.17	-6.01	-64.51
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	*gyrA*	BN194_00070	K0N6S7	1.93	-6.06	-66.94
Pur operon repressor	Transcriptional regulation	*purR_2*	BN194_26960	K0N7M9	3.45	-6.15	-71.09
Phosphoribosylformylglycinamidine synthase subunit PurL (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit II) (Glutamine amidotransferase PurL) (Phosphoribosylformylglycinamidine synthase subunit II)	Nucleic acid/nucleotide metabolism	*purL*	BN194_19330	K0N9H6	1.71	-6.17	-71.87
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	*map*	BN194_12230	K0N7E0	2.10	-6.17	-72.15
50S ribosomal protein L20	Ribosomal proteins	*rplT*	BN194_18800	K0N5Y4	4.37	-6.25	-75.98
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	*rnr*	BN194_11100	K0N3S4	3.66	-6.33	-80.26
Response regulator ArlR	Signal transduction	*arlR*	BN194_18650	K0N5X3	3.45	-6.33	-80.46
Chaperone protein ClpB	Protein folding/turnover	*clpB_2*	BN194_26350	K0N887	3.40	-6.40	-84.61
Uncharacterized protein	Unknown/uncharacterized		BN194_27210	K0N7Q6	3.27	-6.42	-85.50
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	*polA*	BN194_18930	K0N9E7	3.31	-6.47	-88.52
Uncharacterized protein	Unknown/uncharacterized		BN194_20160	K0N5Z4	3.16	-6.49	-89.88
Translation initiation factor IF-3	Protein translation (initiation)	*infC*	BN194_18820	K0NB73	3.52	-6.52	-91.96
50S ribosomal protein L9	Ribosomal proteins	*rplI*	BN194_01130	K0N4K3	7.63	-6.55	-93.40
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhA*	BN194_15080	K0N860	2.24	-6.65	-100.61
50S ribosomal protein L33	Ribosomal proteins	*rpmG*	BN194_20200	K0N697	4.25	-6.86	-116.24
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	4.33	-6.87	-116.72
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	*rex_2,rex*	BN194_23820	K0NBZ5	3.60	-6.88	-118.07
30S ribosomal protein S9	Ribosomal proteins	*rpsI*	BN194_25840	K0MXR0	2.88	-7.23	-150.45
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	*rpoC*	BN194_26330	K0NAN3	4.50	-7.40	-169.29

DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	*rpoA*	BN194_25960	K0N7E5	5.36	-7.52	-184.17
Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)	Nucleic acid/nucleotide metabolism	*purC*	BN194_19360	K0N5S8	4.73	-8.16	-286.55
Alpha-galactosidase 2 (EC 3.2.1.22)	Carbohydrate-related metabolism	*agaS_2*	BN194_22160	K0N6I2	4.33	-8.30	-315.44
Probable catabolite control protein A	Transcriptional regulation	*ccpA*	BN194_08750	K0N323	3.56	-8.69	-413.55

(7d)Protein FC LiCL pH 4.5 Vs LiCL pH 6.5

Protein names	Functional Class	Gene	Gene locus	Protein IDs	-Log t-test p-value	t-test difference	Fold change
Uncharacterized protein	Unknown/uncharacterized		BN194_07550	K0N2T9	2.37	8.95	495.32
Putative thiamine pyrophosphate-containing protein ydaP	Carbohydrate-related metabolism	*ydaP*	BN194_05070	K0N8B1	3.03	5.84	57.17
4-hydroxy-tetrahydrodipicolinate synthase (HTPA synthase) (EC 4.3.3.7)	Amino acid-related metabolism	*dapA*	BN194_01010	K0N1I2	4.47	5.32	39.96
Uncharacterized protein	Unknown/uncharacterized		BN194_24220	K0NC21	4.58	5.29	39.17
Uncharacterized protein	Unknown/uncharacterized		BN194_20070	K0NBE0	3.01	5.28	38.99
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_2*	BN194_03120	K0N7V6	3.63	5.10	34.26
Uncharacterized protein	Unknown/uncharacterized		BN194_25890	K0MXR4	2.35	5.06	33.30
Uncharacterized protein yhfI	General prediction only	*yhfI*	BN194_19200	K0N627	4.25	5.00	31.97
Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	3.31	4.86	29.10
Transaldolase (EC 2.2.1.2)	Central glycolytic/intermediary pathways	*fsa*	BN194_28440	K0MYF0	3.90	4.85	28.78
Inner membrane amino-acid ABC transporter permease protein yecS	ABC-type transporter systems	*yecS_3*	BN194_29780	K0NB99	4.74	4.84	28.69
Uncharacterized protein yqeY	Unknown/uncharacterized	*yqeY*	BN194_17040	K0MVR2	3.73	4.65	25.18
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Cobalamin-independent methionine synthase)	Amino acid-related metabolism	*metE*	BN194_06880	K0N658	4.46	4.56	23.56

(Methionine synthase, vitamin-B12 independent isozyme)							
Probable amino-acid ABC transporter-binding protein HI_1080	*ABC-type transporter systems*		BN194_06710	K0N2R6	6.95	4.52	22.89
Surface antigen	Cell wall biogenesis		BN194_21500	K0N6S2	4.94	4.25	19.04
Putative secreted protein	cell wall biogenesis		BN194_02820	K0N7S8	4.41	4.18	18.18
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC*	BN194_24670	K0NC50	4.39	4.15	17.76
Probable dipeptidase A (EC 3.4.-.-)	Amino acid-related metabolism	*pepDA*	BN194_00410	K0N1E0	3.47	4.12	17.36
Uncharacterized peptidase yqhT (EC 3.4.-.-)	Amino acid-related metabolism	*yqhT*	BN194_18260	K0N5K4	3.99	4.08	16.90
Esterase/lipase	General prediction only	*yneB*	BN194_20230	K0N9P7	4.07	4.02	16.25
Uncharacterized protein	Unknown/uncharacterized		BN194_01080	K0N4J7	4.62	3.95	15.49
30S ribosomal protein S14	Ribosomal proteins	*rpsN*	BN194_09950	K0N3D1	2.57	3.93	15.28
Cytochrome d ubiquinol oxidase subunit 1 (EC 1.10.3.-)	Membrane bioenergetics	*cydA_2*	BN194_23410	K0N6Y2	4.14	3.84	14.35
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	*ilvE*	BN194_21620	K0NBM4	4.56	3.79	13.80
Glucose 1-dehydrogenase 2 (EC 1.1.1.47)	Central glycolytic/intermediary pathways	*gdhII*	BN194_23130	K0NA64	2.97	3.78	13.73
Hydroxyacid oxidase (EC 1.1.3.15)	Central glycolytic/intermediary pathways	*haox*	BN194_24790	K0MXH5	2.40	3.78	13.70
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE*	BN194_01720	K0N7C1	4.74	3.77	13.60
Penicillin-binding protein 2B	Cytokinesis	*pbpB*	BN194_14700	K0N4S9	5.59	3.75	13.42
Uncharacterized protein	Unknown/uncharacterized		BN194_05660	K0N2I2	2.46	3.62	12.30
Deoxyguanosine kinase (EC 2.7.1.113)	*Nucleic acid/nucleotide metabolism*		BN194_14000	K0N4M7	2.44	3.58	11.98
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	*rpoZ*	BN194_18100	K0N5T7	3.43	3.55	11.68
Gluconate 5-dehydrogenase (EC 1.1.1.69)	General prediction only	*idnO*	BN194_08150	K0N2Z5	4.86	3.45	10.95
Malolactic enzyme (EC 1.-.-.-)	Tricarboxylic acid pathway	*mleA*	BN194_08070	K0N949	3.80	3.38	10.41
Possible TrsG protein	Unknown/uncharacterized		BN194_00240	K0MRM8	4.00	3.34	10.15
Lipoprotein	ABC-type transporter systems	*metQ_2*	BN194_13740	K0MV23	4.66	3.34	10.12

ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25510	K0N7B2	3.76	3.34	10.10
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF_2*	BN194_19090	K0MWB2	5.10	3.28	9.71
Peptidase T (EC 3.-.-.-) (EC 3.4.11.-) (EC 3.4.11.4)	Amino acid-related metabolism	*pepT*	BN194_03110	K0N213	3.48	3.27	9.64
Hypothetical lipoprotein	Unknown/uncharacterized		BN194_12440	K0MUR1	4.14	3.26	9.56
Penicillin-binding protein 3	Cell wall biogenesis	*pbpC*	BN194_03320	K0N7W9	4.00	3.14	8.80
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_3*	BN194_14020	K0NAD1	3.92	3.03	8.16
tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	tRNA/Ribosome assembly/processing	*mnmG,gidA*	BN194_30590	K0MYX4	3.54	2.98	7.91
Glutamate--cysteine ligase/gamma-glutamylcysteine synthetase	Cofactor-related metabolism	*gshAB*	BN194_13910	K0N4F0	3.46	2.94	7.69
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*yqeC*	BN194_02330	K0N532	3.73	2.87	7.32
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA*	BN194_09090	K0MTR3	5.54	2.81	6.99
Uncharacterized protein	Unknown/uncharacterized		BN194_12200	K0N464	4.94	2.73	6.64
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_4*	BN194_22020	K0NBQ1	4.42	2.73	6.63
Methionine import ATP-binding protein MetN (EC 3.6.3.-)	ABC-type transporter systems	*metN*	BN194_13750	K0N4L1	3.92	2.71	6.53
Exodeoxyribonuclease 7 small subunit (EC 3.1.11.6) (Exodeoxyribonuclease VII small subunit)	DNA repair/recombination	*xseB*	BN194_18190	K0MW55	2.08	2.70	6.50
Uncharacterized protein	Unknown/uncharacterized		BN194_11890	K0MUG0	6.18	2.69	6.44
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	*luxS*	BN194_08330	K0N6J0	3.71	2.63	6.19
Alpha-galactosidase 2 (EC 3.2.1.22)	Carbohydrate-related metabolism	*agaS_2*	BN194_22160	K0N6I2	0.58	2.61	6.11
Uncharacterized protein	Unknown/uncharacterized		BN194_16570	K0NAT3	1.77	2.58	5.97
Penicillin-binding protein 1A	Cell wall biogenesis	*ponA*	BN194_16720	K0NAU3	4.29	2.57	5.92
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_27170	K0NCZ6	3.42	2.52	5.72
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	*mtlD_3mtlD*	BN194_30400	K0N9C8	3.67	2.50	5.65
Putative integral membrane protein	Unknown/uncharacterized		BN194_01660	K0N1M7	1.90	2.47	5.56
Virulence factor mviM	General prediction only	*mviM*	BN194_13310	K0N4B2	3.35	2.37	5.17

2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	*dkgB*	BN194_08260	K0N347	2.90	2.35	5.11
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB_2*	BN194_29110	K0N8A4	2.92	2.33	5.02
Uncharacterized protein	Unknown/uncharacterized		BN194_15520	K0NAK2	2.27	2.32	4.99
Esterase/lipase	General prediction only		BN194_30390	K0MYV7	2.22	2.27	4.83
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	*dhaK_2*	BN194_04980	K0N5Q3	4.36	2.22	4.66
Putative N-acetylmuramoyl-L-alanine amidase YrvJ (EC 3.5.1.28)	Cytokinesis	*yrvJ*	BN194_17200	K0N5G4	3.17	2.22	4.65
4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase) (EC 1.17.1.8)	Amino acid-related metabolism	*dapB*	BN194_01000	K0N166	3.10	2.21	4.62
Uncharacterized protein	*Central glycolytic/intermediary pathways*		BN194_04970	K0N8A3	3.32	2.16	4.46
Uncharacterized protein ynbB	Cell defense/detoxification	*ynbB*	BN194_18380	K0N9B7	3.16	2.15	4.45
Uncharacterized protein	Unknown/uncharacterized		BN194_20240	K0MWI3	0.81	2.11	4.33
NAD-dependent epimerase/dehydratase:3-beta hydroxysteroid dehydrogenase/isomerase:NmrA-like	General prediction only		BN194_25520	K0NCC8	2.88	2.11	4.32
Uncharacterized protein	Unknown/uncharacterized		BN194_19210	K0N5R7	2.33	2.11	4.31
Uncharacterized protein	*Cell surface proteins/internalins*		BN194_20060	K0N5Y7	1.36	2.10	4.29
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*pip_2*	BN194_27140	K0MY30	3.42	2.10	4.28
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	*clpP_2, clpP*	BN194_10510	K0N3M4	3.38	2.09	4.25
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	*pheS*	BN194_18570	K0NB64	3.67	2.06	4.18
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.-)	Lipid-related metabolism	*plsC*	BN194_17710	K0N5F1	2.82	2.05	4.15
Glycosyl transferase family 2	Cell wall biogenesis		BN194_02460	K0N1U7	0.57	2.01	4.04
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	*fabF*	BN194_22540	K0MX40	3.10	2.01	4.04
Mannose permease IID component	Phosphotransferase systems	*manZ_9*	BN194_29700	K0N954	3.08	2.01	4.04
ErfK family protein	Cell wall biogenesis		BN194_26570	K0NCS1	4.20	2.01	4.03
DltD protein	Cell wall biogenesis		BN194_08620	K0N978	2.93	2.00	4.00
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)		*accC*	BN194_22510	K0N6M5	2.15	2.00	4.00

ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136) (ADP-dependent NAD(P)HX dehydratase)	Cofactor-related metabolism	*nnrD*	BN194_09250	K0N360	2.52	1.99	3.97
Large-conductance mechanosensitive channel	Other transporter proteins	*mscL*	BN194_26890	K0MY02	1.58	1.99	3.96
Sporulation initiation inhibitor protein soj	Cytokinesis	*soj*	BN194_02040	K0MS45	2.55	1.96	3.90
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	*map*	BN194_12230	K0N7E0	5.58	1.94	3.84
Protein lacX, plasmid	Carbohydrate-related metabolism	*lacX*	BN194_27070	K0NCY0	4.43	1.93	3.81
Sorbose permease IIC component	Phosphotransferase systems	*sorA_4*	BN194_29710	K0N8G4	2.65	1.93	3.81
UPF0342 protein yheA	Unknown/uncharacterized	*yheA*	BN194_19080	K0N9F7	3.71	1.92	3.79
Uncharacterized protein				K0N2Q1;K0MXJ1	3.15	1.89	3.72
Glycosyl transferase group 1	Cell wall biogenesis		BN194_09760	K0N3F8	0.80	1.89	3.70
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	*pepN*	BN194_05410	K0N2F5	2.89	1.85	3.61
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	*pepDB*	BN194_21110	K0N678	3.28	1.84	3.57
Uncharacterized protein			BN194_22500	K0N788	0.54	1.84	3.57
Uncharacterized protein	Unknown/uncharacterized		BN194_15540	K0MVD8	2.36	1.83	3.56
Uncharacterized protein ydcI	General prediction only	*ydcI*	BN194_14310	K0N4I1	1.27	1.83	3.55
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*gnd*	BN194_18660	K0N5N2	2.79	1.82	3.53
Uncharacterized protein YPL245W	Unknown/uncharacterized		BN194_25000	K0N7U3	1.56	1.81	3.52
Uncharacterized protein ypuA	Unknown/uncharacterized	*ypuA*	BN194_27250	K0N8I3	3.46	1.79	3.46
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	*prsA*	BN194_19060	K0N5Q8	4.76	1.78	3.43
Uncharacterized protein	Unknown/uncharacterized	*yvcC*	BN194_05260	K0N2E5	4.11	1.78	3.43
GTPase HflX (GTP-binding protein HflX)	tRNA/Ribosome assembly/processing	*hflX*	BN194_21260	K0N689	2.09	1.77	3.40
Putative 2-hydroxyacid dehydrogenase SH0752 (EC 1.1.1.-)	General prediction only		BN194_01890	K0MS33	2.38	1.76	3.38
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI_2*	BN194_16210	K0N508	1.27	1.75	3.37
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_02890	K0MSD4	1.61	1.75	3.37
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	*BN194_21350*	BN194_21780	K0N6Q5	3.90	1.74	3.35

S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	*queA*	BN194_08370	K0N965	2.29	1.74	3.34
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatC*	BN194_11950	K0N436	6.25	1.73	3.32
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	*dhaM*	BN194_04960	K0N2C2	1.62	1.73	3.31
GTP pyrophosphokinase yjbM (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*yjbM*	BN194_09870	K0N9G5	1.84	1.72	3.29
Uncharacterized glycosyltransferase HI_0868 (EC 2.4.-.-)	Cell wall biogenesis		BN194_02410	K0N1U3	1.08	1.69	3.24
TPR repeats containing protein	Unknown/uncharacterized		BN194_14960	K0N4M8	2.62	1.69	3.22
Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase)	Nucleic acid/nucleotide metabolism	*pyrB*	BN194_16480	K0N8N2	2.54	1.69	3.22
Uncharacterized protein ACIAD3023	Cell defense/detoxification		BN194_07010	K0N2T5	1.18	1.69	3.22
Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	General prediction only	*yqiG*	BN194_25330	K0NAG4	0.95	1.68	3.21
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	*pepQ*	BN194_08740	K0MTP0	2.65	1.65	3.15
D-alanine--poly(phosphoribitol) ligase subunit 2 (EC 6.1.1.13) (D-alanyl carrier protein)	Cell wall biogenesis	*dltC*	BN194_08610	K0N361	1.98	1.65	3.14
Hydrolase of the alpha/beta superfamily	General prediction only		BN194_08240	K0MTK6	2.32	1.64	3.11
Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Phosphoglucose isomerase) (Phosphohexose isomerase)	Central glycolytic/intermediary pathways	*pgi*	BN194_12580	K0N7I6	2.58	1.62	3.08
Signal peptidase I (EC 3.4.21.89)	Protein export	*lepB*	BN194_02610	K0N1V9	2.59	1.62	3.08
Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	*Steap4*	BN194_01990	K0MS41	2.84	1.61	3.06
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC*	BN194_00080	K0N486	1.26	1.61	3.05
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA2,gpmA*	BN194_22740	K0MX58	2.89	1.61	3.04
Transcriptional regulator, PadR-like family	Transcriptional regulation		BN194_26580	K0NAQ3	0.50	1.60	3.04
Uncharacterized protein yjbK	General prediction only	*yjbK*	BN194_09860	K0N3G6	1.21	1.60	3.03
SPFH/Band 7/PHB domain protein	Unknown/uncharacterized		BN194_29820	K0NDM1	1.88	1.59	3.02
Glycolate oxidase subunit glcD	General prediction only	*glcD*	BN194_24440	K0MXF3	1.52	1.59	3.01

Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	*ptp3*	BN194_23520	K0NBX6	1.26	1.59	3.00
Guanylate kinase (EC 2.7.4.8)	Nucleic acid/nucleotide metabolism	*gmk_2*	BN194_21480	K0N9Y7	1.66	1.58	3.00
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	*pgcA*	BN194_10370	K0N9K8	5.38	1.57	2.98
Uncharacterized protein yaaQ	Unknown/uncharacterized	*yaaQ*	BN194_23940	K0MXD1	1.96	1.55	2.93
Uncharacterized protein	Unknown/uncharacterized		BN194_12100	K0N456	1.04	1.55	2.92
Uncharacterized protein yutG	Lipid-related metabolism	*yutG*	BN194_08940	K0MTQ3	3.45	1.53	2.90
UPF0755 protein yrrL	Unknown/uncharacterized	*yrrL*	BN194_18550	K0N5W7	3.68	1.52	2.87
Heat-inducible transcription repressor HrcA	Transcriptional regulation	*hrcA*	BN194_17480	K0N915	2.21	1.52	2.87
Uncharacterized protein	Unknown/uncharacterized		BN194_20190	K0MWI0	2.56	1.52	2.86
Uncharacterized protein	General prediction only		BN194_01300	K0N194	1.86	1.52	2.86
Transcription-repair-coupling factor (TRCF) (EC 3.6.4.-)	DNA repair/recombination	*mfd*	BN194_26540	K0MXW9	1.44	1.51	2.84
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	*msrA_2,msrA*	BN194_15860	K0N4W6	0.78	1.49	2.80
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP*	BN194_08180	K0N6I0	0.75	1.48	2.78
Predicted pyrophosphatase	General prediction only		BN194_15360	K0N4R6	0.94	1.48	2.78
Ribonuclease H (EC 3.1.26.4)	DNA repair/recombination	*rnhA*	BN194_27580	K0NAX8	3.56	1.47	2.78
Glycine betaine/carnitine/choline-binding protein OpuCC	ABC-type transporter systems	*opuCC*	BN194_00670	K0N6Z3	2.92	1.47	2.77
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism		BN194_22460	K0N6M0	2.90	1.46	2.76
Uncharacterized protein YxeH	General prediction only	*yxeH*	BN194_04750	K0N1Y7	1.40	1.45	2.74
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	*glyA*	BN194_13540	K0MV12	2.05	1.43	2.69
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	*ykwC*	BN194_02520	K0N7M3	3.04	1.43	2.69
Probable calcium-transporting ATPase (EC 3.6.3.8)	Other transporter proteins	*pacL*	BN194_11490	K0MUB1	1.95	1.43	2.69
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	*gatA*	BN194_11960	K0N3Z6	2.73	1.42	2.68
NADH-dependent butanol dehydrogenase A (EC 1.1.1.-)	Carbohydrate-related metabolism	*bdhA*	BN194_22640	K0MX50	0.84	1.42	2.68

Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	*rp2*	BN194_17060	K0N598	1.45	1.41	2.66
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	*murC*	BN194_18950	K0N600	2.13	1.41	2.65
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1_2*	BN194_12550	K0N496	1.15	1.41	2.65
Threonylcarbamoyl-AMP synthase (TC-AMP synthase) (EC 2.7.7.87) (L-threonylcarbamoyladenylate synthase)	tRNA/Ribosome assembly/processing	*ywlC*	BN194_13530	K0N7S6	0.98	1.40	2.63
Anaerobic ribonucleoside-triphosphate reductase-activating protein (EC 1.97.1.-)	Nucleic acid/nucleotide metabolism	*nrdG*	BN194_19270	K0NB93	2.10	1.39	2.61
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	2.27	1.38	2.60
D-2-hydroxyacid dehydrogenase (EC 1.1.1.-)	General prediction only	*ddh*	BN194_16660	K0N557	2.16	1.37	2.59
ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	*atpF*	BN194_13580	K0N7S9	2.48	1.37	2.59
Phosphohydrolase (MutT/nudix family protein)	General prediction only		BN194_27160	K0N7P9	1.52	1.37	2.58
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	*agaS*	BN194_02940	K0MSD9	2.97	1.36	2.57
Uncharacterized protein ywnB	General prediction only	*ywnB_2*	BN194_20050	K0N687	2.31	1.36	2.56
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	*dnaN*	BN194_00020	K0N6S3	4.24	1.36	2.56
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA*	BN194_17880	K0N983	4.07	1.36	2.56
Transcriptional regulator lytR	Transcriptional regulation	*lytR_4*	BN194_23780	K0NA85	3.32	1.35	2.56
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	*agl*	BN194_27950	K0N8T1	3.36	1.34	2.53
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	*accA*	BN194_22470	K0NBS6	2.39	1.34	2.53
Membrane protein	Unknown/uncharacterized		BN194_22700	K0N7C6	0.61	1.34	2.53
Xre-like DNA-binding protein	Transcriptional regulation		BN194_10050	K0N3E1	1.88	1.33	2.52
Uncharacterized protein yxjH	Amino acid-related metabolism	*yxjH*	BN194_08320	K0N962	0.86	1.32	2.49
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA_2*	BN194_29210	K0N8B2	2.63	1.31	2.48
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	*citX*	BN194_20300	K0N6A3	0.93	1.31	2.48
Uncharacterized protein	RNA degradation		BN194_11250	K0N3V2	1.36	1.31	2.47
S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	*metK*	BN194_09150	K0N352	1.75	1.30	2.46

Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatB*	BN194_11970	K0NA01	2.81	1.29	2.44
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase 2 (EC 5.4.2.1)	Central glycolytic/intermediary pathways	*gpmA2_2*	BN194_27560	K0N7W0	1.51	1.29	2.44
Protein QmcA	Unknown/uncharacterized	*qmcA*	BN194_12070	K0NA10	3.74	1.28	2.43
Uncharacterized protein ybbP	Unknown/uncharacterized	*ybbP*	BN194_11530	K0N776	1.46	1.28	2.43
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	*glpK_2,glpK*	BN194_27720	K0ND65	0.99	1.27	2.40
Uncharacterized protein yeaE	General prediction only	*yeaE*	BN194_07040	K0MT72	1.36	1.25	2.39
50S ribosomal protein L32	Ribosomal proteins	*rpmF*	BN194_15510	K0N4T0	2.48	1.25	2.38
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE_2*	BN194_19740	K0MWF1	1.98	1.25	2.37
Histidinol-phosphatase	General prediction only		BN194_14010	K0N4F8	1.00	1.24	2.36
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03940	K0MSJ3	2.11	1.23	2.35
Putative competence-damage inducible protein	General prediction only	*cinA*	BN194_10070	K0N9I3	1.15	1.23	2.35
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	*grpE*	BN194_17470	K0NAZ2	1.43	1.22	2.33
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	*tpiA*	BN194_11030	K0N736	3.06	1.22	2.32
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	*yjlD*	BN194_24330	K0NAA7	2.30	1.21	2.31
Glutathione reductase, chloroplastic (EC 1.8.1.7)	Cofactor-related metabolism	*GOR*	BN194_23200	K0N7H3	1.33	1.20	2.30
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdE2*	BN194_16600	K0N5A1	2.45	1.20	2.29
Cell shape-determining protein MreC (Cell shape protein MreC)	Cytokinesis	*mreC*	BN194_14560	K0N4K0	2.60	1.19	2.29
MreB-like protein	Cytokinesis	*mbl*	BN194_13650	K0N4K5	2.23	1.19	2.29
Uncharacterized protein ycaC	General prediction only	*ycaC*	BN194_29650	K0N948	1.49	1.19	2.28
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB*	BN194_17900	K0N5S3	2.18	1.18	2.27
Uncharacterized protein	Unknown/uncharacterized		BN194_27530	K0NAX5	1.70	1.18	2.26
Alternansucrase	Cell wall biogenesis		BN194_02430	K0N547	3.35	1.18	2.26
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)	Nucleic acid/nucleotide metabolism	*ntd*	BN194_24240	K0MXE6	1.82	1.17	2.25
Probable catabolite control protein A	Transcriptional regulation	*ccpA*	BN194_08750	K0N323	2.85	1.17	2.25

DNA polymerase III PolC-type (PolIII) (EC 2.7.7.7)	DNA replication-related	*polC*	BN194_17600	K0N5L6	0.82	1.17	2.25
Uncharacterized protein	Unknown/uncharacterized		BN194_20720	K0NBH5	2.23	1.14	2.21
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	*rpoC*	BN194_26330	K0NAN3	2.15	1.14	2.21
Cell division protein DivIB	Cytokinesis	*divIB*	BN194_14740	K0MV80	0.97	1.14	2.20
Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*nrdD*	BN194_01250	K0N190	0.51	1.13	2.20
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	*deoB*	BN194_02800	K0N1N0	1.75	1.13	2.19
Nucleoid-associated protein BN194_23980	General prediction only		BN194_23980	K0NA95	1.07	1.12	2.17
Guanine deaminase (EC 3.5.4.3)	Nucleic acid/nucleotide metabolism	*guaD*	BN194_13320	K0NA96	2.42	1.11	2.16
5'-nucleotidase (EC 3.1.3.5)	General prediction only		BN194_08220	K0N957	1.69	1.11	2.16
Maf-like protein maf	General prediction only	*maf*	BN194_23700	K0N7K3	1.06	1.11	2.16
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	*gpsB*	BN194_16690	K0MVN5	2.30	1.09	2.13
D-lactate dehydrogenase (EC 1.1.1.28)	Carbohydrate-related metabolism	*dld*	BN194_06590	K0MT28	1.70	1.06	2.09
Uncharacterized protein	Unknown/uncharacterized		BN194_29450	K0N932	3.49	1.06	2.08
Uncharacterized protein yqhL	General prediction only	*yqhL*	BN194_18410	K0N5L5	1.56	1.06	2.08
Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	Carbohydrate-related metabolism	*scrB*	BN194_22440	K0MX27	0.61	1.05	2.07
Oxidoreductase YdhF (EC 1.-.-.-)	General prediction only	*ydhF*	BN194_25320	K0NCA1	3.35	1.04	2.06
SMC domain protein	DNA repair/recombination		BN194_07540	K0MTC3	1.70	1.04	2.06
Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-)		*rsmB*	BN194_18040	K0MW45	1.40	1.03	2.05
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA*	BN194_01620	K0N7B1	0.52	1.03	2.04
Uncharacterized protein	Unknown/uncharacterized		BN194_15850	K0N527	2.32	1.03	2.04
Probable copper-transporting P-type ATPase B (EC 3.6.3.-)	Other transporter proteins	*copB*	BN194_19280	K0N9H1	1.37	1.03	2.04
DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	*gyrB*	BN194_00060	K0N1B8	2.53	1.02	2.03
Predicted Zn-dependent peptidase	*Amino acid-related metabolism*		BN194_10020	K0N9H8	0.47	1.02	2.03
Diaminopimelate decarboxylase (DAP decarboxylase) (DAPDC) (EC 4.1.1.20)	Amino acid-related metabolism	*lysA*	BN194_01030	K0N4I7	0.38	1.02	2.03
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	*thiD_2*	BN194_07650	K0N2U9	0.84	1.02	2.02

60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	*groL,groEL*	BN194_23750	K0N7K7	2.98	1.00	2.00
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (ACCase subunit beta) (Acetyl-CoA carboxylase carboxyltransferase subunit beta) (EC 6.4.1.2)	Lipid-related metabolism	*accD*	BN194_22480	K0NA32	2.33	1.00	2.00
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	*mco*	BN194_25410	K0N7A4	1.42	1.00	2.00
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	*rpoB*	BN194_26340	K0MXV4	2.35	1.00	1.99
NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	4.09	0.99	1.99
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_29810	K0N8H4	2.36	0.98	1.97
Predicted acetyltransferase			BN194_11820	K0N9Y9	1.00	0.98	1.97
FeS cluster assembly protein sufB	Cofactor-related metabolism	*sufB*	BN194_13810	K0N4E5	4.04	0.97	1.97
18 kDa heat shock protein	Protein folding/turnover	*hsp18*	BN194_07570	K0N8Z3	0.39	0.97	1.96
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP_2, acpP*	BN194_22590	K0MX45	1.47	0.97	1.95
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh*	BN194_26560	K0N7J5	2.88	0.96	1.95
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	*gltX*	BN194_24470	K0NC38	1.72	0.96	1.94
CBS domain-containing protein	Unknown/uncharacterized		BN194_26610	K0N7J7	1.75	0.96	1.94
Uncharacterized lipoprotein yerH	General prediction only	*yerH*	BN194_11940	K0MUH2	2.86	0.96	1.94
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*fruK*	BN194_15420	K0NAJ6	3.02	0.95	1.94
Uncharacterized protein	Unknown/uncharacterized		BN194_25820	K0NCG9	3.07	0.93	1.91
Glycerol-3-phosphate ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_11260	K0N3T6	1.90	0.93	1.91
UPF0039 protein SAR1027	General prediction only		BN194_19510	K0N5U0	1.87	0.93	1.91
Uncharacterized protein ytxK	DNA repair/recombination	*ytxK*	BN194_11680	K0N791	1.02	0.93	1.90
Uncharacterized protein	Unknown/uncharacterized		BN194_08190	K0MTK3	0.92	0.92	1.89
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*pheT*	BN194_18560	K0N5M4	2.52	0.91	1.88
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA1,gpmA*	BN194_24750	K0N7R7	0.90	0.91	1.88

Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_3*	BN194_21990	K0MWY0	0.54	0.91	1.88
Transcriptional regulator lytR	Transcriptional regulation	*lytR_3*	BN194_21700	K0N6U3	0.96	0.90	1.87
Transcriptional regulator lytR	Transcriptional regulation	*lytR*	BN194_02540	K0MS94	2.41	0.90	1.87
Pyridoxine 5'-phosphate oxidase V related favin-nucleotide-binding protein	Cofactor-related metabolism		BN194_01900	K0N1E7	0.72	0.90	1.87
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ysgA*	BN194_18610	K0N5M8	2.77	0.90	1.87
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacA*	BN194_07500	K0N2T4	1.61	0.90	1.86
DNA polymerase III subunit delta (EC 2.7.7.7)	DNA replication-related	*holB*	BN194_23930	K0NA93	0.44	0.90	1.86
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	*dltA*	BN194_08590	K0MTN0	1.64	0.89	1.86
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB*	BN194_19860	K0N5X0	3.41	0.89	1.85
Putative RNA methyltransferase YpsC (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ypsC*	BN194_16670	K0NAU0	1.56	0.89	1.85
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	1.55	0.88	1.85
tRNA pseudouridine synthase A (EC 5.4.99.12) (tRNA pseudouridine(38-40) synthase) (tRNA pseudouridylate synthase I) (tRNA-uridine isomerase I)	tRNA/Ribosome assembly/processing	*truA*	BN194_25910	K0N7E2	0.89	0.88	1.84
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	*atpD*	BN194_13620	K0NAB3	2.14	0.88	1.84
Protein translocase subunit SecY	Protein export	*secY*	BN194_26020	K0NCJ6	1.01	0.88	1.84
Uncharacterized protein yieF	General prediction only	*yieF_2*	BN194_06540	K0MT25	0.44	0.87	1.83
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	*pdhD*	BN194_15110	K0N4P1	1.44	0.86	1.82
Maltose ABC transporter, periplasmic maltose-binding protein	*ABC-type transporter systems*		BN194_11200	K0N3U4	1.32	0.86	1.81
Uncharacterized protein	Unknown/uncharacterized		BN194_23650	K0N7J8	2.26	0.86	1.81
Septation ring formation regulator EzrA	Cytokinesis	*ezrA*	BN194_14460	K0N4J2	1.54	0.86	1.81
UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	1.83	0.85	1.81
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	*sph*	BN194_04930	K0N5Q0	1.88	0.85	1.80
Uncharacterized protein	Unknown/uncharacterized		BN194_13840	K0MV29	1.73	0.85	1.80

N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*manD*	BN194_02950	K0N1P4	1.49	0.85	1.80
Uncharacterized protein yeaO	Unknown/uncharacterized	*yeaO*	BN194_08040	K0MTJ2	1.29	0.85	1.80
Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	2.06	0.84	1.79
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	*ssdA*	BN194_24140	K0MXE0	2.52	0.84	1.79
Uncharacterized RNA methyltransferase lp_1151 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_11990	K0MUI2	1.62	0.84	1.79
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF*	BN194_08770	K0N987	1.82	0.84	1.79
Cell wall surface anchor family protein	*Cell surface proteins/internalins*		BN194_05290	K0MSU3	1.23	0.83	1.78
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox*	BN194_01780	K0N4U4	0.45	0.83	1.77
DNA mismatch repair protein MutL	DNA repair/recombination	*mutL*	BN194_23710	K0N6Z8	0.96	0.82	1.76
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	1.12	0.82	1.76
GNAT family acetyltransferase	General prediction only		BN194_29620	K0NDL0	0.51	0.82	1.76
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO*	BN194_12030	K0N7B7	0.95	0.82	1.76
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification		BN194_25280	K0NAG2	0.36	0.81	1.76
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	*fabK*	BN194_22580	K0NA38	1.33	0.81	1.76
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF*	BN194_17910	K0N5I3	1.93	0.81	1.76
Uncharacterized ABC transporter ATP-binding protein YdiF	General prediction only	*ydiF*	BN194_23830	K0NA88	0.52	0.80	1.75
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhA*	BN194_15080	K0N860	1.22	0.80	1.74
Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.193)	tRNA/Ribosome assembly/processing	*rsmE*	BN194_17250	K0N5G8	0.58	0.80	1.74
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1*	BN194_09110	K0N399	2.80	0.79	1.73
Uncharacterized ABC transporter ATP-binding protein YdbJ	ABC-type transporter systems	*ydbJ*	BN194_24600	K0N7Q8	0.51	0.79	1.73
Uncharacterized protein	Unknown/uncharacterized		BN194_27210	K0N7Q6	1.57	0.79	1.73
Acyltransferase 3			BN194_15460	K0N4S6	1.34	0.79	1.73
Integral membrane protein	Unknown/uncharacterized		BN194_07890	K0MTI0	0.45	0.79	1.73
50S ribosomal protein L24	Ribosomal proteins	*rplX*	BN194_26110	K0N7F9	1.95	0.79	1.73

Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	1.11	0.79	1.72
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC*	BN194_17890	K0MW34	0.97	0.78	1.72
Uncharacterized protein	Unknown/uncharacterized		BN194_08020	K0N947	2.73	0.78	1.72
Acid shock protein	Protein folding/turnover		BN194_29440	K0MYM2	0.74	0.78	1.72
Putative tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207) (tRNA (cytidine/uridine-2'-O-)-methyltransferase)	*tRNA/Ribosome assembly/processing*		BN194_09990	K0MTX9	0.77	0.78	1.72
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	*purA*	BN194_01160	K0N1J0	3.39	0.77	1.71
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC_2*	BN194_24680	K0NAC2	1.97	0.77	1.70
Alkyl hydroperoxide reductase subunit C (EC 1.11.1.15)	Cell defense/detoxification	*ahpC*	BN194_26250	K0N876	0.35	0.77	1.70
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshA*	BN194_26700	K0N8C7	1.81	0.76	1.69
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	*thrS*	BN194_18860	K0N5P5	2.84	0.75	1.69
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	*accB*	BN194_22530	K0NA35	0.70	0.75	1.69
Cell division protein FtsX	Cytokinesis	*ftsX*	BN194_10200	K0N3G0	1.61	0.75	1.68
Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	ABC-type transporter systems	*ecfA2, ecfA*	BN194_25920	K0NCI4	0.92	0.75	1.68
Exopolyphosphatase	Membrane bioenergetics		BN194_27280	K0NAV4	1.86	0.74	1.67
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	1.63	0.74	1.67
Predicted hydrolase of the HAD superfamily	General prediction only	*mtlD*	BN194_30450	K0N9D4	0.78	0.74	1.67
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	*fabZ*	BN194_22520	K0NBS8	1.05	0.73	1.65
L-sorbose 1-phosphate reductase (EC 1.1.1.-)	Carbohydrate-related metabolism	*sorE*	BN194_04300	K0N1W2	0.21	0.73	1.65
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	*eno*	BN194_11040	K0MU67	1.41	0.72	1.65
Uncharacterized protein	Unknown/uncharacterized		BN194_08270	K0N959	0.51	0.72	1.65
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	*murI*	BN194_08640	K0MTN4	2.15	0.72	1.65
Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	0.82	0.72	1.65
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA_2*	BN194_18340	K0MW64	2.30	0.72	1.64

50S ribosomal protein L18	Ribosomal proteins	*rplR*	BN194_26060	K0N7F4	0.89	0.70	1.63
50S ribosomal protein L20	Ribosomal proteins	*rplT*	BN194_18800	K0N5Y4	1.05	0.70	1.63
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	Central glycolytic/intermediary pathways	*gap*	BN194_11010	K0N3R3	2.71	0.70	1.62
Monooxygenase	General prediction only		BN194_07600	K0N2U5	0.20	0.70	1.62
Transcriptional regulator GltC	Transcriptional regulation	*nac*	BN194_16620	K0NAT7	2.26	0.70	1.62
tRNA modification GTPase MnmE (EC 3.6.-.-)	tRNA/Ribosome assembly/processing	*mnmE,trmE*	BN194_30600	K0N9F0	0.69	0.69	1.62
Uncharacterized protein	Unknown/uncharacterized		BN194_19050	K0N613	0.42	0.69	1.61
Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) (Peptide-methionine (R)-S-oxide reductase)	Posttranslational modification	*msrB*	BN194_17090	K0MVR6	0.30	0.68	1.61
Cell division protein FtsZ	Cytokinesis	*ftsZ*	BN194_14760	K0N4L6	2.12	0.68	1.60
Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Phosphotransferase system, enzyme I)		*ptsI*	BN194_19410	K0N5T2	1.92	0.68	1.60
Uncharacterized protein	Cell wall biogenesis		BN194_02360	K0N1U1	1.71	0.68	1.60
UPF0478 protein SAOUHSC_01855	Signal transduction		BN194_08710	K0N365	1.43	0.67	1.59
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	*clpC*	BN194_21680	K0N9Z7	2.27	0.67	1.59
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		BN194_21400	K0N6R1	1.17	0.66	1.58
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	*glgD*	BN194_21590	K0MWU4	1.32	0.65	1.57
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		BN194_03130	K0N5D9	0.65	0.65	1.57
Uncharacterized protein	General prediction only	*gpm1*	BN194_13960	K0N4F5	0.89	0.64	1.56
Uncharacterized protein	Unknown/uncharacterized		BN194_28350	K0N8V3	1.48	0.63	1.55
Protein LemA	Unknown/uncharacterized	*lemA*	BN194_27350	K0N8J7	1.66	0.62	1.54
UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	2.39	0.62	1.53
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	*deoD*	BN194_02810	K0N1Z0	1.41	0.62	1.53
Rod shape-determining protein MreB	Cytokinesis	*mreB*	BN194_14550	K0N4R7	1.38	0.61	1.52
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	1.46	0.61	1.52
Glucose-1-phosphate thymidylyltransferase		*rmlA*		K0N699;K0MWW4	1.86	0.60	1.52
LPXTG-motif cell wall anchor domain protein			BN194_26300	K0N883	0.83	0.59	1.51

Uncharacterized protein yitL	General prediction only	*yitL*	BN194_15600	K0N505	1.08	0.59	1.51
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	*bkr4*	BN194_22550	K0N799	0.83	0.59	1.51
Holo-[acyl-carrier-protein] synthase (Holo-ACP synthase) (EC 2.7.8.7) (4'-phosphopantetheinyl transferase AcpS)	Cofactor-related metabolism	*acpS*	BN194_26690	K0MXY2	0.60	0.59	1.51
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrDA, pyrD*	BN194_19150	K0N623	2.93	0.59	1.50
Uncharacterized protein in fgs 3'region	General prediction only		BN194_14530	K0N802	0.34	0.59	1.50
Uncharacterized protein	Phosphotransferase systems		BN194_04820	K0N885	0.42	0.59	1.50
Ribosome biogenesis GTPase A	tRNA/Ribosome assembly/processing	*rbgA*	BN194_15940	K0MVH2	0.18	0.58	1.50
Alanine racemase (EC 5.1.1.1)	Amino acid-related metabolism	*alr*	BN194_26680	K0NAR1	1.08	0.58	1.50
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		BN194_18780	K0N9E0	0.63	0.58	1.49
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB2,pstB*	BN194_10280	K0N6X8	0.23	0.58	1.49
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhB*	BN194_15090	K0MVA7	1.17	0.58	1.49
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	*groS,grES*	BN194_23760	K0N700	0.85	0.58	1.49
Uncharacterized protein	Prophage genome		BN194_09330	K0N6Q4	1.32	0.56	1.47
30S ribosomal protein S16	Ribosomal proteins	*rpsP*	BN194_17810	K0N5H1	0.94	0.56	1.47
Probable tRNA sulfurtransferase (EC 2.8.1.4) (Sulfur carrier protein ThiS sulfurtransferase) (Thiamine biosynthesis protein ThiI) (tRNA 4-thiouridine synthase)	Cofactor-related metabolism	*thiI*	BN194_14480	K0N7Z7	2.48	0.56	1.47
ABC-type antimicrobial peptide transport system,ATPase component	*ABC-type transporter systems*		BN194_19940	K0MWG2	0.53	0.56	1.47
DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	DNA replication-related	*dnaX*	BN194_23990	K0MXD3	0.23	0.56	1.47
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	1.07	0.55	1.47
Uridine phosphorylase (EC 2.4.2.3)	Nucleic acid/nucleotide metabolism	*udp*	BN194_24830	K0NAD0	0.28	0.55	1.46
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	0.64	0.55	1.46
Uncharacterized protein yqgF	Cell wall biogenesis	*yqgF*	BN194_18440	K0MW71	1.88	0.54	1.46
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	0.27	0.54	1.46

Uncharacterized protein	Unknown/uncharacterized		BN194_07460	K0N2W9	0.93	0.54	1.46
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_13380	K0N7S0	1.03	0.54	1.45
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*nagA*	BN194_19890	K0MWF9	2.98	0.53	1.45
Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	*fhs*	BN194_16520	K0NAT0	1.30	0.53	1.44
Kinase, putative	General prediction only		BN194_29890	K0MYR0	0.37	0.53	1.44
UbiE/COQ5 family methyltransferase	General prediction only		BN194_23620	K0NBY4	0.38	0.53	1.44
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	*mnmA*	BN194_14930	K0N844	0.37	0.53	1.44
Putative beta-phosphoglucomutase (EC 5.4.2.6)	Central glycolytic/intermediary pathways	*yvdM*	BN194_11170	K0N9S7	0.52	0.53	1.44
Uncharacterized protein	General prediction only		BN194_13850	K0N4L8	0.22	0.52	1.43
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	*nadE*	BN194_19840	K0MWF6	1.81	0.52	1.43
Uncharacterized protein	General prediction only		BN194_21200	K0N6M8	1.54	0.50	1.42
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	*asd*	BN194_01060	K0N1I5	1.32	0.50	1.41
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	*atpG*	BN194_13610	K0N4D3	0.91	0.50	1.41
Pur operon repressor	Transcriptional regulation	*purR_2*	BN194_26960	K0N7M9	1.05	0.49	1.40
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB*	BN194_21340	K0MWS0	0.13	0.48	1.40
YbbR-like domain-containing protein ybbR	Unknown/uncharacterized	*ybbR*	BN194_11540	K0MUB6	0.95	0.48	1.39
UvrABC system protein A	DNA repair/recombination	*uvrA_3*	BN194_27500	K0N8M1	0.66	0.47	1.39
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	*pfkA*	BN194_15570	K0NAK6	1.24	0.47	1.38
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ_2*	BN194_20470	K0NBG3	0.27	0.46	1.38
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	*galE*	BN194_07350	K0N2R3	1.33	0.46	1.38
Uncharacterized protein	Unknown/uncharacterized		BN194_02900	K0N1P1	0.53	0.46	1.38
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	*npr*	BN194_04740	K0MSP8	0.71	0.46	1.37
Tyrosine--tRNA ligase (EC 6.1.1.1)		*tyrS*	BN194_21510	K0N6A9	0.98	0.46	1.37
DNA translocase SftA	Cytokinesis	*sftA*	BN194_18960	K0N5Q1	0.44	0.46	1.37

Probable flavodoxin-1	Membrane bioenergetics	*ykuN_2*	BN194_12220	K0NA19	0.15	0.45	1.36
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_01410	K0N1L0	0.89	0.44	1.36
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	*hisS*	BN194_17110	K0N5A0	1.01	0.44	1.36
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	*garB*	BN194_27400	K0N8K3	1.19	0.44	1.36
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	*polA*	BN194_18930	K0N9E7	0.46	0.44	1.36
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	*apbE_3*	BN194_21550	K0N6S8	0.21	0.44	1.36
30S ribosomal protein S3	Ribosomal proteins	*rpsC*	BN194_26160	K0N7G5	0.79	0.44	1.35
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	*coaD*	BN194_15200	K0N4X3	0.78	0.43	1.35
Fructoselysine kinase (EC 2.7.1.-)	Carbohydrate-related metabolism	*frlD*	BN194_22240	K0MX05	0.54	0.43	1.35
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	*atpA*	BN194_13600	K0N4K1	1.58	0.43	1.35
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB_2*	BN194_21770	K0NBN4	2.35	0.43	1.35
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	*trpS*	BN194_27360	K0N7S4	1.33	0.43	1.34
Uncharacterized protein	Unknown/uncharacterized		BN194_25540	K0MXN3	1.42	0.42	1.34
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	*pdhC*	BN194_15100	K0N4W5	1.74	0.42	1.34
Adenosylcobalamin-dependent ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*rtpR*	BN194_24230	K0NAA3	0.23	0.42	1.34
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	*dacA*	BN194_02140	K0MS53	1.35	0.41	1.33
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	*mtnN*	BN194_14890	K0MV90	1.17	0.41	1.33
5-bromo-4-chloroindolyl phosphate hydrolysis protein	General prediction only		BN194_14860	K0N4M3	1.18	0.40	1.32
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	*typA*	BN194_15150	K0N4W9	1.48	0.40	1.32
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	*galK*	BN194_07340	K0MTA3	0.74	0.39	1.31
DNA-binding protein HU	DNA replication-related	*hup*	BN194_15740	K0MVF4	1.13	0.39	1.31

DegV domain-containing protein CPE0026	Unknown/uncharacterized		BN194_12060	K0N405	0.78	0.39	1.31
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP_3*	BN194_21160	K0N682	0.96	0.39	1.31
Uncharacterized protein	Unknown/uncharacterized		BN194_30140	K0MYT6	0.28	0.38	1.30
Bifunctional protein FolD	Cofactor-related metabolism	*folD*	BN194_18210	K0N5K0	0.23	0.38	1.30
Uncharacterized protein	General prediction only		BN194_21910	K0N6F1	0.58	0.38	1.30
Uncharacterized zinc protease ymfH (EC 3.4.24.-)	Amino acid-related metabolism	*ymfH*	BN194_10030	K0N6V9	0.26	0.38	1.30
Glycosyl transferase family 8	Cell wall biogenesis		BN194_11730	K0N795	0.57	0.37	1.30
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	*aspS*	BN194_17100	K0N5F3	0.80	0.37	1.29
GCN5-related N-acetyltransferase	General prediction only		BN194_19760	K0N5W1	0.29	0.36	1.29
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA*	BN194_05120	K0N8B5	0.17	0.36	1.29
Uncharacterized protein	Unknown/uncharacterized		BN194_01790	K0MS25	0.34	0.36	1.28
Microcin C7 self-immunity protein mccF			BN194_01360	K0N1K5	0.29	0.36	1.28
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	*act*	BN194_16090	K0MVI3	0.18	0.35	1.28
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	*lplJ*	BN194_16640	K0MVN0	0.63	0.35	1.28
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*bglP*	BN194_06940	K0MT60	0.90	0.35	1.27
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2_2,lacD*	BN194_27060	K0N7P0	1.76	0.34	1.27
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	*ispA*	BN194_18180	K0N9A2	0.58	0.34	1.27
Glutamate dehydrogenase	Amino acid-related metabolism	*gdh*	BN194_06980	K0N666	0.25	0.34	1.27
UPF0337 protein yhjA	General prediction only	*yhjA*	BN194_24800	K0N7S1	0.05	0.34	1.27
Chaperone protein DnaJ	Protein folding/turnover	*dnaJ*	BN194_17450	K0N5J4	1.77	0.34	1.27
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	*thyA*	BN194_15800	K0N522	0.68	0.34	1.26
UPF0659 protein YMR090W	General prediction only	*ylbE*	BN194_07030	K0N671	2.09	0.34	1.26
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	*iscS1*	BN194_14900	K0N4U8	0.45	0.34	1.26
Ribosomal protein L11 methyltransferase (L11 Mtase) (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*prmA*	BN194_17260	K0N5B0	0.21	0.33	1.26

Sorbitol PTS, EIIA	Phosphotransferase systems		BN194_09940	K0MTX4	0.46	0.33	1.26
Uncharacterized protein yuaG	Unknown/uncharacterized	*yuaG*	BN194_22920	K0NBV0	0.11	0.32	1.25
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	*pyrG*	BN194_26790	K0MXZ1	0.64	0.32	1.25
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdF*	BN194_16610	K0N552	0.58	0.32	1.25
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	0.34	0.31	1.24
ABC transporter glutamine-binding protein glnH	ABC-type transporter systems	*glnH*	BN194_21430	K0N9Y4	0.98	0.31	1.24
Uncharacterized protein ypmR	General prediction only	*ypmR*	BN194_15840	K0MVG3	0.21	0.30	1.24
Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	*aspC*	BN194_16770	K0NAU6	0.59	0.30	1.24
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		BN194_13770	K0NAC0	0.74	0.30	1.23
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	0.55	0.30	1.23
Zinc metalloprotease (EC 3.4.24.-)	General prediction only	*eep*	BN194_17620	K0NAZ9	1.85	0.30	1.23
Uncharacterized protein	Unknown/uncharacterized		BN194_29560	K0N8E9	0.15	0.30	1.23
Oligoendopeptidase, pepF/M3 family	*Amino acid-related metabolism*		BN194_11580	K0N779	0.60	0.29	1.22
UPF0092 membrane protein yrbF	Protein export	*yrbF*	BN194_08390	K0MTL6	0.27	0.29	1.22
Putative HAD-hydrolase yfnB (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yfnB*	BN194_08780	K0N6M1	0.17	0.29	1.22
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	*prs1,prs*	BN194_26930	K0NAT2	0.85	0.28	1.22
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	*dut*	BN194_24640	K0MXG3	0.99	0.28	1.22
Transport protein	Other transporter proteins		BN194_00630	K0N4D9	0.21	0.28	1.22
tRNA N6-adenosine threonylcarbamoyltransferase (EC 2.3.1.234) (N6-L-threonylcarbamoyladenine synthase) (t(6)A37 threonylcarbamoyladenosine biosynthesis protein TsaD) (tRNA threonylcarbamoyladenosine biosynthesis protein TsaD)	General prediction only	*tsaD,gcp*	BN194_23850	K0N7L3	0.19	0.28	1.22
Uncharacterized protein	Unknown/uncharacterized		BN194_20160	K0N5Z4	0.73	0.28	1.22
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	*rbfA*	BN194_17540	K0MVV7	0.74	0.28	1.21

Uncharacterized protein	Unknown/uncharacterized		BN194_19530	K0N9J0	0.24	0.26	1.20
Probable flavodoxin-1	General prediction only	*ykuN*	BN194_01860	K0N1P2	0.20	0.26	1.20
CBS domain-containing protein ykuL	Unknown/uncharacterized	*ykuL*	BN194_08670	K0N981	0.30	0.26	1.20
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	*msmK*	BN194_11180	K0N747	0.19	0.24	1.18
Glycosyl transferase family protein	Cell wall biogenesis		BN194_02420	K0N7L2	0.49	0.23	1.17
30S ribosomal protein S12	Ribosomal proteins	*rpsL*	BN194_26290	K0MXV0	0.18	0.23	1.17
Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	*pox5*	BN194_19670	K0NBB6	0.14	0.23	1.17
Zinc-type alcohol dehydrogenase-like protein SE_1777	General prediction only		BN194_07910	K0N329	0.46	0.23	1.17
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	*murD*	BN194_14720	K0NAG5	0.31	0.22	1.17
Mannose permease IID component	Phosphotransferase systems	*manZ_4*	BN194_04510	K0N287	0.25	0.22	1.17
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE*	BN194_13710	K0N4D8	0.15	0.22	1.17
Lactose phosphotransferase system repressor	Transcriptional regulation	*lacR*	BN194_07510	K0N2X5	0.16	0.20	1.15
30S ribosomal protein S5	Ribosomal proteins	*rpsE*	BN194_26050	K0N853	0.72	0.20	1.15
Protein ytsP	Signal transduction	*ytsP*	BN194_14450	K0N4Q9	0.08	0.20	1.15
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacB*	BN194_07490	K0MTB7	0.19	0.19	1.14
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh1,ldh*	BN194_06970	K0N8S5	0.09	0.19	1.14
Putative gluconeogenesis factor	General prediction only	*yjiF*	BN194_10480	K0N6Z4	0.20	0.19	1.14
DNA mismatch repair protein MutS	DNA repair/recombination	*mutS*	BN194_23720	K0NBY9	0.06	0.19	1.14
Ferredoxin--NADP reductase (FNR) (Fd-NADP(+) reductase) (EC 1.18.1.2)	Membrane bioenergetics		BN194_08950	K0N337	0.23	0.19	1.14
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	*gpsA*	BN194_10350	K0N3I2	0.40	0.18	1.14
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	*apt*	BN194_17380	K0N902	1.00	0.18	1.14
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yutF*	BN194_08910	K0N383	0.23	0.18	1.13
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	*gmk*	BN194_18110	K0N5J6	0.35	0.18	1.13

D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	*ddl*	BN194_01390	K0MRY4	0.33	0.17	1.13
Exodeoxyribonuclease (EC 3.1.11.2)	DNA repair/recombination	*exoA*	BN194_11390	K0MUA0	0.37	0.17	1.13
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	Cell wall biogenesis	*glmS*	BN194_11560	K0N3V9	0.28	0.17	1.13
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	*hslU*	BN194_16010	K0N4Y1	0.27	0.16	1.12
Putative tRNA-binding protein ytpR	General prediction only	*ytpR*	BN194_18970	K0NB80	0.36	0.16	1.12
Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	Nucleic acid/nucleotide metabolism	*add*	BN194_23440	K0MXB1	0.19	0.16	1.11
50S ribosomal protein L2	Ribosomal proteins	*rplB*	BN194_26190	K0MXU1	0.65	0.15	1.11
Archaeal fructose-1,6-bisphosphatase related enzyme of inositol monophosphatase family	*Carbohydrate-related metabolism*		BN194_15140	K0MVB0	0.42	0.15	1.11
Spermidine/putrescine-binding periplasmic protein	ABC-type transporter systems	*potD*	BN194_11460	K0N3U9	0.30	0.14	1.10
Uncharacterized protein yxkA	General prediction only	*yxkA*	BN194_27230	K0NAV1	0.15	0.14	1.10
Peptide chain release factor 3 (RF-3)	Protein translation (peptide release)	*prfC*	BN194_19480	K0N9I7	0.26	0.14	1.10
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	*ycnE*	BN194_13230	K0N7R3	0.30	0.14	1.10
Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	*rpiA_2, ripA*	BN194_28600	K0N8W9	0.21	0.14	1.10
Spore coat polysaccharide biosynthesis protein spsK				K0N9X8;K0N6D6	0.66	0.13	1.10
Integral membrane protein	Unknown/uncharacterized		BN194_02590	K0MS97	0.42	0.13	1.10
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*yacO*	BN194_24420	K0NC34	0.21	0.13	1.09
Uncharacterized protein	Unknown/uncharacterized		BN194_19470	K0NBA0	0.46	0.12	1.09
Uncharacterized protein ywfO	General prediction only	*ywfO*	BN194_26840	K0MXZ5	0.11	0.12	1.08
Cytidine deaminase (EC 3.5.4.5)	Nucleic acid/nucleotide metabolism	*cdd*	BN194_17000	K0N5D8	0.28	0.11	1.08
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_2*	BN194_29910	K0N8I1	0.23	0.11	1.08
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO_2*	BN194_16630	K0N8Q0	0.65	0.11	1.08
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	*ftsH*	BN194_26460	K0N7I8	0.16	0.11	1.08

Transcriptional regulator	*Posttranslational modification*		BN194_29310	K0N8C2	0.04	0.11	1.08
Probable phosphoketolase (EC 4.1.2.-)	*Central glycolytic/intermediary pathways*		BN194_28700	K0N8X7	0.03	0.10	1.08
Uncharacterized protein	Unknown/uncharacterized		BN194_21380	K0N9Y1	0.31	0.10	1.07
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	*iolS*	BN194_29680	K0NB94	0.39	0.10	1.07
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA1, greA*	BN194_02150	K0N1G7	0.04	0.09	1.07
Uncharacterized protein	Unknown/uncharacterized		BN194_05550	K0N257	0.10	0.09	1.07
Acyl-ACP thioesterase	Lipid-related metabolism		BN194_23910	K0N709	0.12	0.09	1.06
Probable cation-transporting ATPase exp7 (EC 3.6.3.-)	Other transporter proteins	*exp7*	BN194_08170	K0N955	0.19	0.09	1.06
Aspartate racemase (EC 5.1.1.13)	*Amino acid-related metabolism*		BN194_02170	K0N7H2	0.14	0.08	1.06
Uncharacterized RNA pseudouridine synthase YhcT (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*yhcT_2*	BN194_20220	K0NBE7	0.03	0.08	1.06
Site-determining protein	Cytokinesis	*minD*	BN194_14590	K0MV70	0.06	0.08	1.06
FMN-binding domain protein	General prediction only		BN194_24320	K0NC29	0.06	0.08	1.06
Dehydrogenase	General prediction only		BN194_24480	K0NAB4	0.04	0.08	1.05
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	*tpx*	BN194_08090	K0MTJ5	0.09	0.08	1.05
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB1,pstB*	BN194_10270	K0N9K1	0.34	0.07	1.05
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	*ykpA*	BN194_07220	K0N8V6	0.93	0.07	1.05
Uncharacterized protein	Unknown/uncharacterized		BN194_11770	K0N9Y6	0.18	0.07	1.05
Uncharacterized aminotransferase SSO0104 (EC 2.6.1.-)	*Amino acid-related metabolism*		BN194_27600	K0N8N4	0.02	0.07	1.05
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	*fabZ_2*	BN194_22620	K0NBT3	0.23	0.07	1.05
Glycosyltransferase	Cell wall biogenesis		BN194_09050	K0N346	0.03	0.06	1.05
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	*atpH*	BN194_13590	K0MV16	0.07	0.06	1.05
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	0.14	0.06	1.05
Probable phosphoketolase (EC 4.1.2.-)	Central glycolytic/intermediary pathways	*xpkA*	BN194_01710	K0N1M9	0.10	0.06	1.04
tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA (guanine(46)-N(7))-	tRNA/Ribosome assembly/processing	*trmB*	BN194_19000	K0N606	0.08	0.06	1.04

methyltransferase) (tRNA(m7G46)-methyltransferase)							
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*glyS*	BN194_16950	K0N5D3	0.08	0.06	1.04
Uncharacterized protein	Unknown/uncharacterized		BN194_29850	K0N968	0.16	0.06	1.04
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*gmuB*	BN194_23840	K0MXC7	0.02	0.05	1.04
50S ribosomal protein L35	Ribosomal proteins	*rpmI*	BN194_18810	K0N5P1	0.03	0.05	1.04
Uncharacterized N-acetyltransferase ycf52-like (EC 2.3.1.-)	General prediction only	*speE1*	BN194_21490	K0MWT4	0.04	0.05	1.03
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI*	BN194_07860	K0N327	0.02	0.04	1.03
PhoH-like protein	General prediction only	*phoH*	BN194_17020	K0NAW2	0.10	0.04	1.03
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	*ptsH*	BN194_19430	K0N9I2	0.07	0.04	1.03
Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (EC 2.7.7.12) (UDP-glucose--hexose-1-phosphate uridylyltransferase)		*galT*	BN194_07370	K0N8X1	0.02	0.03	1.02
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	*rnc*	BN194_17870	K0NB31	0.03	0.03	1.02
UvrABC system protein A	DNA repair/recombination	*uvrA_2*	BN194_14920	K0NAH3	0.01	0.03	1.02
Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	*pyk*	BN194_15580	K0N8B6	0.11	0.02	1.01
FemAB family protein	General prediction only		BN194_22880	K0NA57	0.02	0.02	1.01
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA_2,ackA*	BN194_23060	K0N6W4	0.02	0.02	1.01
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	*cap4C*	BN194_12280	K0N7E3	0.03	0.01	1.01
FeS cluster assembly protein sufD	Cofactor-related metabolism	*sufD*	BN194_13780	K0N7U0	0.02	0.01	1.01
Queuosine transporter QueT	General prediction only	*queT*	BN194_21930	K0NA07	0.01	0.01	1.00
Uncharacterized protein MJ1445	General prediction only		BN194_08880	K0N6M7	0.00	0.00	1.00
Uncharacterized protein	Unknown/uncharacterized		BN194_22290	K0MX11	0.00	0.00	1.00
Aldose 1-epimerase (EC 5.1.3.3)	*Central glycolytic/intermediary pathways*		BN194_07390	K0MTA8	0.01	-0.01	1.00
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	*fabG*	BN194_22560	K0N6N3	0.01	-0.01	1.00
Uncharacterized protein ybxB	tRNA/Ribosome assembly/processing	*ybxB*	BN194_24020	K0NC08	0.00	-0.01	-1.01
Oligo-1,6-glucosidase (EC 3.2.1.10)	Carbohydrate-related metabolism	*malL*	BN194_04830	K0N5P4	0.00	-0.01	-1.01

Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	*asnB*	BN194_22990	K0MX90	0.02	-0.01	-1.01
Uncharacterized protein	General prediction only		BN194_28370	K0NDC5	0.00	-0.01	-1.01
Cell growth regulatory protein	*IS elements/foreign DNA defense*		BN194_00940	K0MRU4	0.03	-0.02	-1.01
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	*glyr1*	BN194_30100	K0N992	0.01	-0.02	-1.01
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	*alaS*	BN194_08480	K0N6K2	0.04	-0.02	-1.02
Transcriptional regulator, xre family	Transcriptional regulation		BN194_13860	K0N4E8	0.03	-0.02	-1.02
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		BN194_24180	K0NAA2	0.02	-0.02	-1.02
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	*metG*	BN194_27130	K0NAU5	0.13	-0.03	-1.02
Uncharacterized protein	Unknown/uncharacterized		BN194_23540	K0MXB4	0.07	-0.03	-1.02
Phosphoenolpyruvate-dependent sugar phosphotransferase system EIIA, galactitol/fructose specific	Phosphotransferase systems		BN194_27050	K0N8F9	0.14	-0.03	-1.02
NAD kinase (EC 2.7.1.23) (ATP-dependent NAD kinase)		*nadK*	ppnK	K0N6U5	0.11	-0.04	-1.03
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*fruA_3*	BN194_15410	K0N4S1	0.06	-0.04	-1.03
Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	0.05	-0.05	-1.04
Aldose 1-epimerase	*Central glycolytic/intermediary pathways*		BN194_16020	K0NAP4	0.06	-0.06	-1.04
Ribonuclease P protein component (RNase P protein) (RNaseP protein) (EC 3.1.26.5) (Protein C5)	tRNA/Ribosome assembly/processing	*rnpA*	BN194_30620	K0NDS2	0.06	-0.06	-1.04
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ*	BN194_14610	K0N4K4	0.08	-0.06	-1.04
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	*hpt*	BN194_26470	K0NCR2	0.14	-0.06	-1.04
Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)	Nucleic acid/nucleotide metabolism	*purC*	BN194_19360	K0N5S8	0.09	-0.06	-1.04
50S ribosomal protein L16	Ribosomal proteins	*rplP*	BN194_26150	K0N863	0.07	-0.06	-1.05
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	*yuxL*	BN194_19910	K0N5X4	0.20	-0.06	-1.05
Uncharacterized protein HI_0912	General prediction only	*thiF3*	BN194_05090	K0MSS8	0.04	-0.07	-1.05
Bifunctional protein BirA (EC 6.3.4.15)	Lipid-related metabolism	*birA*	BN194_08790	K0MTP3	0.11	-0.07	-1.05
Penicillin acylase (EC 3.5.1.11)	Cell defense/detoxification		BN194_04910	K0N2B8	0.12	-0.07	-1.05
Probable GTP-binding protein EngB	tRNA/Ribosome assembly/processing	*engB*	BN194_15350	K0N4Y5	0.08	-0.08	-1.05

Ribosomal RNA small subunit methyltransferase H (EC 2.1.1.199) (16S rRNA m(4)C1402 methyltransferase) (rRNA (cytosine-N(4)-)-methyltransferase RsmH)	tRNA/Ribosome assembly/processing	*rsmH*	BN194_14680	K0N814	0.18	-0.08	-1.06
Phosphatase YbjI (EC 3.1.3.-)	General prediction only	*ybjI*	BN194_30020	K0NDN5	0.04	-0.09	-1.06
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	*nagB*	BN194_30440	K0MYW0	0.13	-0.09	-1.07
50S ribosomal protein L9	Ribosomal proteins	*rplI*	BN194_01130	K0N4K3	0.17	-0.10	-1.07
Uncharacterized protein	Unknown/uncharacterized		BN194_01150	K0N181	0.18	-0.10	-1.07
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA_2, potA*	BN194_11430	K0N765	0.26	-0.10	-1.07
Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	Nucleic acid/nucleotide metabolism	*purN*	BN194_19310	K0N5S4	0.06	-0.11	-1.08
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	*hmgCS1*	BN194_19680	K0N9K3	0.09	-0.11	-1.08
50S ribosomal protein L10	Ribosomal proteins	*rplJ*	BN194_24090	K0MXD8	0.37	-0.12	-1.08
Putative carboxypeptidase SCO6489 (EC 3.4.16.-)			BN194_01370	K0N787	0.17	-0.12	-1.09
Uncharacterized protein			BN194_07360	K0N2W3	0.32	-0.12	-1.09
Protein veg	Unknown/uncharacterized	*veg*	BN194_27010	K0N7N4	0.18	-0.12	-1.09
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	*ftsY*	BN194_17850	K0N5R8	0.32	-0.13	-1.09
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	*carB*	BN194_16450	K0N587	0.30	-0.13	-1.09
Predicted hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	0.17	-0.14	-1.10
Fumarate hydratase class II (Fumarase C) (EC 4.2.1.2)	Tricarboxylic acid pathway	*fumC*	BN194_25340	K0MXL5	0.79	-0.14	-1.10
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD*	BN194_17920	K0NB35	0.42	-0.15	-1.11
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	*proC*	BN194_19900	K0N677	0.44	-0.15	-1.11
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrD*	BN194_16440	K0MVL3	0.27	-0.16	-1.12
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	*rpe*	BN194_18000	K0N5T1	0.15	-0.17	-1.12
Diphosphomevalonate decarboxylase (EC 4.1.1.33)	Lipid-related metabolism	*mvd1*	BN194_16830	K0N8S2	0.33	-0.17	-1.12
Uncharacterized protein	Unknown/uncharacterized		BN194_00400	K0N116	0.48	-0.17	-1.12
Ribosome-binding ATPase YchF	Protein translation (peptide release)	*engD,ychF*	BN194_02070	K0N7F7	1.93	-0.17	-1.13

Oligoendopeptidase F	Amino acid-related metabolism	*yjbG_2*	BN194_08130	K0N6H7	0.23	-0.17	-1.13
Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)	Nucleic acid/nucleotide metabolism	*pyrF*	BN194_16430	K0N8M7	0.17	-0.18	-1.13
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	*treA*	BN194_06930	K0N662	0.06	-0.18	-1.13
Uncharacterized amino acid permease YfnA	Other transporter proteins	*yfnA*	BN194_06960	K0N2T0	0.12	-0.19	-1.14
50S ribosomal protein L15	Ribosomal proteins	*rplO*	BN194_26030	K0NAK7	0.85	-0.20	-1.15
Zinc-transporting ATPase (EC 3.6.3.5)	Other transporter proteins	*zosA_2*	BN194_29430	K0NB79	0.32	-0.20	-1.15
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	*fabD*	BN194_22570	K0NBT1	0.40	-0.21	-1.15
Protein RibT (EC 2.3.1.-)	Cofactor-related metabolism	*ribT*	BN194_15620	K0NAL0	0.18	-0.21	-1.16
Uncharacterized protein	Cell wall biogenesis		BN194_21890	K0MWX1	0.23	-0.21	-1.16
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	*fabH*	BN194_22600	K0N7B0	0.42	-0.21	-1.16
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	*trxB*	BN194_10360	K0N3L1	0.41	-0.22	-1.16
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	*yhaA*	BN194_30550	K0N9E4	0.14	-0.22	-1.17
Serine/threonine-protein kinase PrkC (EC 2.7.11.1)	Posttranslational modification	*prkC*	BN194_18020	K0NB40	0.38	-0.23	-1.17
Oligoendopeptidase F homolog (EC 3.4.24.-)	Amino acid-related metabolism	*yjbG*	BN194_02530	K0N560	0.53	-0.23	-1.17
Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		BN194_20000	K0N684	0.22	-0.23	-1.17
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		BN194_08960	K0N387	0.37	-0.23	-1.18
Transcription termination/antitermination protein NusG	Transcription-associated proteins	*nusG*	BN194_24260	K0N730	0.40	-0.24	-1.18
ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	*clpX*	BN194_15340	K0MVC6	0.95	-0.24	-1.18
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ*	BN194_11360	K0N3U2	0.57	-0.24	-1.18
GMP reductase (EC 1.7.1.7) (Guanosine 5'-monophosphate oxidoreductase)	Nucleic acid/nucleotide metabolism	*guaC*	BN194_09960	K0N3H4	1.30	-0.24	-1.18
Cold shock protein 1	Transcription-associated proteins	*csp*	BN194_06990	K0MT67	0.10	-0.25	-1.19
Isoprenyl transferase (EC 2.5.1.-)	Lipid-related metabolism	*uppS*	BN194_17640	K0MVX1	0.91	-0.25	-1.19
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*ytzG*	BN194_09230	K0N6P7	0.92	-0.26	-1.19

Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	*pgk*	BN194_11020	K0N9R1	1.21	-0.26	-1.19
30S ribosomal protein S4	Ribosomal proteins	*rpsD*	BN194_14440	K0MV63	0.43	-0.26	-1.19
Uncharacterized protein	Unknown/uncharacterized		BN194_13400	K0N4I9	0.12	-0.26	-1.19
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	*pta*	BN194_11340	K0MU95	0.52	-0.26	-1.20
Uncharacterized protein	Unknown/uncharacterized		BN194_24010	K0N715	0.45	-0.26	-1.20
ABC transporter, ATP-binding protein	*Cell surface proteins/internalins*		BN194_15700	K0N514	0.09	-0.27	-1.20
Probable L-serine dehydratase, alpha chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAA*	BN194_13950	K0N4M4	0.29	-0.27	-1.20
Cell division protein FtsA	Cytokinesis	*ftsA*	BN194_14750	K0N4T3	1.70	-0.27	-1.20
Uncharacterized protein IRC4	Unknown/uncharacterized	*IRC4*	BN194_30110	K0N8K0	0.19	-0.27	-1.20
Protein translocase subunit SecA	Protein export	*secA*	BN194_10170	K0N9J2	0.67	-0.27	-1.21
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	*uvrA*	BN194_10450	K0N3J2	0.97	-0.27	-1.21
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	0.95	-0.27	-1.21
50S ribosomal protein L4	Ribosomal proteins	*rplD*	BN194_26210	K0N7H0	0.44	-0.27	-1.21
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	*fbp*	BN194_21660	K0N6C3	0.30	-0.28	-1.21
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	*valS*	BN194_14510	K0N4J6	0.95	-0.28	-1.21
50S ribosomal protein L31 type B	Ribosomal proteins	*rpmE2*	BN194_26770	K0NCV4	0.54	-0.28	-1.21
50S ribosomal protein L27	Ribosomal proteins	*rpmA*	BN194_18270	K0NB51	0.21	-0.29	-1.22
Carboxy-terminal processing protease CtpA (EC 3.4.21.102)	Protein folding/turnover	*ctpA*	BN194_15880	K0N8G1	1.04	-0.30	-1.23
Methionyl-tRNA formyltransferase (EC 2.1.2.9)	Protein translation (initiation)	*fmt*	BN194_18060	K0N5J2	1.97	-0.30	-1.23
Putative nrdI-like protein	*Nucleic acid/nucleotide metabolism*		BN194_08250	K0N300	1.02	-0.31	-1.24
Uncharacterized protein			BN194_02080	K0N4Z7	0.28	-0.31	-1.24
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	0.81	-0.33	-1.25
Uncharacterized protein yslB	Unknown/uncharacterized	*yslB*	BN194_08630	K0N6L4	0.53	-0.33	-1.25
Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (EC 5.3.3.2) (Isopentenyl diphosphate:dimethylallyl diphosphate isomerase)	Lipid-related metabolism	*fni*	BN194_16840	K0MVP7	1.37	-0.33	-1.25

(Isopentenyl pyrophosphate isomerase) (Type 2 isopentenyl diphosphate isomerase)							
Probable glutamine ABC transporter permease protein glnP	ABC-type transporter systems	*glnP*	BN194_21410	K0N6A4	0.16	-0.33	-1.26
Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain)	Nucleic acid/nucleotide metabolism	*carA*	BN194_16460	K0N535	0.51	-0.34	-1.26
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	*pcp*	BN194_01980	K0N4Y4	1.07	-0.34	-1.26
Uncharacterized protein	Unknown/uncharacterized		BN194_23630	K0NA78	0.60	-0.34	-1.27
Membrane protein insertase YidC 1	Protein export	*yidC1*	BN194_18630	K0N9D1	0.20	-0.35	-1.27
ABC-type Na+ efflux pump permease component-like protein	*ABC-type transporter systems*		BN194_11370	K0N9U5	0.81	-0.35	-1.27
Transcriptional regulator	Transcriptional regulation		BN194_08230	K0N6I4	0.66	-0.35	-1.27
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	*yabR*	BN194_26500	K0N8A7	0.72	-0.35	-1.27
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	1.51	-0.35	-1.28
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*pcrA*	BN194_11920	K0N9Z6	1.38	-0.36	-1.28
Uncharacterized protein	*ABC-type transporter systems*		BN194_21220	K0NBK2	1.51	-0.37	-1.29
HTH-type transcriptional regulator iolR	Transcriptional regulation	*iolR*	BN194_02190	K0MS58	0.73	-0.37	-1.29
Phage capsid protein	Prophage genome		BN194_30330	K0NBD3	0.44	-0.38	-1.30
ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	DNA repair/recombination	*addA*	BN194_16800	K0N5B6	0.23	-0.39	-1.31
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	*pth*	BN194_26550	K0N8B3	0.61	-0.39	-1.31
PTS family mannose/fructose/sorbose porter component IIC	Phosphotransferase systems		BN194_02980	K0N5D0	0.33	-0.40	-1.32
Cof protein	General prediction only		BN194_12010	K0N401	0.33	-0.40	-1.32
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	*proS*	BN194_17610	K0N5E2	1.91	-0.40	-1.32
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_3*	BN194_29920	K0NDN0	0.74	-0.40	-1.32
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E_2,P100*	BN194_05160	K0N2D7	0.19	-0.41	-1.33
Uncharacterized protein ybfG	General prediction only	*ybfG*	BN194_00330	K0N4B3	0.87	-0.42	-1.34
Probable L-serine dehydratase, beta chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAB*	BN194_13940	K0MV34	0.51	-0.42	-1.34
3-keto-L-gulonate-6-phosphate decarboxylase sgbH (EC 4.1.1.85)	Carbohydrate-related metabolism	*sgbH*	BN194_28550	K0N8W6	0.31	-0.43	-1.35

Uncharacterized protein	Unknown/uncharacterized		BN194_19810	K0N5W5	1.16	-0.43	-1.35
Phosphate-binding protein pstS 1	ABC-type transporter systems	*pstS1*	BN194_10240	K0MTZ5	0.55	-0.44	-1.36
Acylphosphatase	Carbohydrate-related metabolism	*acyP*	BN194_18620	K0NB65	1.10	-0.45	-1.36
Elongation factor 4 (EF-4) (EC 3.6.5.n1) (Ribosomal back-translocase LepA)	Protein translation (elongation)	*lepA*	BN194_17440	K0MVU5	0.27	-0.45	-1.37
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	*frr*	BN194_17650	K0N5M3	2.07	-0.45	-1.37
Chromosomal replication initiator protein DnaA	DNA replication-related	*dnaA*	BN194_00010	K0N1B5	0.35	-0.45	-1.37
Uncharacterized oxidoreductase YbdH (EC 1.1.-.-)	Carbohydrate-related metabolism	*ybdH*	BN194_30540	K0MYX0	0.48	-0.45	-1.37
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_19800	K0N670	1.50	-0.45	-1.37
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA*	BN194_11290	K0MU90	0.93	-0.45	-1.37
Mevalonate kinase (EC 2.7.1.36)	Lipid-related metabolism	*mvk*	BN194_12270	K0NA23	1.69	-0.46	-1.37
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	0.29	-0.46	-1.37
Chromosome partition protein Smc	Cytokinesis	*smc*	BN194_17860	K0N5H9	0.28	-0.46	-1.38
30S ribosomal protein S21	Ribosomal proteins	*rpsU*	BN194_17050	K0N5E5	0.29	-0.46	-1.38
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	*rnr*	BN194_11100	K0N3S4	0.99	-0.46	-1.38
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	*rny*	BN194_10100	K0N3E5	0.42	-0.47	-1.38
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	0.38	-0.47	-1.38
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	*mhqD*	BN194_18770	K0NB71	0.27	-0.47	-1.39
Mannose permease IID component	Phosphotransferase systems	*manZ*	BN194_02990	K0MSE1	1.11	-0.48	-1.39
Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*leuS*	BN194_09210	K0N3A9	2.14	-0.48	-1.39
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	*murF*	BN194_26720	K0NCU5	1.02	-0.48	-1.40
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	*prs1_2*	BN194_30370	K0NDQ5	0.98	-0.48	-1.40
Protein hit	tRNA aminoacyl synthesis	*hit*	BN194_19040	K0MWA8	0.74	-0.49	-1.41
Septum site-determining protein DivIVA	Cytokinesis	*divIVA*	BN194_14800	K0N4T8	0.72	-0.50	-1.41
30S ribosomal protein S15	Ribosomal proteins	*rpsO*	BN194_15260	K0N4Q6	1.44	-0.50	-1.41
Nuclease sbcCD subunit D	DNA repair/recombination	*sbcD*	BN194_07530	K0N6B1	0.25	-0.50	-1.41

Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	*fba_2*	BN194_05060	K0N2C9	0.90	-0.50	-1.41
Acetyltransferase	General prediction only		BN194_08200	K0N2Z8	0.94	-0.50	-1.41
Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase)	Cofactor-related metabolism	*coaA*	BN194_21080	K0N9V9	0.45	-0.50	-1.41
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	*cmk*	BN194_15710	K0N4V1	1.03	-0.50	-1.41
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*rluB*	BN194_15650	K0N509	1.12	-0.51	-1.42
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	*glgC*	BN194_21600	K0N6T3	0.81	-0.52	-1.43
50S ribosomal protein L22	Ribosomal proteins	*rplV*	BN194_26170	K0NCM1	2.43	-0.52	-1.43
Uncharacterized protein ysxB	Ribosomal proteins	*ysxB*	BN194_18280	K0N9A9	0.24	-0.53	-1.44
Multifunctional protein: 5-nucleotidase 2,3-cyclic-nucleotide 2-phosphodiesterase	Nucleic acid/nucleotide metabolism	*ushA*	BN194_15530	K0N8A9	0.74	-0.53	-1.44
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E,P100*	BN194_02180	K0N513	4.43	-0.53	-1.44
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	*murE*	BN194_02160	K0N1S5	1.16	-0.53	-1.45
Uncharacterized ABC transporter ATP-binding protein YfiB	ABC-type transporter systems	*yfiB*	BN194_06890	K0MT56	1.04	-0.53	-1.45
Uncharacterized protein yghZ	General prediction only	*yghZ*	BN194_27510	K0N7U8	1.11	-0.54	-1.45
Uncharacterized protein	Lipid-related metabolism		BN194_11980	K0N7B3	1.18	-0.54	-1.46
Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	*rbsK*	BN194_03300	K0N1R2	1.60	-0.55	-1.46
Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)	Nucleic acid/nucleotide metabolism	*pdp*	BN194_23430	K0NA73	1.36	-0.55	-1.46
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	1.37	-0.55	-1.47
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	2.72	-0.55	-1.47
Uncharacterized metallophosphoesterase yunD	Nucleic acid/nucleotide metabolism	*yunD*	BN194_08890	K0MTQ0	1.03	-0.56	-1.47
Sensory transduction protein BceR	Signal transduction	*bceR_2*	BN194_19250	K0N630	1.49	-0.56	-1.47
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	*der*	BN194_15730	K0N8E1	0.31	-0.56	-1.47
Elongation factor P	Protein translation (elongation)	*efp*	BN194_18240	K0MW57	0.91	-0.56	-1.47

Uncharacterized ABC transporter ATP-binding protein YfmR (EC 3.6.3.-)	ABC-type transporter systems	*yfmR*	BN194_15790	K0MVF8	1.60	-0.56	-1.47
Uncharacterized protein	General prediction only		BN194_30000	K0N979	0.60	-0.57	-1.48
Uncharacterized protein yloA	Cell surface proteins/internalins	*yloA*	BN194_16340	K0MVK5	0.82	-0.57	-1.49
UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.3.1.98) (UDP-N-acetylmuramate dehydrogenase)	Cell wall biogenesis	*murB*	BN194_11400	K0N3X0	2.78	-0.58	-1.49
Cysteine desulfurase (EC 2.8.1.7)	Cofactor-related metabolism	*csd*	BN194_13790	K0MV25	1.32	-0.58	-1.49
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	*yqjQ*	BN194_15480	K0N8A1	0.66	-0.58	-1.49
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	1.11	-0.59	-1.51
Primosomal protein DnaI	DNA replication-related	*dnaI*	BN194_18880	K0N9E5	0.35	-0.60	-1.51
DNA topoisomerase 4 subunit B (EC 5.99.1.3) (Topoisomerase IV subunit B)	DNA replication-related	*parE*	BN194_16050	K0N545	2.31	-0.60	-1.51
Ribosomal RNA small subunit methyltransferase G (EC 2.1.1.-) (16S rRNA 7-methylguanosine methyltransferase)	tRNA/Ribosome assembly/processing	*rsmG*	BN194_02020	K0N7F1	1.23	-0.60	-1.51
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	*glmM*	BN194_11550	K0N3Y7	3.56	-0.60	-1.52
NAD-dependent protein deacetylase (EC 3.5.1.-)	General prediction only	*cobB*	BN194_27190	K0MY36	0.83	-0.60	-1.52
Translation initiation factor IF-1	Protein translation (initiation)	*infA*	BN194_26000	K0N847	1.48	-0.61	-1.53
Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	0.24	-0.61	-1.53
tRNA (Adenine(22)-N(1))-methyltransferase (EC 2.1.1.217)	tRNA/Ribosome assembly/processing	*trmK*	BN194_16910	K0N584	1.35	-0.61	-1.53
6-phospho-beta-galactosidase (EC 3.2.1.85) (Beta-D-phosphogalactoside galactohydrolase) (P-beta-Gal)	Carbohydrate-related metabolism	*lacG*	BN194_07320	K0N8W7	0.47	-0.62	-1.53
Thymidine kinase (EC 2.7.1.21)	Nucleic acid/nucleotide metabolism	*tdk*	BN194_13500	K0N4J4	1.51	-0.62	-1.54
Uncharacterized protein	Unknown/uncharacterized		BN194_21450	K0N6R7	0.43	-0.63	-1.55
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	*mhqA_3*	BN194_18760	K0N5N7	0.70	-0.64	-1.55
30S ribosomal protein S18	Ribosomal proteins	*rpsR*	BN194_00120	K0N6T2	1.22	-0.64	-1.55
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	*serS*	BN194_20080	K0N9N4	1.24	-0.64	-1.56
30S ribosomal protein S20	Ribosomal proteins	*rpsT*	BN194_15250	K0N4X9	0.26	-0.64	-1.56
Uncharacterized MscS family protein YkuT	Other transporter proteins	*ykuT*	BN194_08700	K0N322	1.29	-0.64	-1.56
50S ribosomal protein L19	Ribosomal proteins	*rplS*	BN194_17770	K0NB12	0.53	-0.64	-1.56

Dumpy	Cell surface proteins/internalins	*dp*	BN194_05390	K0MSV0	0.86	-0.65	-1.57
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	*pyc*	BN194_15170	K0NAI2	1.35	-0.65	-1.57
50S ribosomal protein L30	Ribosomal proteins	*rpmD*	BN194_26040	K0MXS6	1.65	-0.66	-1.58
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	*pepV*	BN194_08800	K0N324	1.67	-0.66	-1.58
50S ribosomal protein L7/L12	Ribosomal proteins	*rplL*	BN194_24080	K0NA98	0.53	-0.66	-1.58
Cold shock-like protein CspLA	Transcription-associated proteins	*cspLA*	BN194_12460	K0N438	0.77	-0.66	-1.58
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	*ppaC*	BN194_16110	K0N4Z4	1.77	-0.66	-1.59
HTH-type transcriptional regulator galR	Transcriptional regulation	*galR*	BN194_03780	K0N5G9	1.38	-0.67	-1.59
Calcium-transporting ATPase lmo0841 (EC 3.6.3.8)	Other transporter proteins		BN194_19820	K0NBC5	1.79	-0.67	-1.59
tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	*dus1*	BN194_26390	K0MXV9	1.33	-0.67	-1.59
Phosphoesterase (EC 3.1.4.-)	General prediction only	*ysnB*	BN194_08650	K0N317	1.66	-0.69	-1.61
Signal recognition particle protein (Fifty-four homolog)	Protein export	*ffh*	BN194_17820	K0NB27	1.38	-0.70	-1.63
UPF0473 protein BN194_08530	Unknown/uncharacterized		BN194_08530	K0N6K6	1.25	-0.70	-1.63
Uncharacterized protein	Transcriptional regulation		BN194_22670	K0NBT5	1.52	-0.71	-1.63
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	1.59	-0.71	-1.64
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA*	BN194_08450	K0N309	1.66	-0.72	-1.64
Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	*plsX*	BN194_17940	K0MW37	0.76	-0.72	-1.64
HTH-type transcriptional repressor yvoA	Transcriptional regulation	*yvoA_2*	BN194_19880	K0N9L8	1.42	-0.72	-1.65
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_4*	BN194_29900	K0N971	1.36	-0.72	-1.65
GTPase Era	tRNA/Ribosome assembly/processing	*era*	BN194_16990	K0MVQ8	1.00	-0.72	-1.65
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	*murA2,murA*	BN194_26780	K0NAR9	0.82	-0.73	-1.65
Uncharacterized protein	General prediction only		BN194_26820	K0NCV9	0.65	-0.73	-1.66
Single-stranded DNA-binding protein (SSB)	DNA replication-related	*ssb*	BN194_00110	K0N1C2	1.59	-0.73	-1.66

Uncharacterized protein	Posttranslational modification	*pp2C*	BN194_18030	K0N993	3.51	-0.74	-1.67
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_3*	BN194_21440	K0MWS9	2.74	-0.74	-1.67
CCA-adding enzyme (EC 2.7.7.72) (CCA tRNA nucleotidyltransferase) (tRNA CCA-pyrophosphorylase) (tRNA adenylyl-/cytidylyl-transferase) (tRNA nucleotidyltransferase) (tRNA-NT)	tRNA/Ribosome assembly/processing	*cca*	BN194_15770	K0NAM4	0.32	-0.74	-1.67
Uncharacterized protein yaaA	General prediction only	*yaaA*	BN194_00040	K0MRL5	1.35	-0.74	-1.67
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	*ywpJ*	BN194_11320	K0N9U2	1.75	-0.74	-1.67
Lipopolysaccharide synthesis sugar transferase	Cell wall biogenesis		BN194_21390	K0MWS4	1.44	-0.76	-1.69
Sortase	Cell wall biogenesis		BN194_22780	K0NA48	2.87	-0.76	-1.70
Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase)	Cofactor-related metabolism	*coaE*	BN194_18910	K0N5P8	0.46	-0.76	-1.70
Uncharacterized protein ytoI	Transcriptional regulation	*ytoI*	BN194_08440	K0MTM0	1.29	-0.77	-1.70
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	*dnaK*	BN194_17460	K0N5C7	2.34	-0.78	-1.72
ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease RexB)	DNA repair/recombination	*rexB*	BN194_16810	K0N573	0.36	-0.78	-1.72
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	1.00	-0.78	-1.72
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*ileS*	BN194_14810	K0N4L9	2.92	-0.79	-1.73
Transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	1.20	-0.80	-1.74
Uncharacterized protein	Cofactor-related metabolism		BN194_18720	K0NB69	0.77	-0.80	-1.75
Protein dedA	Unknown/uncharacterized	*dedA*	BN194_08930	K0N6M9	0.55	-0.81	-1.76
30S ribosomal protein S1 homolog	Ribosomal proteins	*ypfD*	BN194_15720	K0NAL9	1.63	-0.82	-1.76
Ribonuclease Z (RNase Z) (EC 3.1.26.11) (tRNA 3 endonuclease) (tRNase Z)	tRNA/Ribosome assembly/processing	*rnz*	BN194_15470	K0NAK0	0.32	-0.82	-1.77
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	*pyrH*	BN194_17660	K0N5E6	2.13	-0.82	-1.77
Regulatory protein vanR	Signal transduction	*vanR*	BN194_02120	K0N7G4	2.52	-0.83	-1.78
Septum formation inhibitor MinC, C-terminal domain family	Cytokinesis	*minC*	BN194_14580	K0N805	0.81	-0.84	-1.79
Uncharacterized protein	Signal transduction		BN194_18490	K0MW74	2.83	-0.84	-1.79
UPF0237 protein BN194_09820	Unknown/uncharacterized		BN194_09820	K0N9F9	1.91	-0.84	-1.79

50S ribosomal protein L21	Ribosomal proteins	*rplU*	BN194_18290	K0MW61	1.38	-0.85	-1.80
50S ribosomal protein L29	Ribosomal proteins	*rpmC*	BN194_26140	K0MXT6	1.98	-0.85	-1.80
Type I restriction enzyme EcoR124II M protein (EC 2.1.1.72)	IS elements/foreign DNA defense	*hsdM*	BN194_22340	K0MX17	0.49	-0.85	-1.81
GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	2.42	-0.86	-1.81
Uncharacterized RNA methyltransferase lp_3226 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_19580	K0N9J4	0.43	-0.86	-1.81
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	*phoU*	BN194_10290	K0MTZ9	1.55	-0.86	-1.82
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	*yqeH*	BN194_18740	K0MW90	1.51	-0.87	-1.83
Putative ADP-ribose pyrophosphatase yjhB (EC 3.6.1.-)	General prediction only	*yjhB*	BN194_25530	K0NAH4	0.78	-0.88	-1.84
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	*mtlF*	BN194_30410	K0N8N0	1.38	-0.88	-1.84
Phosphonates import ATP-binding protein PhnC (EC 3.6.3.28)	ABC-type transporter systems	*phnC_2,phnC*	BN194_25690	K0MXP5	1.88	-0.89	-1.85
Sorbose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*sorB_2*	BN194_29180	K0NB63	2.24	-0.90	-1.86
Uncharacterized protein	Unknown/uncharacterized		BN194_01870	K0N7D4	1.96	-0.90	-1.86
UvrABC system protein B (Protein UvrB) (Excinuclease ABC subunit B)	DNA repair/recombination	*uvrB*	BN194_10440	K0MU09	0.98	-0.90	-1.86
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*argS*	BN194_19120	K0NB86	1.60	-0.91	-1.88
Polyphosphate kinase (EC 2.7.4.1) (ATP-polyphosphate phosphotransferase) (Polyphosphoric acid kinase)	Membrane bioenergetics	*ppk*	BN194_27270	K0ND10	1.58	-0.91	-1.89
UPF0346 protein BN194_15870	Unknown/uncharacterized		BN194_15870	K0NAN2	1.51	-0.92	-1.89
Bifunctional protein GlmU	Cell wall biogenesis	*glmU*	BN194_26940	K0MY10	2.14	-0.93	-1.90
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	*rex_2,rex*	BN194_23820	K0NBZ5	1.29	-0.93	-1.90
Uncharacterized isochorismatase family protein pncA (EC 3.-.-.-)	General prediction only	*pncA*	BN194_29120	K0NDH8	0.77	-0.94	-1.93
Uncharacterized oxidoreductase YcsN (EC 1.-.-.-)	General prediction only	*ycsN*	BN194_27290	K0MY45	2.24	-0.95	-1.93
1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157)	Cell wall biogenesis		BN194_09040	K0MTQ9	1.24	-0.95	-1.93
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD(+)])	DNA replication-related	*ligA*	BN194_11930	K0N7A9	2.32	-0.95	-1.93
Uncharacterized protein	General prediction only		BN194_14990	K0MV99	0.58	-0.95	-1.93
Xanthine/uracil/vitamin C permease	Other transporter proteins		BN194_01470	K0N796	0.70	-0.96	-1.94

NifU-like protein	Cofactor-related metabolism	*nifU*	BN194_13800	K0N4L4	2.53	-0.96	-1.95
Manganese transport system ATP-binding protein MntB	ABC-type transporter systems	*mntB*	BN194_25460	K0N7A8	1.97	-0.97	-1.96
Response regulator ArlR	Signal transduction	*arlR*	BN194_18650	K0N5X3	2.49	-0.97	-1.96
Uncharacterized protein	Unknown/uncharacterized		BN194_02470	K0N7L7	1.57	-0.98	-1.97
L-asparaginase (EC 3.5.1.1)	Amino acid-related metabolism	*ansA*	BN194_23900	K0N7L6	1.17	-0.98	-1.98
Elongation factor G (EF-G)	Protein translation (elongation)	*fusA*	BN194_26270	K0NCN8	2.21	-0.99	-1.98
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	*alsS*	BN194_20150	K0N695	0.49	-0.99	-1.98
DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	1.47	-0.99	-1.99
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	*patB_2*	BN194_09790	K0MTW3	1.39	-0.99	-1.99
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	Nucleic acid/nucleotide metabolism	*tmk*	BN194_23950	K0N7L9	2.83	-1.00	-2.00
Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase (EC 4.2.-.-)	*tRNA/Ribosome assembly/processing*		BN194_17370	K0NAY4	2.94	-1.00	-2.00
Phosphoribosylformylglycinamidine synthase subunit PurL (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit II) (Glutamine amidotransferase PurL) (Phosphoribosylformylglycinamidine synthase subunit II)	Nucleic acid/nucleotide metabolism	*purL*	BN194_19330	K0N9H6	3.40	-1.01	-2.01
30S ribosomal protein S11	Ribosomal proteins	*rpsK*	BN194_25970	K0NCJ0	1.99	-1.02	-2.02
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	*tuf*	BN194_15310	K0N4R1	3.60	-1.02	-2.03
Glucitol operon repressor	Transcriptional regulation	*srlR*	BN194_28690	K0MYG3	1.93	-1.03	-2.05
Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	*nfo*	BN194_17070	K0NAW5	1.44	-1.04	-2.06
Glycine betaine/carnitine/choline transport ATP-binding protein OpuCA	ABC-type transporter systems	*opuCA*	BN194_00680	K0N4E4	2.17	-1.04	-2.06
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	*def*	BN194_15060	K0N4N6	1.54	-1.05	-2.07
Transcriptional regulator, TetR family	Transcriptional regulation		BN194_12190	K0MUM1	2.70	-1.05	-2.07
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	*pflB*	BN194_16080	K0N8I5	2.37	-1.05	-2.08
Xanthine permease	Other transporter proteins	*pbuX*	BN194_12500	K0N490	1.35	-1.06	-2.08
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	2.39	-1.07	-2.10

Chaperone protein ClpB	Protein folding/turnover	*clpB*	BN194_15500	K0N4Z8	2.00	-1.07	-2.10
Putative RNA-binding protein ylmH	General prediction only	*ylmH*	BN194_14790	K0MV84	2.00	-1.08	-2.12
Cell division ATP-binding protein FtsE	Cytokinesis	*ftsE*	BN194_10190	K0MTZ2	3.41	-1.10	-2.14
Ribosomal RNA small subunit methyltransferase A (EC 2.1.1.182) (16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase) (16S rRNA dimethyladenosine transferase) (16S rRNA dimethylase) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase)	tRNA/Ribosome assembly/processing	*rsmA,ksgA*	BN194_27020	K0NCX3	1.95	-1.10	-2.14
50S ribosomal protein L23	Ribosomal proteins	*rplW*	BN194_26200	K0N869	1.61	-1.11	-2.15
50S ribosomal protein L3	Ribosomal proteins	*rplC*	BN194_26220	K0NCN1	1.67	-1.11	-2.16
Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	*bceA_2*	BN194_21230	K0N9X1	1.76	-1.12	-2.17
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*helD*	BN194_21130	K0N9W3	2.83	-1.12	-2.17
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	*rpoE*	BN194_26810	K0N7L4	1.77	-1.12	-2.17
Uncharacterized protein	Unknown/uncharacterized		BN194_17360	K0N5B9	0.79	-1.12	-2.17
Uncharacterized protein yeaC		*yeaC*	BN194_29960	K0N8I6	1.96	-1.12	-2.17
Putative transcriptional regulator (DtxR family)	Transcriptional regulation		BN194_08410	K0N354	0.59	-1.12	-2.18
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	4.10	-1.13	-2.18
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	*zwf*	BN194_08420	K0N966	2.56	-1.13	-2.19
Translation initiation factor IF-3	Protein translation (initiation)	*infC*	BN194_18820	K0NB73	3.44	-1.14	-2.20
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	*rpoA*	BN194_25960	K0N7E5	3.78	-1.15	-2.22
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	*ung*	BN194_11330	K0N758	1.51	-1.15	-2.22
30S ribosomal protein S19	Ribosomal proteins	*rpsS*	BN194_26180	K0NAM1	2.44	-1.15	-2.22
Uncharacterized protein YwcC	Carbohydrate-related metabolism	*ywcC*	BN194_09930	K0N6V0	1.97	-1.16	-2.23
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	*clpE*	BN194_19450	K0N644	1.53	-1.16	-2.23
Uncharacterized protein	General prediction only		BN194_17420	K0NAY8	3.80	-1.16	-2.24
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	*tig*	BN194_15330	K0N884	3.61	-1.16	-2.24

Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	*lysS*	BN194_26380	K0NAN7	3.18	-1.17	-2.25
30S ribosomal protein S6	Ribosomal proteins	*rpsF*	BN194_00100	K0N0Z1	1.56	-1.17	-2.25
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB*	BN194_13410	K0N4C0	2.59	-1.17	-2.25
Ribosome maturation factor RimP	tRNA/Ribosome assembly/processing	*rimP*	BN194_17590	K0MVW3	1.21	-1.17	-2.25
Uncharacterized protein ylxR	General prediction only	*ylxR*	BN194_17570	K0NAZ6	2.92	-1.19	-2.28
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC_2*	BN194_20620	K0NBH0	1.63	-1.20	-2.29
Protein RecA (Recombinase A)	DNA repair/recombination	*recA_2,recA*	BN194_27650	K0N8P0	1.44	-1.21	-2.31
Uncharacterized protein ykuJ	Unknown/uncharacterized	*ykuJ*	BN194_09100	K0N348	0.68	-1.21	-2.32
30S ribosomal protein S10	Ribosomal proteins	*rpsJ*	BN194_26230	K0NAM5	1.70	-1.21	-2.32
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_3*	BN194_04780	K0N5N9	1.86	-1.22	-2.32
Uncharacterized protein YdiC	General prediction only	*ydiC_3*	BN194_23870	K0NBZ8	1.05	-1.22	-2.32
Putative ribosome biogenesis GTPase RsgA (EC 3.6.1.-)	tRNA/Ribosome assembly/processing	*rsgA*	BN194_18010	K0N5J0	0.99	-1.22	-2.33
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*asnS*	BN194_16760	K0N569	2.50	-1.22	-2.33
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	*yclJ*	BN194_11790	K0MUE5	3.43	-1.23	-2.35
Phosphoribosylformylglycinamidine synthase subunit PurQ (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit I) (Glutaminase PurQ) (Phosphoribosylformylglycinamidine synthase subunit I)	Nucleic acid/nucleotide metabolism	*purQ*	BN194_19340	K0MWC7	2.14	-1.23	-2.35
3'-5' exoribonuclease yhaM (EC 3.1.-.-)	RNA degradation	*yhaM*	BN194_19070	K0NB84	0.67	-1.24	-2.36
Phosphatase YidA (EC 3.1.3.-)	General prediction only	*yidA*	BN194_28520	K0NDD5	2.93	-1.24	-2.36
PspC domain-containing protein	Unknown/uncharacterized	*ythC*	BN194_10300	K0N3H5	2.96	-1.24	-2.36
Replicative DNA helicase (EC 3.6.4.12)	DNA replication-related	*dnaC*	BN194_01140	K0MRW2	0.66	-1.24	-2.37
Endonuclease MutS2 (EC 3.1.-.-)	DNA repair/recombination	*mutS2*	BN194_08560	K0N359	1.50	-1.25	-2.38
Transcriptional regulator, XRE family	Transcriptional regulation		BN194_30170	K0NDP4	2.09	-1.26	-2.39
Thioredoxin	Posttranslational modification	*trxA_2*	BN194_08570	K0N975	2.52	-1.26	-2.40
Uridine kinase (EC 2.7.1.48)		*udk*	BN194_18540	K0MW76	1.12	-1.28	-2.42

GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*relA*	BN194_17230	K0N8Y0	4.25	-1.28	-2.43
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	3.11	-1.31	-2.48
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	*yfeX*	BN194_07170	K0N8U9	3.91	-1.31	-2.48
50S ribosomal protein L17	Ribosomal proteins	*rplQ*	BN194_25950	K0N841	2.41	-1.32	-2.50
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	*rnjA*	BN194_15020	K0NAH6	2.42	-1.33	-2.51
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	*obg*	BN194_15440	K0MVD3	3.95	-1.33	-2.52
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	*gyrA*	BN194_00070	K0N6S7	2.01	-1.34	-2.54
Uncharacterized protein	Unknown/uncharacterized		BN194_15370	K0NAJ2	2.21	-1.35	-2.55
Uncharacterized protein YqhY	Unknown/uncharacterized	*yqhY*	BN194_18230	K0N9A7	4.16	-1.36	-2.57
Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	*phoP*	BN194_10220	K0N9J6	2.10	-1.36	-2.57
Arginine repressor	Transcriptional regulation	*argR1,argR*	BN194_19110	K0N5R1	2.23	-1.37	-2.59
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	*pmi*	BN194_02920	K0N7U2	3.62	-1.37	-2.59
Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-)	Nucleic acid/nucleotide metabolism	*purK*	BN194_12510	K0N441	2.91	-1.39	-2.61
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	*ybeY*	BN194_17010	K0N594	1.94	-1.42	-2.67
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*manX_5*	BN194_29720	K0NDL4	2.82	-1.42	-2.67
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	*pyrC*	BN194_16470	K0NAS6	2.24	-1.42	-2.68
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	*ohrR*	BN194_10500	K0N3J7	4.08	-1.42	-2.68
50S ribosomal protein L5	Ribosomal proteins	*rplE*	BN194_26100	K0N859	2.52	-1.44	-2.70
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	*hslO*	BN194_26400	K0N893	2.96	-1.44	-2.71
Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	1.07	-1.46	-2.76
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	*nusB*	BN194_18220	K0NB49	2.12	-1.48	-2.78
Uncharacterized protein			BN194_19420	K0NB98	0.28	-1.48	-2.79
Uncharacterized protein YneR	General prediction only	*yneR*	BN194_18480	K0N9C1	1.80	-1.48	-2.79
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	*cysS*	BN194_24430	K0NAB2	0.94	-1.49	-2.80
Ribosomal RNA small subunit methyltransferase F (EC 2.1.1.178)	tRNA/Ribosome assembly/processing	*rsmF*	BN194_16850	K0N5C0	1.99	-1.49	-2.80

Glycine cleavage system H protein	Amino acid-related metabolism	*gcvH*	BN194_13700	K0N4K8	3.00	-1.50	-2.83
Segregation and condensation protein B	Cytokinesis	*scpB*	BN194_15640	K0MVE6	2.08	-1.51	-2.85
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC_2,deoC*	BN194_02790	K0MSB5	2.79	-1.51	-2.86
Recombination protein RecR	DNA repair/recombination	*recR*	BN194_23970	K0NC03	3.36	-1.52	-2.86
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP*	BN194_17930	K0N988	1.68	-1.52	-2.88
50S ribosomal protein L6	Ribosomal proteins	*rplF*	BN194_26070	K0NCK5	2.85	-1.53	-2.89
Transcriptional regulator, xre family	Transcriptional regulation		BN194_05600	K0N260	2.35	-1.53	-2.90
Putative transcriptional regulator, MarR family	Transcriptional regulation		BN194_27490	K0MY64	1.07	-1.54	-2.91
50S ribosomal protein L33	Ribosomal proteins	*rpmG2,rpmG*	BN194_24280	K0NAA5	3.00	-1.56	-2.94
3-hydroxy-3-methylglutaryl coenzyme A reductase (HMG-CoA reductase) (EC 1.1.1.88)	Lipid-related metabolism	*mvaA*	BN194_19690	K0MWE8	2.85	-1.56	-2.96
Uncharacterized protein ypgQ	General prediction only	*ypgQ*	BN194_27480	K0NAX0	1.30	-1.57	-2.98
LexA repressor (EC 3.4.21.-) (EC 3.4.21.88)	DNA repair/recombination	*lexA*	BN194_07970	K0N944	0.58	-1.58	-2.99
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227) (Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase)	Cell wall biogenesis	*murG*	BN194_14730	K0N819	2.72	-1.59	-3.01
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	*maa*	BN194_30010	K0N8I9	2.25	-1.62	-3.06
GNAT family acetyltransferase	General prediction only		BN194_01510	K0N1L8	2.95	-1.62	-3.08
tRNA-specific adenosine deaminase (EC 3.5.4.33)	tRNA/Ribosome assembly/processing	*tadA*	BN194_24000	K0N7M1	0.66	-1.63	-3.10
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	*glcK*	BN194_18420	K0NB57	3.20	-1.64	-3.11
Hex regulon repressor	Transcriptional regulation		BN194_02320	K0N7J9	2.58	-1.64	-3.11
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		BN194_11600	K0N3Z3	2.50	-1.65	-3.13
Uncharacterized protein SE_0534	*tRNA/Ribosome assembly/processing*		BN194_10150	K0N3F2	3.01	-1.65	-3.14
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	*ndk*	BN194_08160	K0N340	1.34	-1.66	-3.15
50S ribosomal protein L1	Ribosomal proteins	*rplA*	BN194_24150	K0N7M7	5.66	-1.67	-3.19
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	*yabO*	BN194_26520	K0NCR8	2.31	-1.68	-3.20

Thioredoxin-like protein ytpP	Posttranslational modification	*ytpP*	BN194_18980	K0N9F1	2.72	-1.69	-3.22
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA_2*	BN194_20640	K0MWL6	3.71	-1.69	-3.23
DNA topoisomerase 1 (EC 5.99.1.2) (DNA topoisomerase I)	DNA replication-related	*topA*	BN194_15970	K0NAP0	2.51	-1.70	-3.25
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	*HBN1*	BN194_16550	K0N597	2.73	-1.70	-3.26
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	*guaA*	BN194_21070	K0NBJ2	2.98	-1.71	-3.26
Beta-galactosidase 17 (EC 3.2.1.23)	Carbohydrate-related metabolism	*BGAL17*	BN194_02960	K0N204	0.65	-1.71	-3.27
Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	*gntK*	BN194_02340	K0MS76	1.73	-1.74	-3.33
Transcriptional repressor CcpN	Transcriptional regulation	*ccpN*	BN194_24740	K0MXH2	2.19	-1.75	-3.36
DegV domain-containing protein SP_1112	Unknown/uncharacterized		BN194_15830	K0N8F3	3.36	-1.77	-3.41
Uncharacterized protein			BN194_21520	K0NBL8	2.98	-1.83	-3.57
Uncharacterized protein yueI	Unknown/uncharacterized	*yueI*	BN194_13920	K0NAC7	2.26	-1.84	-3.57
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	4.30	-1.84	-3.58
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	*prfB*	BN194_10180	K0N6W9	3.26	-1.84	-3.58
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA_2*	BN194_22950	K0N7F8	2.76	-1.84	-3.59
Transcriptional repressor smtB homolog	Transcriptional regulation	*ziaR*	BN194_01180	K0N4L0	1.19	-1.85	-3.59
Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		BN194_08520	K0N972	2.77	-1.85	-3.61
Uncharacterized protein	Unknown/uncharacterized		BN194_12110	K0N410	3.04	-1.87	-3.65
Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase)	Nucleic acid/nucleotide metabolism	*purM*	BN194_19320	K0NB95	3.15	-1.87	-3.66
Uncharacterized protein	Unknown/uncharacterized		BN194_01600	K0N1B9	2.32	-1.90	-3.74
Folate transporter FolT	Unknown/uncharacterized	*folT*	BN194_23890	K0MXC9	1.03	-1.90	-3.74
50S ribosomal protein L11	Ribosomal proteins	*rplK*	BN194_24160	K0N724	2.24	-1.92	-3.78
Dihydrofolate reductase (EC 1.5.1.3)	Cofactor-related metabolism	*folA*	BN194_15810	K0N4W0	1.42	-1.92	-3.78
Double-stranded beta-helix related protein	Transcriptional regulation		BN194_11420	K0N9U8	1.05	-1.93	-3.80
DNA replication protein dnaD	DNA replication-related	*dnaD*	BN194_16750	K0N5B1	1.41	-1.93	-3.82

Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_23190	K0MXA1	2.12	-1.94	-3.83
Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	*adk*	BN194_26010	K0N7F0	2.85	-1.94	-3.85
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	*aldB*	BN194_20140	K0MWH5	3.55	-1.94	-3.85
Bifunctional purine biosynthesis protein PurH	Nucleic acid/nucleotide metabolism	*purH*	BN194_19300	K0N634	3.35	-1.95	-3.87
Transcription termination/antitermination protein NusA	Transcription-associated proteins	*nusA*	BN194_17580	K0N927	3.59	-1.96	-3.89
Cadmium efflux system accessory protein	Other transporter proteins	*cadC*	BN194_21540	K0MWU0	2.45	-1.97	-3.91
Phosphoribosylformylglycinamidine synthase subunit PurS (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit III) (Phosphoribosylformylglycinamidine synthase subunit III)	Nucleic acid/nucleotide metabolism	*yexA,purS*	BN194_19350	K0N638	3.20	-1.98	-3.93
Transcriptional regulator, xre family	Transcriptional regulation		BN194_23510	K0N6Y7	4.11	-1.98	-3.94
Uncharacterized protein MJ0282	Cofactor-related metabolism		BN194_03700	K0N1T2	5.25	-2.00	-4.00
Uncharacterized ABC transporter ATP-binding protein TM_0288	*ABC-type transporter systems*		BN194_06900	K0N2K4	1.12	-2.01	-4.01
tRNA pseudouridine synthase B (EC 5.4.99.25) (tRNA pseudouridine(55) synthase) (tRNA pseudouridylate synthase) (tRNA-uridine isomerase)	tRNA/Ribosome assembly/processing	*truB*	BN194_17520	K0NAZ5	2.44	-2.01	-4.02
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_2*	BN194_15390	K0MVD0	4.87	-2.01	-4.03
Uncharacterized protein	Unknown/uncharacterized		BN194_21170	K0NBJ9	2.78	-2.01	-4.04
50S ribosomal protein L13	Ribosomal proteins	*rplM*	BN194_25850	K0N828	2.99	-2.02	-4.07
N5-carboxyaminoimidazole ribonucleotide mutase (N5-CAIR mutase) (EC 5.4.99.18) (5-(carboxyamino)imidazole ribonucleotide mutase)	Nucleic acid/nucleotide metabolism	*purE*	BN194_19380	K0N9H9	3.88	-2.03	-4.09
Predicted ORF			BN194_P0560	K0MZ29	3.03	-2.05	-4.13
HTH-type transcriptional repressor glcR	Transcriptional regulation	*glcR*	BN194_02570	K0N7M8	3.41	-2.07	-4.20
SsrA-binding protein (Small protein B)	Posttranslational modification	*smpB*	BN194_11110	K0N3S3	2.71	-2.07	-4.20
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	*prfA*	BN194_13510	K0N4C6	2.98	-2.08	-4.23
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	*yhfP*	BN194_07740	K0MTE1	3.14	-2.09	-4.26
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	*guaB*	BN194_02100	K0N1G3	4.77	-2.11	-4.31

Transcriptional repressor NrdR	Transcriptional regulation	*nrdR*	BN194_18900	K0N5Z5	2.79	-2.11	-4.32
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	*cysK*	BN194_05520	K0N8E6	3.42	-2.13	-4.37
Glutathione peroxidase	Cell defense/detoxification	*gpo*	BN194_09780	K0N6T6	2.69	-2.13	-4.38
30S ribosomal protein S9	Ribosomal proteins	*rpsI*	BN194_25840	K0MXR0	1.88	-2.14	-4.39
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25570	K0NCD4	2.61	-2.15	-4.45
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	*hprK*	BN194_10330	K0N6Y3	3.65	-2.16	-4.46
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	*pycB*	BN194_20290	K0MWI8	2.93	-2.16	-4.48
HTH-type transcriptional regulator yodB	Transcriptional regulation	*yodB*	BN194_18590	K0MW80	0.97	-2.17	-4.49
Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	DNA repair/recombination	*recJ*	BN194_17390	K0MVT7	3.55	-2.18	-4.53
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2,lacD*	BN194_07480	K0N6A8	3.18	-2.22	-4.65
30S ribosomal protein S2	Ribosomal proteins	*rpsB*	BN194_17680	K0N936	4.33	-2.23	-4.70
Chaperone protein ClpB	Protein folding/turnover	*clpB_2*	BN194_26350	K0N887	4.05	-2.25	-4.75
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citE*	BN194_20320	K0NBF4	4.30	-2.27	-4.82
Nucleotide-binding protein BN194_10470	General prediction only		BN194_10470	K0N9L7	3.43	-2.28	-4.87
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB_2*	BN194_20630	K0N9S5	1.27	-2.29	-4.89
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE*	BN194_02970	K0N7U7	3.46	-2.30	-4.93
50S ribosomal protein L14	Ribosomal proteins	*rplN*	BN194_26120	K0NCL3	3.36	-2.31	-4.95
D-ribose-binding protein	ABC-type transporter systems	*rbsB*	BN194_03290	K0MSF6	3.26	-2.32	-5.00
30S ribosomal protein S13	Ribosomal proteins	*rpsM*	BN194_25980	K0NAK3	2.04	-2.36	-5.13
ABC-type phosphate/phosphonate transport system,periplasmic component	*ABC-type transporter systems*		BN194_25680	K0NAI1	4.14	-2.36	-5.13
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox_2*	BN194_02850	K0N1N9	4.84	-2.39	-5.23
Uncharacterized protein	Unknown/uncharacterized	*FNV1452*	BN194_18830	K0N9E3	3.84	-2.40	-5.28
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	*xpt*	BN194_12490	K0MUR6	3.05	-2.41	-5.31
30S ribosomal protein S8	Ribosomal proteins	*rpsH*	BN194_26080	K0NAL1	3.91	-2.45	-5.46

N5-carboxyaminoimidazole ribonucleotide synthase (N5-CAIR synthase) (EC 6.3.4.18) (5-(carboxyamino)imidazole ribonucleotide synthetase)	Nucleic acid/nucleotide metabolism	*purK_2, purK*	BN194_19370	K0NB96	3.53	-2.50	-5.64
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA*	BN194_18520	K0NB62	4.04	-2.50	-5.64
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	*tsf*	BN194_17670	K0NB01	6.19	-2.50	-5.65
Uncharacterized protein			BN194_16060	K0N4Y8	3.56	-2.50	-5.67
Elongation factor P	Protein translation (elongation)	*efp_2*	BN194_22050	K0N712	1.91	-2.52	-5.73
30S ribosomal protein S7	Ribosomal proteins	*rpsG*	BN194_26280	K0NAM9	4.72	-2.53	-5.77
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	1.80	-2.53	-5.78
Stage 0 sporulation protein J	Cytokinesis	*spo0J*	BN194_02050	K0N1F9	3.49	-2.53	-5.79
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	*yqeL,rsfS*	BN194_18710	K0N5N6	3.99	-2.54	-5.82
Ribosome maturation factor RimM	tRNA/Ribosome assembly/processing	*rimM*	BN194_17790	K0MVZ6	3.23	-2.56	-5.89
30S ribosomal protein S17	Ribosomal proteins	*rpsQ*	BN194_26130	K0NAL6	2.28	-2.58	-5.99
Nod factor export ATP-binding protein I (EC 3.6.3.-)	ABC-type transporter systems	*nodI*	BN194_06850	K0N2J7	2.68	-2.60	-6.06
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*lacC*	BN194_07470	K0N8Y4	4.82	-2.64	-6.25
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citF*	BN194_20310	K0N607	3.42	-2.67	-6.38
TPR repeat-containing protein ypiA	Unknown/uncharacterized	*ypiA*	BN194_15750	K0N517	5.24	-2.68	-6.39
RNA polymerase sigma factor SigA	RNA polymerase	*rpoD,sigA*	BN194_16920	K0NAV6	3.95	-2.72	-6.57
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	2.84	-2.76	-6.77
DNA topoisomerase 4 subunit A (EC 5.99.1.-)		*parC*	BN194_16070	K0NAP8	3.79	-2.77	-6.84
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	*purB*	BN194_12520	K0NA41	5.93	-2.79	-6.92
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF_2*	BN194_20590	K0MWL1	3.07	-2.84	-7.16
Coenzyme A biosynthesis bifunctional protein CoaBC (EC 4.1.1.36) (EC 6.3.2.5)		*coaBC*	BN194_18090	K0MW49	3.55	-2.88	-7.36
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	*htrA*	BN194_29460	K0N8D9	4.14	-2.89	-7.41
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	*pepS*	BN194_12180	K0N7D5	2.01	-2.89	-7.42
Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	Nucleic acid/nucleotide metabolism	*purD*	BN194_19290	K0MWC4	3.40	-2.90	-7.47

Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	*upp*	BN194_13550	K0N4J8	3.19	-2.96	-7.80
Adapter protein MecA	Competence (DNA uptake)	*mecA*	BN194_19170	K0NB89	1.88	-2.99	-7.97
MarR family transcriptional regulator	Transcriptional regulation		BN194_22610	K0N6N9	4.00	-3.01	-8.08
30S ribosomal protein S14 type Z	Ribosomal proteins	*rpsZ,rpsN*	BN194_26090	K0MXS9	0.80	-3.09	-8.50
Translation initiation factor IF-2	Protein translation (initiation)	*infB*	BN194_17550	K0N5K7	4.44	-3.13	-8.78
Uncharacterized protein	*Nucleic acid/nucleotide metabolism*		BN194_27260	K0N7R1	3.29	-3.14	-8.84
41 kDa protein		*repA*	BN194_P0550	K0NBI6	2.05	-3.18	-9.05
Uncharacterized protein	Unknown/uncharacterized		BN194_01760	K0N1N3	1.99	-3.23	-9.37
Uncharacterized protein MJ1651	General prediction only		BN194_04410	K0N281	3.25	-3.24	-9.45
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_2*	BN194_20600	K0N6C6	3.48	-3.28	-9.73
Uncharacterized protein	Unknown/uncharacterized		BN194_16650	K0N5A4	4.37	-3.30	-9.82
UPF0337 protein lp_1708	General prediction only		BN194_05810	K0N2J8	1.07	-3.31	-9.89
Uncharacterized protein yjdJ	General prediction only	*yjdJ*	BN194_24650	K0N7R2	2.14	-3.32	-9.97
Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	*ADH2*	BN194_08400	K0N307	3.08	-3.36	-10.29
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	*citD*	BN194_20330	K0N9Q5	4.17	-3.36	-10.30
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB_2*	BN194_21970	K0NBP6	2.68	-3.39	-10.48
Transcriptional regulatory protein YycF	Signal transduction	*yycF_2*	BN194_29510	K0N8E4	3.17	-3.48	-11.16
Putative sporulation transcription regulator WhiA	Transcriptional regulation	*whiA*	BN194_10490	K0MU14	5.08	-3.51	-11.38
Probable transcription repressor NiaR	Transcriptional regulation	*niaR*	BN194_08730	K0N6L8	4.26	-3.52	-11.51
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshB*	BN194_08460	K0N356	4.02	-3.55	-11.68
Nucleoid occlusion protein	Cytokinesis	*noc*	BN194_02030	K0N4Z1	3.91	-3.71	-13.07
Manganese ABC transporter substrate-binding lipoprotein	ABC-type transporter systems	*fimA*	BN194_25450	K0N7Y2	1.77	-3.78	-13.75
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_2*	BN194_04490	K0MSM9	2.83	-3.93	-15.21
MFS permease-like protein	Other transporter proteins		BN194_06910	K0N2S6	3.41	-3.93	-15.26
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	*hslV*	BN194_16000	K0N542	2.07	-4.11	-17.32

Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*yfmL*	BN194_12120	K0NA13	4.98	-4.13	-17.56
50S ribosomal protein L33	Ribosomal proteins	*rpmG*	BN194_20200	K0N697	0.87	-4.28	-19.36
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07710	K0N2Z3	5.80	-4.43	-21.60
Uncharacterized protein RP368	ABC-type transporter systems		BN194_07720	K0N914	5.51	-4.66	-25.22
ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_07700	K0N2V5	5.36	-5.59	-48.30
ABC-type uncharacterized transport system, ATPase component	ABC-type transporter systems		BN194_07730	K0N6C9	5.67	-6.30	-78.69

(7e)Protein FC LiCL pH 4.5 Vs CFE pH 4.5

Protein names	Functional Class	Gene	Gene locus	Protein IDs	-Log t-test p-value	t-test difference	Fold change
50S ribosomal protein L32	Ribosomal proteins	*rpmF*	BN194_15510	K0N4T0	4.92	10.39	1343.80
Uncharacterized protein	Unknown/uncharacterized		BN194_01080	K0N4J7	4.97	8.64	397.55
Alternansucrase	Cell wall biogenesis		BN194_02430	K0N547	6.37	8.24	302.79
Uncharacterized protein yitL	General prediction only	*yitL*	BN194_15600	K0N505	2.30	7.38	167.10
Putative N-acetylmuramoyl-L-alanine amidase YrvJ (EC 3.5.1.28)	Cytokinesis	*yrvJ*	BN194_17200	K0N5G4	3.39	6.78	110.13
Uncharacterized protein	Unknown/uncharacterized		BN194_07550	K0N2T9	3.00	6.70	103.75
Putative secreted protein	cell wall biogenesis		BN194_02820	K0N7S8	4.61	6.22	74.69
Uncharacterized protein	Unknown/uncharacterized		BN194_23630	K0NA78	4.81	6.19	73.16
Ribonuclease H (EC 3.1.26.4)	DNA repair/recombination	*rnhA*	BN194_27580	K0NAX8	5.51	5.51	45.43
Uncharacterized protein	Unknown/uncharacterized		BN194_05550	K0N257	3.42	5.48	44.76
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	*dut*	BN194_24640	K0MXG3	5.50	5.46	44.10
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ysgA*	BN194_18610	K0N5M8	4.18	5.29	39.11
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF_2*	BN194_19090	K0MWB2	5.02	5.17	35.90
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*rluB*	BN194_15650	K0N509	3.15	5.14	35.31

ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_07700	K0N2V5	3.32	5.13	35.03
Possible TrsG protein	Unknown/uncharacterized		BN194_00240	K0MRM8	4.79	5.03	32.73
Gluconate 5-dehydrogenase (EC 1.1.1.69)	General prediction only	*idnO*	BN194_08150	K0N2Z5	3.81	4.93	30.51
Uncharacterized protein yaaA	General prediction only	*yaaA*	BN194_00040	K0MRL5	4.73	4.78	27.39
Surface antigen	Cell wall biogenesis		BN194_21500	K0N6S2	4.88	4.72	26.32
Uncharacterized protein	Unknown/uncharacterized		BN194_12200	K0N464	2.60	4.70	26.06
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	*yabO*	BN194_26520	K0NCR8	3.13	4.63	24.73
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ*	BN194_14610	K0N4K4	2.07	4.51	22.75
HTH-type transcriptional regulator galR	Transcriptional regulation	*galR*	BN194_03780	K0N5G9	3.91	4.47	22.14
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	*rpe*	BN194_18000	K0N5T1	2.31	4.46	22.05
Transcriptional regulator lytR	Transcriptional regulation	*lytR*	BN194_02540	K0MS94	5.07	4.14	17.58
Transcriptional regulator lytR	Transcriptional regulation	*lytR_4*	BN194_23780	K0NA85	5.27	4.13	17.45
Uncharacterized protein	Unknown/uncharacterized	*yvcC*	BN194_05260	K0N2E5	5.78	4.11	17.31
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	*bkr4*	BN194_22550	K0N799	3.58	3.99	15.91
Inner membrane amino-acid ABC transporter permease protein yecS	ABC-type transporter systems	*yecS_3*	BN194_29780	K0NB99	3.26	3.95	15.42
Uncharacterized protein	Cell wall biogenesis		BN194_02360	K0N1U1	1.70	3.92	15.09
Uncharacterized protein	Unknown/uncharacterized		BN194_20240	K0MWI3	2.17	3.88	14.68
D-2-hydroxyacid dehydrogenase (EC 1.1.1.-)	General prediction only	*ddh*	BN194_16660	K0N557	3.63	3.83	14.25
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB*	BN194_17900	K0N5S3	2.51	3.79	13.87
Uncharacterized protein	Unknown/uncharacterized		BN194_21380	K0N9Y1	5.41	3.74	13.32
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	*yabR*	BN194_26500	K0N8A7	4.39	3.66	12.67
UPF0337 protein yhjA	General prediction only	*yhjA*	BN194_24800	K0N7S1	1.04	3.66	12.65
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	*fabZ*	BN194_22520	K0NBS8	3.40	3.59	12.06
Cell wall surface anchor family protein	*Cell surface proteins/internalins*		BN194_05290	K0MSU3	3.23	3.46	11.04
DNA topoisomerase 1 (EC 5.99.1.2) (DNA topoisomerase I)	DNA replication-related	*topA*	BN194_15970	K0NAP0	1.23	3.43	10.80
ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136) (ADP-dependent NAD(P)HX dehydratase)	Cofactor-related metabolism	*nnrD*	BN194_09250	K0N360	3.49	3.42	10.68

Isoprenyl transferase (EC 2.5.1.-)	Lipid-related metabolism	*uppS*	BN194_17640	K0MVX1	5.41	3.40	10.55
Arginine repressor	Transcriptional regulation	*argR1,argR*	BN194_19110	K0N5R1	2.18	3.34	10.14
Uncharacterized protein	Unknown/uncharacterized		BN194_02900	K0N1P1	3.03	3.33	10.07
Uncharacterized protein	Unknown/uncharacterized		BN194_15370	K0NAJ2	3.54	3.33	10.06
Penicillin-binding protein 2B	Cytokinesis	*pbpB*	BN194_14700	K0N4S9	4.36	3.33	10.03
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*ytzG*	BN194_09230	K0N6P7	1.63	3.31	9.95
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*yqeC*	BN194_02330	K0N532	2.47	3.24	9.47
Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)	Nucleic acid/nucleotide metabolism	*pyrF*	BN194_16430	K0N8M7	3.27	3.22	9.31
ABC transporter, ATP-binding protein	*Cell surface proteins/internalins*		BN194_15700	K0N514	1.33	3.20	9.18
Uncharacterized protein	Unknown/uncharacterized		BN194_24220	K0NC21	2.26	3.19	9.14
tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA (guanine(46)-N(7))-methyltransferase) (tRNA(m7G46)-methyltransferase)	tRNA/Ribosome assembly/processing	*trmB*	BN194_19000	K0N606	2.78	3.16	8.92
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	4.40	3.15	8.90
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*bglP*	BN194_06940	K0MT60	3.53	3.12	8.69
Penicillin-binding protein 1A	Cell wall biogenesis	*ponA*	BN194_16720	K0NAU3	4.64	3.12	8.66
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF*	BN194_08770	K0N987	3.74	3.09	8.53
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB_2*	BN194_21770	K0NBN4	5.53	3.09	8.53
Uncharacterized protein ypuA	Unknown/uncharacterized	*ypuA*	BN194_27250	K0N8I3	4.63	3.04	8.23
Xre-like DNA-binding protein	Transcriptional regulation		BN194_10050	K0N3E1	0.97	3.00	7.99
50S ribosomal protein L35	Ribosomal proteins	*rpmI*	BN194_18810	K0N5P1	2.23	2.88	7.34
Uncharacterized protein	Unknown/uncharacterized		BN194_01790	K0MS25	1.63	2.86	7.24
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA_2*	BN194_20640	K0MWL6	4.88	2.83	7.09
50S ribosomal protein L24	Ribosomal proteins	*rplX*	BN194_26110	K0N7F9	4.06	2.77	6.83
Ribonuclease P protein component (RNase P protein) (RNaseP protein) (EC 3.1.26.5) (Protein C5)	tRNA/Ribosome assembly/processing	*rnpA*	BN194_30620	K0NDS2	2.51	2.76	6.79
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	*fabG*	BN194_22560	K0N6N3	4.51	2.74	6.69
30S ribosomal protein S16	Ribosomal proteins	*rpsP*	BN194_17810	K0N5H1	2.97	2.70	6.50
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25510	K0N7B2	4.00	2.64	6.24

Uncharacterized oxidoreductase YcsN (EC 1.-.-.-)	General prediction only	*ycsN*	BN194_27290	K0MY45	3.91	2.62	6.15
30S ribosomal protein S21	Ribosomal proteins	*rpsU*	BN194_17050	K0N5E5	1.81	2.61	6.09
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	*clpP_2, clpP*	BN194_10510	K0N3M4	3.97	2.59	6.02
Exopolyphosphatase	Membrane bioenergetics		BN194_27280	K0NAV4	3.11	2.58	5.97
4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase) (EC 1.17.1.8)	Amino acid-related metabolism	*dapB*	BN194_01000	K0N166	3.26	2.54	5.81
Diphosphomevalonate decarboxylase (EC 4.1.1.33)	Lipid-related metabolism	*mvd1*	BN194_16830	K0N8S2	2.43	2.52	5.75
HTH-type transcriptional repressor yvoA	Transcriptional regulation	*yvoA_2*	BN194_19880	K0N9L8	3.06	2.48	5.59
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	*htrA*	BN194_29460	K0N8D9	5.01	2.47	5.55
NAD kinase (EC 2.7.1.23) (ATP-dependent NAD kinase)		*nadK*	ppnK	K0N6U5	2.45	2.42	5.37
Sorbose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*sorB_2*	BN194_29180	K0NB63	1.37	2.42	5.36
UPF0337 protein lp_1708	General prediction only		BN194_05810	K0N2J8	0.75	2.40	5.27
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	4.41	2.39	5.23
Uncharacterized protein	Prophage genome		BN194_09330	K0N6Q4	3.65	2.37	5.16
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*yacO*	BN194_24420	K0NC34	3.33	2.33	5.02
Sortase	Cell wall biogenesis		BN194_22780	K0NA48	4.54	2.33	5.01
UPF0346 protein BN194_15870	Unknown/uncharacterized		BN194_15870	K0NAN2	2.12	2.32	4.98
50S ribosomal protein L16	Ribosomal proteins	*rplP*	BN194_26150	K0N863	2.85	2.29	4.88
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	3.50	2.24	4.74
50S ribosomal protein L21	Ribosomal proteins	*rplU*	BN194_18290	K0MW61	2.79	2.23	4.68
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	*murF*	BN194_26720	K0NCU5	3.08	2.22	4.67
ErfK family protein	Cell wall biogenesis		BN194_26570	K0NCS1	3.43	2.21	4.62
Acyltransferase 3			BN194_15460	K0N4S6	1.93	2.19	4.55
Queuosine transporter QueT	General prediction only	*queT*	BN194_21930	K0NA07	1.46	2.19	4.55
Transcriptional regulator GltC	Transcriptional regulation	*nac*	BN194_16620	K0NAT7	4.63	2.17	4.50
Putative RNA-binding protein ylmH	General prediction only	*ylmH*	BN194_14790	K0MV84	1.59	2.13	4.39
Uncharacterized protein	Unknown/uncharacterized		BN194_16650	K0N5A4	1.12	2.13	4.38

50S ribosomal protein L33	Ribosomal proteins	*rpmG2,rpmG*	BN194_24280	K0NAA5	3.61	2.10	4.28
50S ribosomal protein L9	Ribosomal proteins	*rplI*	BN194_01130	K0N4K3	3.37	2.06	4.17
Cell division protein FtsX	Cytokinesis	*ftsX*	BN194_10200	K0N3G0	3.29	2.05	4.13
Uncharacterized protein yeaO	Unknown/uncharacterized	*yeaO*	BN194_08040	K0MTJ2	2.01	2.04	4.12
Uncharacterized protein	Unknown/uncharacterized		BN194_08020	K0N947	4.03	2.00	4.00
4-hydroxy-tetrahydrodipicolinate synthase (HTPA synthase) (EC 4.3.3.7)	Amino acid-related metabolism	*dapA*	BN194_01010	K0N1I2	2.77	1.97	3.91
Hypothetical lipoprotein	Unknown/uncharacterized		BN194_12440	K0MUR1	2.05	1.95	3.87
Uncharacterized protein	General prediction only		BN194_01300	K0N194	2.59	1.95	3.87
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	*cap4C*	BN194_12280	K0N7E3	3.38	1.95	3.86
DNA-binding protein HU	DNA replication-related	*hup*	BN194_15740	K0MVF4	3.46	1.92	3.78
SsrA-binding protein (Small protein B)	Posttranslational modification	*smpB*	BN194_11110	K0N3S3	0.67	1.91	3.76
Transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	2.39	1.88	3.68
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	1.15	1.87	3.65
50S ribosomal protein L15	Ribosomal proteins	*rplO*	BN194_26030	K0NAK7	4.89	1.87	3.64
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*fruK*	BN194_15420	K0NAJ6	3.55	1.80	3.47
Translation initiation factor IF-3	Protein translation (initiation)	*infC*	BN194_18820	K0NB73	4.12	1.79	3.47
Membrane protein	Unknown/uncharacterized		BN194_22700	K0N7C6	0.78	1.76	3.40
Manganese ABC transporter substrate-binding lipoprotein	ABC-type transporter systems	*fimA*	BN194_25450	K0N7Y2	0.84	1.74	3.35
Uncharacterized protein	Unknown/uncharacterized		BN194_01760	K0N1N3	1.14	1.74	3.34
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	*gltX*	BN194_24470	K0NC38	2.63	1.72	3.28
Pur operon repressor	Transcriptional regulation	*purR_2*	BN194_26960	K0N7M9	2.58	1.69	3.22
Ribosome maturation factor RimP	tRNA/Ribosome assembly/processing	*rimP*	BN194_17590	K0MVW3	1.00	1.67	3.17
50S ribosomal protein L27	Ribosomal proteins	*rpmA*	BN194_18270	K0NB51	1.44	1.65	3.14
Cytochrome d ubiquinol oxidase subunit 1 (EC 1.10.3.-)	Membrane bioenergetics	*cydA_2*	BN194_23410	K0N6Y2	2.48	1.64	3.11
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	*coaD*	BN194_15200	K0N4X3	2.48	1.61	3.06
Lipoprotein	ABC-type transporter systems	*metQ_2*	BN194_13740	K0MV23	3.41	1.61	3.05

Penicillin-binding protein 3	Cell wall biogenesis	*pbpC*	BN194_03320	K0N7W9	2.61	1.61	3.05
Uncharacterized amino acid permease YfnA	Other transporter proteins	*yfnA*	BN194_06960	K0N2T0	1.36	1.60	3.03
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	*dkgB*	BN194_08260	K0N347	2.31	1.60	3.03
50S ribosomal protein L30	Ribosomal proteins	*rpmD*	BN194_26040	K0MXS6	3.54	1.53	2.88
Carboxy-terminal processing protease CtpA (EC 3.4.21.102)	Protein folding/turnover	*ctpA*	BN194_15880	K0N8G1	3.61	1.52	2.87
Polyphosphate kinase (EC 2.7.4.1) (ATP-polyphosphate phosphotransferase) (Polyphosphoric acid kinase)	Membrane bioenergetics	*ppk*	BN194_27270	K0ND10	2.34	1.48	2.79
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_07710	K0N2Z3	4.02	1.47	2.77
Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	DNA repair/recombination	*recJ*	BN194_17390	K0MVT7	1.22	1.44	2.71
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_2*	BN194_29910	K0N8I1	2.77	1.44	2.71
Oxidoreductase YdhF (EC 1.-.-.-)	General prediction only	*ydhF*	BN194_25320	K0NCA1	0.93	1.43	2.69
Uncharacterized protein	Unknown/uncharacterized		BN194_11890	K0MUG0	5.56	1.41	2.67
Aspartate racemase (EC 5.1.1.13)	*Amino acid-related metabolism*		BN194_02170	K0N7H2	2.10	1.37	2.58
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227) (Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase)	Cell wall biogenesis	*murG*	BN194_14730	K0N819	2.42	1.37	2.58
Uncharacterized protein	Unknown/uncharacterized		BN194_11770	K0N9Y6	0.88	1.34	2.54
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	*hslO*	BN194_26400	K0N893	1.85	1.33	2.51
Translation initiation factor IF-1	Protein translation (initiation)	*infA*	BN194_26000	K0N847	2.60	1.32	2.50
Predicted ORF			BN194_P0560	K0MZ29	0.85	1.31	2.48
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	*dnaN*	BN194_00020	K0N6S3	4.12	1.29	2.44
50S ribosomal protein L10	Ribosomal proteins	*rplJ*	BN194_24090	K0MXD8	4.65	1.27	2.42
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	*HBN1*	BN194_16550	K0N597	2.86	1.27	2.41
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB_2*	BN194_20630	K0N9S5	0.58	1.26	2.40
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP*	BN194_17930	K0N988	1.08	1.26	2.40
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	*ndk*	BN194_08160	K0N340	0.99	1.26	2.39
Uncharacterized protein	Unknown/uncharacterized		BN194_12100	K0N456	1.31	1.23	2.35

Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_3*	BN194_14020	K0NAD1	1.93	1.20	2.29
Coenzyme A biosynthesis bifunctional protein CoaBC (EC 4.1.1.36) (EC 6.3.2.5)		*coaBC*	BN194_18090	K0MW49	2.04	1.20	2.29
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	*pta*	BN194_11340	K0MU95	2.29	1.18	2.27
Transaldolase (EC 2.2.1.2)	Central glycolytic/intermediary pathways	*fsa*	BN194_28440	K0MYF0	1.65	1.17	2.26
Uncharacterized MscS family protein YkuT	Other transporter proteins	*ykuT*	BN194_08700	K0N322	1.26	1.17	2.24
Transcriptional repressor smtB homolog	Transcriptional regulation	*ziaR*	BN194_01180	K0N4L0	0.55	1.16	2.24
Bifunctional protein BirA (EC 6.3.4.15)	Lipid-related metabolism	*birA*	BN194_08790	K0MTP3	2.27	1.15	2.22
SPFH/Band 7/PHB domain protein	Unknown/uncharacterized		BN194_29820	K0NDM1	0.92	1.15	2.22
Protein translocase subunit SecY	Protein export	*secY*	BN194_26020	K0NCJ6	1.39	1.15	2.22
UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	2.35	1.14	2.21
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	0.83	1.14	2.21
Elongation factor P	Protein translation (elongation)	*efp*	BN194_18240	K0MW57	2.07	1.13	2.19
Protein dedA	Unknown/uncharacterized	*dedA*	BN194_08930	K0N6M9	0.26	1.12	2.17
Hex regulon repressor	Transcriptional regulation		BN194_02320	K0N7J9	1.62	1.12	2.17
Protein veg	Unknown/uncharacterized	*veg*	BN194_27010	K0N7N4	1.14	1.11	2.16
Putative RNA methyltransferase YpsC (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ypsC*	BN194_16670	K0NAU0	1.85	1.06	2.08
Acetyltransferase	General prediction only		BN194_08200	K0N2Z8	1.55	1.06	2.08
30S ribosomal protein S1 homolog	Ribosomal proteins	*ypfD*	BN194_15720	K0NAL9	1.97	1.05	2.08
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_4*	BN194_29900	K0N971	2.01	1.05	2.08
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	*dacA*	BN194_02140	K0MS53	2.73	1.05	2.07
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	1.82	1.04	2.06
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	*fabZ_2*	BN194_22620	K0NBT3	3.22	1.03	2.05
CBS domain-containing protein	Unknown/uncharacterized		BN194_26610	K0N7J7	1.86	1.03	2.04
Segregation and condensation protein B	Cytokinesis	*scpB*	BN194_15640	K0MVE6	3.77	1.02	2.03
Uncharacterized protein yeaC		*yeaC*	BN194_29960	K0N8I6	0.95	1.00	2.00
30S ribosomal protein S15	Ribosomal proteins	*rpsO*	BN194_15260	K0N4Q6	2.43	1.00	1.99
Putative sporulation transcription regulator WhiA	Transcriptional regulation	*whiA*	BN194_10490	K0MU14	1.40	0.99	1.99
Xanthine permease	Other transporter proteins	*pbuX*	BN194_12500	K0N490	1.04	0.97	1.95

Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase (EC 4.2.-.-)	*tRNA/Ribosome assembly/processing*		BN194_17370	K0NAY4	1.39	0.97	1.95
CBS domain-containing protein ykuL	Unknown/uncharacterized	*ykuL*	BN194_08670	K0N981	1.23	0.96	1.95
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*nagA*	BN194_19890	K0MWF9	4.62	0.95	1.93
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	*lysS*	BN194_26380	K0NAN7	2.84	0.95	1.93
Transcriptional regulator	Transcriptional regulation		BN194_08230	K0N6I4	1.78	0.95	1.93
Cell shape-determining protein MreC (Cell shape protein MreC)	Cytokinesis	*mreC*	BN194_14560	K0N4K0	2.26	0.94	1.92
Uncharacterized lipoprotein yerH	General prediction only	*yerH*	BN194_11940	K0MUH2	2.90	0.93	1.91
Archaeal fructose-1,6-bisphosphatase related enzyme of inositol monophosphatase family	*Carbohydrate-related metabolism*		BN194_15140	K0MVB0	2.30	0.93	1.91
50S ribosomal protein L22	Ribosomal proteins	*rplV*	BN194_26170	K0NCM1	3.11	0.93	1.91
Endonuclease MutS2 (EC 3.1.-.-)	DNA repair/recombination	*mutS2*	BN194_08560	K0N359	1.46	0.93	1.91
D-ribose-binding protein	ABC-type transporter systems	*rbsB*	BN194_03290	K0MSF6	0.45	0.93	1.90
Uncharacterized protein	Unknown/uncharacterized		BN194_19210	K0N5R7	1.43	0.92	1.89
Ribosomal RNA small subunit methyltransferase F (EC 2.1.1.178)	tRNA/Ribosome assembly/processing	*rsmF*	BN194_16850	K0N5C0	1.59	0.91	1.88
Signal peptidase I (EC 3.4.21.89)	Protein export	*lepB*	BN194_02610	K0N1V9	2.18	0.89	1.85
Manganese transport system ATP-binding protein MntB	ABC-type transporter systems	*mntB*	BN194_25460	K0N7A8	1.04	0.89	1.85
UPF0342 protein yheA	Unknown/uncharacterized	*yheA*	BN194_19080	K0N9F7	1.22	0.88	1.84
Probable copper-transporting P-type ATPase B (EC 3.6.3.-)	Other transporter proteins	*copB*	BN194_19280	K0N9H1	0.81	0.87	1.83
Cell division protein DivIB	Cytokinesis	*divIB*	BN194_14740	K0MV80	0.53	0.87	1.82
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	2.52	0.86	1.82
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_19800	K0N670	2.21	0.82	1.77
Uridine kinase (EC 2.7.1.48)		*udk*	BN194_18540	K0MW76	0.78	0.81	1.76
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshB*	BN194_08460	K0N356	1.59	0.81	1.75
Aldose 1-epimerase	*Central glycolytic/intermediary pathways*		BN194_16020	K0NAP4	1.23	0.81	1.75
Ribosomal RNA small subunit methyltransferase H (EC 2.1.1.199) (16S rRNA m(4)C1402 methyltransferase) (rRNA (cytosine-N(4)-)-methyltransferase RsmH)	tRNA/Ribosome assembly/processing	*rsmH*	BN194_14680	K0N814	1.00	0.78	1.72
Uncharacterized protein yutG	Lipid-related metabolism	*yutG*	BN194_08940	K0MTQ3	4.20	0.78	1.72

Integral membrane protein	Unknown/uncharacterized		BN194_02590	K0MS97	1.25	0.74	1.67
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	*phoU*	BN194_10290	K0MTZ9	1.08	0.73	1.66
Uncharacterized protein	Unknown/uncharacterized		BN194_19470	K0NBA0	2.63	0.73	1.66
Uncharacterized protein	Unknown/uncharacterized		BN194_08270	K0N959	0.32	0.71	1.63
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	*grpE*	BN194_17470	K0NAZ2	1.05	0.69	1.62
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.-)	Lipid-related metabolism	*plsC*	BN194_17710	K0N5F1	0.76	0.69	1.61
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	*rbfA*	BN194_17540	K0MVV7	1.67	0.68	1.61
Probable catabolite control protein A	Transcriptional regulation	*ccpA*	BN194_08750	K0N323	2.00	0.67	1.60
Uncharacterized protein	Unknown/uncharacterized		BN194_15850	K0N527	1.73	0.67	1.59
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	*gpsB*	BN194_16690	K0MVN5	1.64	0.64	1.56
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	*ispA*	BN194_18180	K0N9A2	2.60	0.64	1.56
Uncharacterized protein	General prediction only		BN194_21200	K0N6M8	2.49	0.64	1.56
Uncharacterized protein ACIAD3023	Cell defense/detoxification		BN194_07010	K0N2T5	0.66	0.63	1.55
Membrane protein insertase YidC 1	Protein export	*yidC1*	BN194_18630	K0N9D1	0.51	0.62	1.54
Transcriptional regulator lytR	Transcriptional regulation	*lytR_3*	BN194_21700	K0N6U3	0.63	0.62	1.53
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	*prsA*	BN194_19060	K0N5Q8	2.88	0.62	1.53
Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	*fba_2*	BN194_05060	K0N2C9	1.28	0.60	1.52
UPF0039 protein SAR1027	General prediction only		BN194_19510	K0N5U0	0.73	0.60	1.51
Anaerobic ribonucleoside-triphosphate reductase-activating protein (EC 1.97.1.-)	Nucleic acid/nucleotide metabolism	*nrdG*	BN194_19270	K0NB93	0.56	0.59	1.50
Uncharacterized protein	Unknown/uncharacterized		BN194_25540	K0MXN3	1.77	0.58	1.50
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism		BN194_22460	K0N6M0	1.30	0.58	1.49
Probable GTP-binding protein EngB	tRNA/Ribosome assembly/processing	*engB*	BN194_15350	K0N4Y5	0.90	0.57	1.49
ABC transporter glutamine-binding protein glnH	ABC-type transporter systems	*glnH*	BN194_21430	K0N9Y4	2.07	0.56	1.48
Methionine import ATP-binding protein MetN (EC 3.6.3.-)	ABC-type transporter systems	*metN*	BN194_13750	K0N4L1	1.30	0.54	1.45
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	1.69	0.54	1.45
Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	*bceA_2*	BN194_21230	K0N9X1	1.03	0.53	1.45
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA*	BN194_11290	K0MU90	1.41	0.53	1.44

FMN-binding domain protein	General prediction only		BN194_24320	K0NC29	0.47	0.53	1.44
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	*cysK*	BN194_05520	K0N8E6	1.29	0.53	1.44
Uncharacterized protein	Unknown/uncharacterized		BN194_20070	K0NBE0	0.34	0.50	1.41
Uncharacterized protein	Unknown/uncharacterized		BN194_15520	K0NAK2	1.17	0.50	1.41
Uncharacterized protein	Lipid-related metabolism		BN194_11980	K0N7B3	1.04	0.48	1.40
UPF0755 protein yrrL	Unknown/uncharacterized	*yrrL*	BN194_18550	K0N5W7	1.44	0.48	1.39
D-alanine--poly(phosphoribitol) ligase subunit 2 (EC 6.1.1.13) (D-alanyl carrier protein)	Cell wall biogenesis	*dltC*	BN194_08610	K0N361	0.65	0.48	1.39
Uncharacterized ABC transporter ATP-binding protein TM_0288	*ABC-type transporter systems*		BN194_06900	K0N2K4	0.21	0.48	1.39
Transcriptional repressor CcpN	Transcriptional regulation	*ccpN*	BN194_24740	K0MXH2	1.44	0.47	1.39
Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (EC 5.3.3.2) (Isopentenyl diphosphate:dimethylallyl diphosphate isomerase) (Isopentenyl pyrophosphate isomerase) (Type 2 isopentenyl diphosphate isomerase)	Lipid-related metabolism	*fni*	BN194_16840	K0MVP7	1.04	0.46	1.38
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	*pyrC*	BN194_16470	K0NAS6	0.91	0.46	1.38
Uncharacterized protein	Unknown/uncharacterized		BN194_00400	K0N116	1.20	0.46	1.37
50S ribosomal protein L7/L12	Ribosomal proteins	*rplL*	BN194_24080	K0NA98	0.34	0.45	1.37
Uncharacterized protein	Unknown/uncharacterized		BN194_23540	K0MXB4	1.12	0.45	1.37
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB*	BN194_13410	K0N4C0	0.53	0.45	1.36
Zinc metalloprotease (EC 3.4.24.-)	General prediction only	*eep*	BN194_17620	K0NAZ9	1.74	0.44	1.36
Glycine betaine/carnitine/choline-binding protein OpuCC	ABC-type transporter systems	*opuCC*	BN194_00670	K0N6Z3	1.17	0.43	1.35
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	*hprK*	BN194_10330	K0N6Y3	1.18	0.43	1.35
Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	0.44	0.42	1.34
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_3*	BN194_29920	K0NDN0	0.76	0.42	1.34
HTH-type transcriptional repressor glcR	Transcriptional regulation	*glcR*	BN194_02570	K0N7M8	0.96	0.41	1.33
Uncharacterized protein			BN194_02080	K0N4Z7	0.36	0.41	1.33
Recombination protein RecR	DNA repair/recombination	*recR*	BN194_23970	K0NC03	0.33	0.41	1.33
Phosphohydrolase (MutT/nudix family protein)	General prediction only		BN194_27160	K0N7P9	0.40	0.41	1.33
Nucleoid-associated protein BN194_23980	General prediction only		BN194_23980	K0NA95	0.48	0.41	1.33

Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF_2*	BN194_20590	K0MWL1	0.57	0.40	1.32
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	0.42	0.40	1.32
Serine/threonine-protein kinase PrkC (EC 2.7.11.1)	Posttranslational modification	*prkC*	BN194_18020	K0NB40	0.32	0.39	1.31
Phosphate-binding protein pstS 1	ABC-type transporter systems	*pstS1*	BN194_10240	K0MTZ5	0.34	0.39	1.31
Glycerol-3-phosphate ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_11260	K0N3T6	0.82	0.38	1.30
30S ribosomal protein S17	Ribosomal proteins	*rpsQ*	BN194_26130	K0NAL6	0.33	0.38	1.30
Uncharacterized protein YneR	General prediction only	*yneR*	BN194_18480	K0N9C1	0.53	0.36	1.28
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	*murE*	BN194_02160	K0N1S5	0.73	0.34	1.27
Probable tRNA sulfurtransferase (EC 2.8.1.4) (Sulfur carrier protein ThiS sulfurtransferase) (Thiamine biosynthesis protein ThiI) (tRNA 4-thiouridine synthase)	Cofactor-related metabolism	*thiI*	BN194_14480	K0N7Z7	1.87	0.34	1.26
Putative transcriptional regulator, MarR family	Transcriptional regulation		BN194_27490	K0MY64	0.19	0.33	1.26
50S ribosomal protein L29	Ribosomal proteins	*rpmC*	BN194_26140	K0MXT6	0.81	0.33	1.26
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Cobalamin-independent methionine synthase) (Methionine synthase, vitamin-B12 independent isozyme)	Amino acid-related metabolism	*metE*	BN194_06880	K0N658	0.69	0.32	1.25
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	*rpoE*	BN194_26810	K0N7L4	0.51	0.32	1.25
Probable amino-acid ABC transporter-binding protein HI_1080	*ABC-type transporter systems*		BN194_06710	K0N2R6	1.73	0.32	1.24
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	*rnc*	BN194_17870	K0NB31	0.21	0.32	1.24
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_29810	K0N8H4	0.83	0.31	1.24
Uncharacterized protein	Unknown/uncharacterized		BN194_15540	K0MVD8	0.47	0.30	1.23
30S ribosomal protein S20	Ribosomal proteins	*rpsT*	BN194_15250	K0N4X9	0.11	0.29	1.23
Uncharacterized ABC transporter ATP-binding protein YfiB	ABC-type transporter systems	*yfiB*	BN194_06890	K0MT56	0.79	0.29	1.22
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1_2*	BN194_12550	K0N496	0.20	0.29	1.22
Uncharacterized protein yslB	Unknown/uncharacterized	*yslB*	BN194_08630	K0N6L4	0.36	0.29	1.22
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03940	K0MSJ3	0.23	0.28	1.22
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA_2,ackA*	BN194_23060	K0N6W4	0.60	0.28	1.21

Uncharacterized protein yqhL	General prediction only	*yqhL*	BN194_18410	K0N5L5	0.35	0.26	1.19
DNA topoisomerase 4 subunit B (EC 5.99.1.3) (Topoisomerase IV subunit B)	DNA replication-related	*parE*	BN194_16050	K0N545	1.11	0.25	1.19
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA_2*	BN194_18340	K0MW64	0.96	0.24	1.18
Uncharacterized protein			BN194_07360	K0N2W3	1.39	0.22	1.17
Bifunctional protein FolD	Cofactor-related metabolism	*folD*	BN194_18210	K0N5K0	0.07	0.21	1.15
Exodeoxyribonuclease 7 small subunit (EC 3.1.11.6) (Exodeoxyribonuclease VII small subunit)	DNA repair/recombination	*xseB*	BN194_18190	K0MW55	0.23	0.20	1.15
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	*pflB*	BN194_16080	K0N8I5	0.27	0.19	1.14
Thymidine kinase (EC 2.7.1.21)	Nucleic acid/nucleotide metabolism	*tdk*	BN194_13500	K0N4J4	0.11	0.18	1.14
Maf-like protein maf	General prediction only	*maf*	BN194_23700	K0N7K3	0.10	0.18	1.13
Exodeoxyribonuclease (EC 3.1.11.2)	DNA repair/recombination	*exoA*	BN194_11390	K0MUA0	0.18	0.18	1.13
Uncharacterized protein	Transcriptional regulation		BN194_22670	K0NBT5	0.35	0.18	1.13
Uncharacterized protein	Unknown/uncharacterized		BN194_13840	K0MV29	0.33	0.18	1.13
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	*pdhD*	BN194_15110	K0N4P1	0.16	0.17	1.13
ABC-type phosphate/phosphonate transport system,periplasmic component	*ABC-type transporter systems*		BN194_25680	K0NAI1	0.54	0.16	1.12
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA1,gpmA*	BN194_24750	K0N7R7	0.09	0.16	1.11
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	*pyc*	BN194_15170	K0NAI2	0.37	0.16	1.11
Uncharacterized protein yqeY	Unknown/uncharacterized	*yqeY*	BN194_17040	K0MVR2	0.30	0.15	1.11
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshA*	BN194_26700	K0N8C7	0.26	0.15	1.11
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	*clpC*	BN194_21680	K0N9Z7	0.62	0.14	1.10
Nucleoid occlusion protein	Cytokinesis	*noc*	BN194_02030	K0N4Z1	0.23	0.14	1.10
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	0.30	0.14	1.10
Uncharacterized protein	Unknown/uncharacterized		BN194_12110	K0N410	0.06	0.14	1.10
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	*rnjA*	BN194_15020	K0NAH6	0.24	0.13	1.10
Hydrolase of the alpha/beta superfamily	General prediction only		BN194_08240	K0MTK6	0.18	0.13	1.09
Cell growth regulatory protein	*IS elements/foreign DNA defense*		BN194_00940	K0MRU4	0.69	0.13	1.09

Maltose ABC transporter, periplasmic maltose-binding protein	*ABC-type transporter systems*		BN194_11200	K0N3U4	0.18	0.12	1.09
Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	*ADH2*	BN194_08400	K0N307	0.10	0.12	1.09
Uncharacterized protein HI_0912	General prediction only	*thiF3*	BN194_05090	K0MSS8	0.05	0.12	1.08
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	*gpsA*	BN194_10350	K0N3I2	0.24	0.11	1.08
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	*queA*	BN194_08370	K0N965	0.13	0.11	1.08
Uncharacterized protein	Unknown/uncharacterized		BN194_28350	K0N8V3	0.25	0.11	1.08
Mannose permease IID component	Phosphotransferase systems	*manZ_9*	BN194_29700	K0N954	0.18	0.10	1.07
Uncharacterized protein ywnB	General prediction only	*ywnB_2*	BN194_20050	K0N687	0.15	0.10	1.07
Diaminopimelate decarboxylase (DAP decarboxylase) (DAPDC) (EC 4.1.1.20)	Amino acid-related metabolism	*lysA*	BN194_01030	K0N4I7	0.04	0.09	1.07
Protein LemA	Unknown/uncharacterized	*lemA*	BN194_27350	K0N8J7	0.19	0.08	1.06
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	*eno*	BN194_11040	K0MU67	0.13	0.07	1.05
YbbR-like domain-containing protein ybbR	Unknown/uncharacterized	*ybbR*	BN194_11540	K0MUB6	0.05	0.06	1.04
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1*	BN194_09110	K0N399	0.41	0.06	1.04
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	*yqeH*	BN194_18740	K0MW90	0.10	0.05	1.04
Probable flavodoxin-1	General prediction only	*ykuN*	BN194_01860	K0N1P2	0.04	0.04	1.03
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	*proC*	BN194_19900	K0N677	0.07	0.04	1.03
HTH-type transcriptional regulator iolR	Transcriptional regulation	*iolR*	BN194_02190	K0MS58	0.02	0.04	1.03
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	*apt*	BN194_17380	K0N902	0.19	0.03	1.02
Uncharacterized protein	Unknown/uncharacterized		BN194_27210	K0N7Q6	0.03	0.03	1.02
DegV domain-containing protein SP_1112	Unknown/uncharacterized		BN194_15830	K0N8F3	0.06	0.03	1.02
Single-stranded DNA-binding protein (SSB)	DNA replication-related	*ssb*	BN194_00110	K0N1C2	0.04	0.03	1.02
3-keto-L-gulonate-6-phosphate decarboxylase sgbH (EC 4.1.1.85)	Carbohydrate-related metabolism	*sgbH*	BN194_28550	K0N8W6	0.02	0.02	1.01
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	*act*	BN194_16090	K0MVI3	0.01	0.02	1.01
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	*rnr*	BN194_11100	K0N3S4	0.01	0.00	1.00
50S ribosomal protein L23	Ribosomal proteins	*rplW*	BN194_26200	K0N869	0.01	-0.01	1.00

Uncharacterized protein	Unknown/uncharacterized		BN194_27530	K0NAX5	0.01	-0.01	-1.01
Probable transcription repressor NiaR	Transcriptional regulation	*niaR*	BN194_08730	K0N6L8	0.02	-0.01	-1.01
Protein RibT (EC 2.3.1.-)	Cofactor-related metabolism	*ribT*	BN194_15620	K0NAL0	0.01	-0.01	-1.01
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	*ftsY*	BN194_17850	K0N5R8	0.03	-0.01	-1.01
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB1,pstB*	BN194_10270	K0N9K1	0.03	-0.02	-1.02
Uncharacterized protein	Unknown/uncharacterized		BN194_05660	K0N2I2	0.05	-0.03	-1.02
Uncharacterized protein	Unknown/uncharacterized		BN194_29560	K0N8E9	0.02	-0.03	-1.02
Putative gluconeogenesis factor	General prediction only	*yjiF*	BN194_10480	K0N6Z4	0.02	-0.03	-1.02
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	*xpt*	BN194_12490	K0MUR6	0.04	-0.04	-1.03
HTH-type transcriptional regulator yodB	Transcriptional regulation	*yodB*	BN194_18590	K0MW80	0.01	-0.04	-1.03
Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	*plsX*	BN194_17940	K0MW37	0.03	-0.04	-1.03
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE*	BN194_01720	K0N7C1	0.10	-0.05	-1.03
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*pcrA*	BN194_11920	K0N9Z6	0.11	-0.05	-1.03
Glycine cleavage system H protein	Amino acid-related metabolism	*gcvH*	BN194_13700	K0N4K8	0.12	-0.08	-1.05
30S ribosomal protein S5	Ribosomal proteins	*rpsE*	BN194_26050	K0N853	0.24	-0.08	-1.06
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_3*	BN194_21440	K0MWS9	1.11	-0.09	-1.06
Uncharacterized RNA pseudouridine synthase YhcT (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*yhcT_2*	BN194_20220	K0NBE7	0.10	-0.09	-1.06
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	*yjlD*	BN194_24330	K0NAA7	0.21	-0.11	-1.08
Glucose 1-dehydrogenase 2 (EC 1.1.1.47)	Central glycolytic/intermediary pathways	*gdhII*	BN194_23130	K0NA64	0.28	-0.11	-1.08
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	0.67	-0.11	-1.08
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	Nucleic acid/nucleotide metabolism	*tmk*	BN194_23950	K0N7L9	0.39	-0.11	-1.08
Fumarate hydratase class II (Fumarase C) (EC 4.2.1.2)	Tricarboxylic acid pathway	*fumC*	BN194_25340	K0MXL5	0.45	-0.12	-1.09
Chaperone protein ClpB	Protein folding/turnover	*clpB*	BN194_15500	K0N4Z8	0.16	-0.13	-1.10
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	*pfkA*	BN194_15570	K0NAK6	0.30	-0.14	-1.10

Uncharacterized protein yuaG	Unknown/uncharacterized	*yuaG*	BN194_22920	K0NBV0	0.20	-0.14	-1.10
Spermidine/putrescine-binding periplasmic protein	ABC-type transporter systems	*potD*	BN194_11460	K0N3U9	0.30	-0.14	-1.10
Uncharacterized protein YqhY	Unknown/uncharacterized	*yqhY*	BN194_18230	K0N9A7	0.29	-0.14	-1.10
DNA topoisomerase 4 subunit A (EC 5.99.1.-)		*parC*	BN194_16070	K0NAP8	0.27	-0.14	-1.10
ABC-type Na+ efflux pump permease component-like protein	*ABC-type transporter systems*		BN194_11370	K0N9U5	0.32	-0.14	-1.10
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP_2, acpP*	BN194_22590	K0MX45	0.45	-0.14	-1.11
Mannose permease IID component	Phosphotransferase systems	*manZ_4*	BN194_04510	K0N287	0.19	-0.15	-1.11
Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	0.05	-0.16	-1.12
GMP reductase (EC 1.7.1.7) (Guanosine 5'-monophosphate oxidoreductase)	Nucleic acid/nucleotide metabolism	*guaC*	BN194_09960	K0N3H4	1.03	-0.16	-1.12
50S ribosomal protein L18	Ribosomal proteins	*rplR*	BN194_26060	K0N7F4	0.17	-0.16	-1.12
UPF0473 protein BN194_08530	Unknown/uncharacterized		BN194_08530	K0N6K6	0.25	-0.16	-1.12
Sorbitol PTS, EIIA	Phosphotransferase systems		BN194_09940	K0MTX4	0.18	-0.16	-1.12
Large-conductance mechanosensitive channel	Other transporter proteins	*mscL*	BN194_26890	K0MY02	0.14	-0.17	-1.12
Uncharacterized protein yqgF	Cell wall biogenesis	*yqgF*	BN194_18440	K0MW71	0.64	-0.18	-1.13
Cadmium efflux system accessory protein	Other transporter proteins	*cadC*	BN194_21540	K0MWU0	0.25	-0.18	-1.13
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	0.49	-0.19	-1.14
GTPase Era	tRNA/Ribosome assembly/processing	*era*	BN194_16990	K0MVQ8	0.34	-0.19	-1.14
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*fruA_3*	BN194_15410	K0N4S1	0.33	-0.19	-1.14
Uncharacterized protein			BN194_16060	K0N4Y8	0.38	-0.19	-1.14
Uncharacterized protein ylxR	General prediction only	*ylxR*	BN194_17570	K0NAZ6	0.85	-0.20	-1.15
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	*fabF*	BN194_22540	K0MX40	0.41	-0.20	-1.15
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	*ptsH*	BN194_19430	K0N9I2	0.69	-0.21	-1.16
Transcriptional regulator, XRE family	Transcriptional regulation		BN194_30170	K0NDP4	0.38	-0.22	-1.17
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC_2*	BN194_20620	K0NBH0	0.19	-0.23	-1.17
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox*	BN194_01780	K0N4U4	0.50	-0.23	-1.18
Glutathione reductase, chloroplastic (EC 1.8.1.7)	Cofactor-related metabolism	*GOR*	BN194_23200	K0N7H3	0.22	-0.23	-1.18
3-hydroxy-3-methylglutaryl coenzyme A reductase (HMG-CoA reductase) (EC 1.1.1.88)	Lipid-related metabolism	*mvaA*	BN194_19690	K0MWE8	0.55	-0.24	-1.18

Uncharacterized protein ybfG	General prediction only	*ybfG*	BN194_00330	K0N4B3	0.46	-0.24	-1.18
50S ribosomal protein L6	Ribosomal proteins	*rplF*	BN194_26070	K0NCK5	0.55	-0.24	-1.18
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	*prs1_2*	BN194_30370	K0NDQ5	0.37	-0.24	-1.18
UPF0659 protein YMR090W	General prediction only	*ylbE*	BN194_07030	K0N671	1.78	-0.25	-1.19
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)		*accC*	BN194_22510	K0N6M5	0.29	-0.26	-1.20
Transport protein	Other transporter proteins		BN194_00630	K0N4D9	0.37	-0.27	-1.21
UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	0.88	-0.28	-1.21
Putative beta-phosphoglucomutase (EC 5.4.2.6)	Central glycolytic/intermediary pathways	*yvdM*	BN194_11170	K0N9S7	0.30	-0.28	-1.22
Putative HAD-hydrolase yfnB (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yfnB*	BN194_08780	K0N6M1	0.21	-0.29	-1.22
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	*ybeY*	BN194_17010	K0N594	0.29	-0.29	-1.22
ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	*atpF*	BN194_13580	K0N7S9	0.62	-0.30	-1.23
41 kDa protein		*repA*	BN194_P0550	K0NBI6	0.17	-0.30	-1.23
Uncharacterized protein ypmR	General prediction only	*ypmR*	BN194_15840	K0MVG3	0.30	-0.30	-1.23
Ferredoxin--NADP reductase (FNR) (Fd-NADP(+) reductase) (EC 1.18.1.2)	Membrane bioenergetics		BN194_08950	K0N337	0.38	-0.31	-1.24
Uncharacterized protein	General prediction only		BN194_14990	K0MV99	0.16	-0.31	-1.24
Virulence factor mviM	General prediction only	*mviM*	BN194_13310	K0N4B2	0.82	-0.31	-1.24
Holo-[acyl-carrier-protein] synthase (Holo-ACP synthase) (EC 2.7.8.7) (4'-phosphopantetheinyl transferase AcpS)	Cofactor-related metabolism	*acpS*	BN194_26690	K0MXY2	0.29	-0.31	-1.24
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC*	BN194_17890	K0MW34	0.37	-0.32	-1.25
Uncharacterized protein	Unknown/uncharacterized		BN194_08190	K0MTK3	0.08	-0.32	-1.25
Uncharacterized protein	Unknown/uncharacterized		BN194_20190	K0MWI0	0.69	-0.32	-1.25
tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	tRNA/Ribosome assembly/processing	*mnmG,gidA*	BN194_30590	K0MYX4	0.57	-0.32	-1.25
Uncharacterized protein	General prediction only		BN194_21910	K0N6F1	0.51	-0.33	-1.26
tRNA-specific adenosine deaminase (EC 3.5.4.33)	tRNA/Ribosome assembly/processing	*tadA*	BN194_24000	K0N7M1	0.11	-0.33	-1.26
Phosphatase YidA (EC 3.1.3.-)	General prediction only	*yidA*	BN194_28520	K0NDD5	1.08	-0.33	-1.26
Bifunctional protein GlmU	Cell wall biogenesis	*glmU*	BN194_26940	K0MY10	0.81	-0.33	-1.26

RNA polymerase sigma factor SigA	RNA polymerase	*rpoD,sigA*	BN194_16920	K0NAV6	1.69	-0.35	-1.28
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_4*	BN194_22020	K0NBQ1	1.24	-0.36	-1.28
NifU-like protein	Cofactor-related metabolism	*nifU*	BN194_13800	K0N4L4	1.01	-0.36	-1.29
TPR repeats containing protein	Unknown/uncharacterized		BN194_14960	K0N4M8	0.87	-0.37	-1.29
Uncharacterized protein ydcI	General prediction only	*ydcI*	BN194_14310	K0N4I1	0.12	-0.37	-1.29
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA2,gpmA*	BN194_22740	K0MX58	0.87	-0.37	-1.29
Mevalonate kinase (EC 2.7.1.36)	Lipid-related metabolism	*mvk*	BN194_12270	K0NA23	1.40	-0.38	-1.30
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	0.46	-0.38	-1.30
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	*atpG*	BN194_13610	K0N4D3	0.66	-0.38	-1.30
UPF0092 membrane protein yrbF	Protein export	*yrbF*	BN194_08390	K0MTL6	0.32	-0.38	-1.30
Probable cation-transporting ATPase exp7 (EC 3.6.3.-)	Other transporter proteins	*exp7*	BN194_08170	K0N955	0.68	-0.38	-1.30
Cell division ATP-binding protein FtsE	Cytokinesis	*ftsE*	BN194_10190	K0MTZ2	2.04	-0.39	-1.31
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	1.01	-0.40	-1.32
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	*yclJ*	BN194_11790	K0MUE5	0.72	-0.41	-1.32
Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	Nucleic acid/nucleotide metabolism	*purN*	BN194_19310	K0N5S4	0.20	-0.41	-1.33
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_2*	BN194_15390	K0MVD0	2.31	-0.42	-1.34
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	*ykwC*	BN194_02520	K0N7M3	1.34	-0.43	-1.35
tRNA (Adenine(22)-N(1))-methyltransferase (EC 2.1.1.217)	tRNA/Ribosome assembly/processing	*trmK*	BN194_16910	K0N584	1.77	-0.43	-1.35
Uncharacterized protein	Cell wall biogenesis		BN194_21890	K0MWX1	0.59	-0.43	-1.35
Uncharacterized protein ytoI	Transcriptional regulation	*ytoI*	BN194_08440	K0MTM0	1.24	-0.44	-1.35
Uncharacterized protein ybbP	Unknown/uncharacterized	*ybbP*	BN194_11530	K0N776	0.90	-0.44	-1.35
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	*glcK*	BN194_18420	K0NB57	1.49	-0.44	-1.36
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25570	K0NCD4	0.52	-0.44	-1.36
Double-stranded beta-helix related protein	Transcriptional regulation		BN194_11420	K0N9U8	0.17	-0.45	-1.37
FemAB family protein	General prediction only		BN194_22880	K0NA57	0.69	-0.46	-1.37
Uncharacterized protein	Unknown/uncharacterized		BN194_01600	K0N1B9	0.57	-0.47	-1.39

Sorbose permease IIC component	Phosphotransferase systems	*sorA_4*	BN194_29710	K0N8G4	1.18	-0.47	-1.39
ABC-type uncharacterized transport system, ATPase component	*ABC-type transporter systems*		BN194_07730	K0N6C9	0.45	-0.47	-1.39
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ*	BN194_11360	K0N3U2	1.36	-0.48	-1.39
DNA polymerase III subunit delta (EC 2.7.7.7)	DNA replication-related	*holB*	BN194_23930	K0NA93	0.27	-0.49	-1.40
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	*atpD*	BN194_13620	K0NAB3	1.35	-0.49	-1.40
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	1.38	-0.49	-1.40
N5-carboxyaminoimidazole ribonucleotide synthase (N5-CAIR synthase) (EC 6.3.4.18) (5-(carboxyamino)imidazole ribonucleotide synthetase)	Nucleic acid/nucleotide metabolism	*purK_2, purK*	BN194_19370	K0NB96	1.26	-0.49	-1.41
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	*murD*	BN194_14720	K0NAG5	0.82	-0.50	-1.41
Chaperone protein DnaJ	Protein folding/turnover	*dnaJ*	BN194_17450	K0N5J4	1.96	-0.50	-1.42
Putative tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207) (tRNA (cytidine/uridine-2'-O-)-methyltransferase)	*tRNA/Ribosome assembly/processing*		BN194_09990	K0MTX9	0.48	-0.51	-1.42
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD*	BN194_17920	K0NB35	1.79	-0.52	-1.43
Mannose permease IID component	Phosphotransferase systems	*manZ*	BN194_02990	K0MSE1	1.35	-0.52	-1.44
30S ribosomal protein S19	Ribosomal proteins	*rpsS*	BN194_26180	K0NAM1	1.16	-0.52	-1.44
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	*gyrA*	BN194_00070	K0N6S7	0.84	-0.53	-1.44
Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	0.21	-0.53	-1.44
30S ribosomal protein S18	Ribosomal proteins	*rpsR*	BN194_00120	K0N6T2	0.79	-0.53	-1.45
GNAT family acetyltransferase	General prediction only		BN194_29620	K0NDL0	0.24	-0.54	-1.45
Uncharacterized protein	Posttranslational modification	*pp2C*	BN194_18030	K0N993	0.39	-0.54	-1.46
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	*atpH*	BN194_13590	K0MV16	0.85	-0.55	-1.46
DltD protein	Cell wall biogenesis		BN194_08620	K0N978	1.06	-0.55	-1.46
Uncharacterized protein MJ1445	General prediction only		BN194_08880	K0N6M7	1.18	-0.55	-1.46
Phosphonates import ATP-binding protein PhnC (EC 3.6.3.28)	ABC-type transporter systems	*phnC_2,phnC*	BN194_25690	K0MXP5	1.20	-0.55	-1.47

Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	0.79	-0.56	-1.48
Cytidine deaminase (EC 3.5.4.5)	Nucleic acid/nucleotide metabolism	*cdd*	BN194_17000	K0N5D8	0.88	-0.57	-1.48
Uncharacterized glycosyltransferase HI_0868 (EC 2.4.-.-)	Cell wall biogenesis		BN194_02410	K0N1U3	3.83	-0.57	-1.49
Septum formation inhibitor MinC, C-terminal domain family	Cytokinesis	*minC*	BN194_14580	K0N805	0.54	-0.58	-1.50
Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (EC 2.7.7.12) (UDP-glucose--hexose-1-phosphate uridylyltransferase)		*galT*	BN194_07370	K0N8X1	0.93	-0.58	-1.50
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	*ohrR*	BN194_10500	K0N3J7	1.67	-0.59	-1.50
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	*ftsH*	BN194_26460	K0N7I8	1.10	-0.60	-1.51
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	1.06	-0.60	-1.52
tRNA pseudouridine synthase A (EC 5.4.99.12) (tRNA pseudouridine(38-40) synthase) (tRNA pseudouridylate synthase I) (tRNA-uridine isomerase I)	tRNA/Ribosome assembly/processing	*truA*	BN194_25910	K0N7E2	0.68	-0.61	-1.52
Zinc-transporting ATPase (EC 3.6.3.5)	Other transporter proteins	*zosA_2*	BN194_29430	K0NB79	1.12	-0.61	-1.52
Uncharacterized protein	Unknown/uncharacterized		BN194_29850	K0N968	1.49	-0.62	-1.53
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	*msmK*	BN194_11180	K0N747	0.36	-0.62	-1.53
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	*ddl*	BN194_01390	K0MRY4	1.44	-0.62	-1.54
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	*thrS*	BN194_18860	K0N5P5	2.55	-0.62	-1.54
Translation initiation factor IF-2	Protein translation (initiation)	*infB*	BN194_17550	K0N5K7	1.08	-0.63	-1.55
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*manX_5*	BN194_29720	K0NDL4	2.20	-0.63	-1.55
Transcription-repair-coupling factor (TRCF) (EC 3.6.4.-)	DNA repair/recombination	*mfd*	BN194_26540	K0MXW9	0.39	-0.63	-1.55
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	*metG*	BN194_27130	K0NAU5	3.44	-0.64	-1.55
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	*murC*	BN194_18950	K0N600	1.07	-0.64	-1.56
Glycine betaine/carnitine/choline transport ATP-binding protein OpuCA	ABC-type transporter systems	*opuCA*	BN194_00680	K0N4E4	1.47	-0.64	-1.56
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	*atpA*	BN194_13600	K0N4K1	2.22	-0.64	-1.56

Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	Central glycolytic/intermediary pathways	*gap*	BN194_11010	K0N3R3	2.74	-0.64	-1.56
UPF0237 protein BN194_09820	Unknown/uncharacterized		BN194_09820	K0N9F9	0.83	-0.65	-1.57
6-phospho-beta-galactosidase (EC 3.2.1.85) (Beta-D-phosphogalactoside galactohydrolase) (P-beta-Gal)	Carbohydrate-related metabolism	*lacG*	BN194_07320	K0N8W7	1.42	-0.65	-1.57
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	1.75	-0.67	-1.59
Putative nrdI-like protein	*Nucleic acid/nucleotide metabolism*		BN194_08250	K0N300	2.10	-0.67	-1.59
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	*glpK_2,glpK*	BN194_27720	K0ND65	0.57	-0.68	-1.60
Transcription termination/antitermination protein NusG	Transcription-associated proteins	*nusG*	BN194_24260	K0N730	1.21	-0.68	-1.60
Cold shock-like protein CspLA	Transcription-associated proteins	*cspLA*	BN194_12460	K0N438	0.97	-0.68	-1.60
Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-)	Nucleic acid/nucleotide metabolism	*purK*	BN194_12510	K0N441	2.28	-0.68	-1.60
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	*yqjQ*	BN194_15480	K0N8A1	0.58	-0.69	-1.61
Uncharacterized protein MJ0282	Cofactor-related metabolism		BN194_03700	K0N1T2	2.63	-0.69	-1.61
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	*rpoA*	BN194_25960	K0N7E5	2.79	-0.69	-1.61
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	*tpiA*	BN194_11030	K0N736	2.36	-0.69	-1.62
50S ribosomal protein L11	Ribosomal proteins	*rplK*	BN194_24160	K0N724	0.88	-0.70	-1.62
Glycosyl transferase family 2	Cell wall biogenesis		BN194_02460	K0N1U7	1.37	-0.70	-1.62
Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	*rpiA_2, ripA*	BN194_28600	K0N8W9	1.28	-0.70	-1.62
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	1.55	-0.71	-1.63
Integral membrane protein	Unknown/uncharacterized		BN194_07890	K0MTI0	0.41	-0.72	-1.64
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_2*	BN194_20600	K0N6C6	0.89	-0.72	-1.65
DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	1.06	-0.72	-1.65
Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	*upp*	BN194_13550	K0N4J8	1.12	-0.73	-1.66
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_01410	K0N1L0	1.52	-0.74	-1.66
PspC domain-containing protein	Unknown/uncharacterized	*ythC*	BN194_10300	K0N3H5	2.23	-0.74	-1.67
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	*purB*	BN194_12520	K0NA41	2.07	-0.74	-1.67

Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA*	BN194_17880	K0N983	2.86	-0.75	-1.68
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	*yhfP*	BN194_07740	K0MTE1	1.54	-0.75	-1.68
Uncharacterized protein yloA	Cell surface proteins/internalins	*yloA*	BN194_16340	K0MVK5	1.08	-0.76	-1.69
30S ribosomal protein S14	Ribosomal proteins	*rpsN*	BN194_09950	K0N3D1	0.99	-0.76	-1.69
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_02890	K0MSD4	0.70	-0.77	-1.71
Uncharacterized protein	Phosphotransferase systems		BN194_04820	K0N885	0.65	-0.78	-1.72
UPF0478 protein SAOUHSC_01855	Signal transduction		BN194_08710	K0N365	1.99	-0.81	-1.75
50S ribosomal protein L17	Ribosomal proteins	*rplQ*	BN194_25950	K0N841	2.19	-0.81	-1.75
30S ribosomal protein S8	Ribosomal proteins	*rpsH*	BN194_26080	K0NAL1	2.20	-0.82	-1.77
50S ribosomal protein L13	Ribosomal proteins	*rplM*	BN194_25850	K0N828	1.69	-0.82	-1.77
Phosphoribosylformylglycinamidine synthase subunit PurS (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit III) (Phosphoribosylformylglycinamidine synthase subunit III)	Nucleic acid/nucleotide metabolism	*yexA,purS*	BN194_19350	K0N638	1.27	-0.83	-1.77
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF*	BN194_17910	K0N5I3	2.73	-0.83	-1.78
Uncharacterized protein	Unknown/uncharacterized		BN194_01150	K0N181	1.28	-0.84	-1.79
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	*asnB*	BN194_22990	K0MX90	2.74	-0.85	-1.80
30S ribosomal protein S11	Ribosomal proteins	*rpsK*	BN194_25970	K0NCJ0	1.91	-0.85	-1.81
Transcriptional regulator, PadR-like family	Transcriptional regulation		BN194_26580	K0NAQ3	0.55	-0.85	-1.81
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	*deoD*	BN194_02810	K0N1Z0	1.94	-0.86	-1.81
Malolactic enzyme (EC 1.-.-.-)	Tricarboxylic acid pathway	*mleA*	BN194_08070	K0N949	1.68	-0.86	-1.81
GTP pyrophosphokinase yjbM (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*yjbM*	BN194_09870	K0N9G5	0.97	-0.86	-1.81
Dehydrogenase	General prediction only		BN194_24480	K0NAB4	0.76	-0.87	-1.83
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	*fabD*	BN194_22570	K0NBT1	1.78	-0.87	-1.83
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	*pdhC*	BN194_15100	K0N4W5	3.20	-0.87	-1.83
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	*trxB*	BN194_10360	K0N3L1	1.85	-0.88	-1.84
Sensory transduction protein BceR	Signal transduction	*bceR_2*	BN194_19250	K0N630	2.09	-0.88	-1.84

Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	*rbsK*	BN194_03300	K0N1R2	2.71	-0.88	-1.84
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	*tuf*	BN194_15310	K0N4R1	2.52	-0.89	-1.85
Putative integral membrane protein	Unknown/uncharacterized		BN194_01660	K0N1M7	0.67	-0.89	-1.86
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		BN194_13770	K0NAC0	2.29	-0.89	-1.86
GNAT family acetyltransferase	General prediction only		BN194_01510	K0N1L8	1.94	-0.89	-1.86
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	*uvrA*	BN194_10450	K0N3J2	2.53	-0.90	-1.86
Uncharacterized protein	*ABC-type transporter systems*		BN194_21220	K0NBK2	3.04	-0.90	-1.87
MarR family transcriptional regulator	Transcriptional regulation		BN194_22610	K0N6N9	0.81	-0.90	-1.87
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	*fbp*	BN194_21660	K0N6C3	1.03	-0.90	-1.87
Nod factor export ATP-binding protein I (EC 3.6.3.-)	ABC-type transporter systems	*nodI*	BN194_06850	K0N2J7	1.21	-0.90	-1.87
Putative 2-hydroxyacid dehydrogenase SH0752 (EC 1.1.1.-)	General prediction only		BN194_01890	K0MS33	1.55	-0.92	-1.89
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	*pth*	BN194_26550	K0N8B3	1.37	-0.92	-1.89
Uncharacterized N-acetyltransferase ycf52-like (EC 2.3.1.-)	General prediction only	*speE1*	BN194_21490	K0MWT4	1.06	-0.93	-1.91
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	1.30	-0.93	-1.91
30S ribosomal protein S10	Ribosomal proteins	*rpsJ*	BN194_26230	K0NAM5	1.27	-0.94	-1.91
Uncharacterized protein yueI	Unknown/uncharacterized	*yueI*	BN194_13920	K0NAC7	2.27	-0.94	-1.92
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	*rex_2,rex*	BN194_23820	K0NBZ5	1.30	-0.94	-1.92
Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		BN194_08520	K0N972	1.78	-0.94	-1.92
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	*citX*	BN194_20300	K0N6A3	1.53	-0.95	-1.93
ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	*clpX*	BN194_15340	K0MVC6	3.05	-0.95	-1.93
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	*prs1,prs*	BN194_26930	K0NAT2	2.49	-0.95	-1.93
Oligo-1,6-glucosidase (EC 3.2.1.10)	Carbohydrate-related metabolism	*malL*	BN194_04830	K0N5P4	1.72	-0.96	-1.95
Ribosomal protein L11 methyltransferase (L11 Mtase) (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*prmA*	BN194_17260	K0N5B0	1.23	-0.98	-1.98

Phosphoenolpyruvate-dependent sugar phosphotransferase system EIIA, galactitol/fructose specific	Phosphotransferase systems		BN194_27050	K0N8F9	4.31	-0.99	-1.99
Uncharacterized protein	Unknown/uncharacterized	*FNV1452*	BN194_18830	K0N9E3	1.05	-0.99	-1.99
Calcium-transporting ATPase lmo0841 (EC 3.6.3.8)	Other transporter proteins		BN194_19820	K0NBC5	2.52	-0.99	-1.99
Protein translocase subunit SecA	Protein export	*secA*	BN194_10170	K0N9J2	2.37	-0.99	-1.99
Nucleotide-binding protein BN194_10470	General prediction only		BN194_10470	K0N9L7	2.08	-1.00	-1.99
Regulatory protein vanR	Signal transduction	*vanR*	BN194_02120	K0N7G4	2.72	-1.01	-2.02
Uncharacterized protein RP368	*ABC-type transporter systems*		BN194_07720	K0N914	0.99	-1.04	-2.05
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	*glgD*	BN194_21590	K0MWU4	1.25	-1.04	-2.05
Lactose phosphotransferase system repressor	Transcriptional regulation	*lacR*	BN194_07510	K0N2X5	0.61	-1.04	-2.05
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	*frr*	BN194_17650	K0N5M3	4.25	-1.04	-2.06
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		BN194_03130	K0N5D9	1.40	-1.05	-2.06
Uncharacterized protein ytxK	DNA repair/recombination	*ytxK*	BN194_11680	K0N791	1.15	-1.05	-2.06
Cold shock protein 1	Transcription-associated proteins	*csp*	BN194_06990	K0MT67	0.53	-1.05	-2.07
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	*gmk*	BN194_18110	K0N5J6	3.13	-1.05	-2.07
Elongation factor G (EF-G)	Protein translation (elongation)	*fusA*	BN194_26270	K0NCN8	2.52	-1.05	-2.07
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	*yqeL,rsfS*	BN194_18710	K0N5N6	2.28	-1.05	-2.08
Phosphatase YbjI (EC 3.1.3.-)	General prediction only	*ybjI*	BN194_30020	K0NDN5	0.65	-1.06	-2.08
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	*luxS*	BN194_08330	K0N6J0	2.35	-1.06	-2.08
30S ribosomal protein S9	Ribosomal proteins	*rpsI*	BN194_25840	K0MXR0	1.98	-1.06	-2.08
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	*tig*	BN194_15330	K0N884	3.07	-1.06	-2.08
Transcriptional regulator, xre family	Transcriptional regulation		BN194_05600	K0N260	1.71	-1.06	-2.09
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	*ppaC*	BN194_16110	K0N4Z4	2.82	-1.07	-2.10
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	1.88	-1.07	-2.10
tRNA pseudouridine synthase B (EC 5.4.99.25) (tRNA pseudouridine(55) synthase) (tRNA pseudouridylate synthase) (tRNA-uridine isomerase)	tRNA/Ribosome assembly/processing	*truB*	BN194_17520	K0NAZ5	1.64	-1.07	-2.10

Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	*adk*	BN194_26010	K0N7F0	2.23	-1.08	-2.11
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE*	BN194_02970	K0N7U7	2.40	-1.08	-2.11
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	1.30	-1.08	-2.12
Uncharacterized protein	Unknown/uncharacterized		BN194_07460	K0N2W9	3.27	-1.08	-2.12
Protein hit	tRNA aminoacyl synthesis	*hit*	BN194_19040	K0MWA8	1.72	-1.08	-2.12
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	4.24	-1.08	-2.12
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_3*	BN194_04780	K0N5N9	1.69	-1.09	-2.13
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	*ssdA*	BN194_24140	K0MXE0	2.89	-1.10	-2.15
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		BN194_18780	K0N9E0	1.17	-1.10	-2.15
Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	1.79	-1.10	-2.15
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	*clpE*	BN194_19450	K0N644	1.48	-1.13	-2.18
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification		BN194_25280	K0NAG2	0.67	-1.13	-2.18
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	4.20	-1.13	-2.18
Uncharacterized protein SE_0534	*tRNA/Ribosome assembly/processing*		BN194_10150	K0N3F2	2.46	-1.13	-2.19
Uncharacterized peptidase yqhT (EC 3.4.-.-)	Amino acid-related metabolism	*yqhT*	BN194_18260	K0N5K4	1.91	-1.14	-2.21
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	*pepV*	BN194_08800	K0N324	2.76	-1.15	-2.21
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	*hisS*	BN194_17110	K0N5A0	2.33	-1.15	-2.21
Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	*gntK*	BN194_02340	K0MS76	1.47	-1.15	-2.22
5-bromo-4-chloroindolyl phosphate hydrolysis protein	General prediction only		BN194_14860	K0N4M3	3.00	-1.16	-2.23
MFS permease-like protein	Other transporter proteins		BN194_06910	K0N2S6	1.26	-1.16	-2.23
Putative ADP-ribose pyrophosphatase yjhB (EC 3.6.1.-)	General prediction only	*yjhB*	BN194_25530	K0NAH4	1.29	-1.16	-2.23
Putative thiamine pyrophosphate-containing protein ydaP	Carbohydrate-related metabolism	*ydaP*	BN194_05070	K0N8B1	2.28	-1.16	-2.24
Uncharacterized protein	Unknown/uncharacterized		BN194_21170	K0NBJ9	3.18	-1.16	-2.24
Cof protein	General prediction only		BN194_12010	K0N401	0.65	-1.16	-2.24
Uncharacterized protein yghZ	General prediction only	*yghZ*	BN194_27510	K0N7U8	2.23	-1.17	-2.25
Bifunctional purine biosynthesis protein PurH	Nucleic acid/nucleotide metabolism	*purH*	BN194_19300	K0N634	1.42	-1.17	-2.25

Chaperone protein ClpB	Protein folding/turnover	*clpB_2*	BN194_26350	K0N887	2.25	-1.18	-2.27
Uncharacterized protein	Unknown/uncharacterized		BN194_13400	K0N4I9	1.49	-1.20	-2.29
Signal recognition particle protein (Fifty-four homolog)	Protein export	*ffh*	BN194_17820	K0NB27	1.42	-1.20	-2.29
Stage 0 sporulation protein J	Cytokinesis	*spo0J*	BN194_02050	K0N1F9	2.33	-1.20	-2.30
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	*rpoZ*	BN194_18100	K0N5T7	1.74	-1.20	-2.30
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdF*	BN194_16610	K0N552	2.21	-1.21	-2.31
Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)	Nucleic acid/nucleotide metabolism	*pdp*	BN194_23430	K0NA73	2.59	-1.21	-2.31
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	*dhaM*	BN194_04960	K0N2C2	1.17	-1.21	-2.31
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA_2, potA*	BN194_11430	K0N765	3.08	-1.22	-2.32
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	*tpx*	BN194_08090	K0MTJ5	1.78	-1.22	-2.33
Uncharacterized protein yhfI	General prediction only	*yhfI*	BN194_19200	K0N627	3.34	-1.22	-2.33
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	*pyrH*	BN194_17660	K0N5E6	2.54	-1.22	-2.34
Uncharacterized protein in fgs 3'region	General prediction only		BN194_14530	K0N802	0.67	-1.23	-2.35
Glycosyltransferase	Cell wall biogenesis		BN194_09050	K0N346	0.62	-1.23	-2.35
Uncharacterized protein	General prediction only		BN194_17420	K0NAY8	2.27	-1.23	-2.35
N5-carboxyaminoimidazole ribonucleotide mutase (N5-CAIR mutase) (EC 5.4.99.18) (5-(carboxyamino)imidazole ribonucleotide mutase)	Nucleic acid/nucleotide metabolism	*purE*	BN194_19380	K0N9H9	3.72	-1.24	-2.36
Adapter protein MecA	Competence (DNA uptake)	*mecA*	BN194_19170	K0NB89	0.43	-1.24	-2.36
Uncharacterized protein	*Nucleic acid/nucleotide metabolism*		BN194_27260	K0N7R1	1.48	-1.25	-2.37
Putative ribosome biogenesis GTPase RsgA (EC 3.6.1.-)	tRNA/Ribosome assembly/processing	*rsgA*	BN194_18010	K0N5J0	0.86	-1.25	-2.38
18 kDa heat shock protein	Protein folding/turnover	*hsp18*	BN194_07570	K0N8Z3	0.60	-1.25	-2.38
30S ribosomal protein S2	Ribosomal proteins	*rpsB*	BN194_17680	K0N936	3.25	-1.25	-2.38
Uncharacterized protein	*Cell surface proteins/internalins*		BN194_20060	K0N5Y7	2.87	-1.25	-2.39
Uncharacterized protein	Unknown/uncharacterized		BN194_19050	K0N613	1.73	-1.25	-2.39
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	*typA*	BN194_15150	K0N4W9	2.85	-1.26	-2.39

Predicted pyrophosphatase	General prediction only		BN194_15360	K0N4R6	1.66	-1.26	-2.40
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	*groL,groEL*	BN194_23750	K0N7K7	3.11	-1.26	-2.40
Ribosome-binding ATPase YchF	Protein translation (peptide release)	*engD,ychF*	BN194_02070	K0N7F7	4.05	-1.27	-2.41
Elongation factor P	Protein translation (elongation)	*efp_2*	BN194_22050	K0N712	0.97	-1.27	-2.41
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	*nusB*	BN194_18220	K0NB49	3.08	-1.27	-2.42
Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	*pyk*	BN194_15580	K0N8B6	5.58	-1.28	-2.43
Cell division protein FtsA	Cytokinesis	*ftsA*	BN194_14750	K0N4T3	4.41	-1.28	-2.43
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*helD*	BN194_21130	K0N9W3	3.03	-1.28	-2.43
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	*ycnE*	BN194_13230	K0N7R3	1.79	-1.28	-2.43
50S ribosomal protein L14	Ribosomal proteins	*rplN*	BN194_26120	K0NCL3	2.13	-1.28	-2.44
50S ribosomal protein L31 type B	Ribosomal proteins	*rpmE2*	BN194_26770	K0NCV4	4.24	-1.29	-2.44
MreB-like protein	Cytokinesis	*mbl*	BN194_13650	K0N4K5	2.34	-1.29	-2.45
Uncharacterized protein	Unknown/uncharacterized		BN194_02470	K0N7L7	1.91	-1.29	-2.45
Uncharacterized protein	Unknown/uncharacterized		BN194_19810	K0N5W5	2.52	-1.29	-2.45
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrD*	BN194_16440	K0MVL3	2.26	-1.29	-2.45
GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*relA*	BN194_17230	K0N8Y0	2.60	-1.29	-2.45
LPXTG-motif cell wall anchor domain protein			BN194_26300	K0N883	1.90	-1.29	-2.45
Nuclease sbcCD subunit D	DNA repair/recombination	*sbcD*	BN194_07530	K0N6B1	0.71	-1.30	-2.46
SMC domain protein	DNA repair/recombination		BN194_07540	K0MTC3	0.57	-1.30	-2.46
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		BN194_11600	K0N3Z3	2.65	-1.32	-2.49
Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*nrdD*	BN194_01250	K0N190	0.64	-1.32	-2.50
DegV domain-containing protein CPE0026	Unknown/uncharacterized		BN194_12060	K0N405	2.38	-1.34	-2.53
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	*dltA*	BN194_08590	K0MTN0	2.23	-1.34	-2.53
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	*tsf*	BN194_17670	K0NB01	5.41	-1.34	-2.54
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	*glgC*	BN194_21600	K0N6T3	1.08	-1.34	-2.54
Septum site-determining protein DivIVA	Cytokinesis	*divIVA*	BN194_14800	K0N4T8	1.92	-1.37	-2.58

50S ribosomal protein L4	Ribosomal proteins	*rplD*	BN194_26210	K0N7H0	2.20	-1.37	-2.58
DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	*gyrB*	BN194_00060	K0N1B8	3.25	-1.37	-2.58
50S ribosomal protein L5	Ribosomal proteins	*rplE*	BN194_26100	K0N859	2.41	-1.37	-2.59
30S ribosomal protein S13	Ribosomal proteins	*rpsM*	BN194_25980	K0NAK3	1.32	-1.38	-2.61
Alpha-galactosidase 2 (EC 3.2.1.22)	Carbohydrate-related metabolism	*agaS_2*	BN194_22160	K0N6I2	1.57	-1.39	-2.61
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	*prfA*	BN194_13510	K0N4C6	2.43	-1.39	-2.61
Putative competence-damage inducible protein	General prediction only	*cinA*	BN194_10070	K0N9I3	1.25	-1.39	-2.62
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD(+)])	DNA replication-related	*ligA*	BN194_11930	K0N7A9	2.29	-1.42	-2.68
Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.193)	tRNA/Ribosome assembly/processing	*rsmE*	BN194_17250	K0N5G8	1.71	-1.42	-2.68
50S ribosomal protein L3	Ribosomal proteins	*rplC*	BN194_26220	K0NCN1	2.04	-1.43	-2.69
Transcriptional regulator, TetR family	Transcriptional regulation		BN194_12190	K0MUM1	4.63	-1.43	-2.70
Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Phosphotransferase system, enzyme I)		*ptsI*	BN194_19410	K0N5T2	2.95	-1.43	-2.70
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*argS*	BN194_19120	K0NB86	2.31	-1.44	-2.71
Cell division protein FtsZ	Cytokinesis	*ftsZ*	BN194_14760	K0N4L6	3.54	-1.44	-2.71
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	*ywpJ*	BN194_11320	K0N9U2	3.14	-1.46	-2.76
Protein lacX, plasmid	Carbohydrate-related metabolism	*lacX*	BN194_27070	K0NCY0	4.63	-1.46	-2.76
UbiE/COQ5 family methyltransferase	General prediction only		BN194_23620	K0NBY4	1.32	-1.47	-2.78
Uncharacterized protein	General prediction only		BN194_13850	K0N4L8	0.80	-1.48	-2.78
Ribosome maturation factor RimM	tRNA/Ribosome assembly/processing	*rimM*	BN194_17790	K0MVZ6	2.34	-1.48	-2.79
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	*murA2,murA*	BN194_26780	K0NAR9	2.33	-1.49	-2.81
Xanthine/uracil/vitamin C permease	Other transporter proteins		BN194_01470	K0N796	1.13	-1.51	-2.84
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	*groS,grES*	BN194_23760	K0N700	2.20	-1.51	-2.84
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhA*	BN194_15080	K0N860	2.23	-1.51	-2.84
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	*dhaK_2*	BN194_04980	K0N5Q3	4.56	-1.51	-2.85

Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC_2,deoC*	BN194_02790	K0MSB5	2.35	-1.51	-2.86
Putative transcriptional regulator (DtxR family)	Transcriptional regulation		BN194_08410	K0N354	0.83	-1.52	-2.86
Transcriptional regulatory protein YycF	Signal transduction	*yycF_2*	BN194_29510	K0N8E4	1.85	-1.52	-2.86
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*yfmL*	BN194_12120	K0NA13	2.99	-1.54	-2.91
Predicted hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	2.20	-1.55	-2.92
Uncharacterized isochorismatase family protein pncA (EC 3.-.-.-)	General prediction only	*pncA*	BN194_29120	K0NDH8	0.97	-1.55	-2.92
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE_2*	BN194_19740	K0MWF1	2.42	-1.55	-2.93
Uncharacterized protein	Cofactor-related metabolism		BN194_18720	K0NB69	1.33	-1.55	-2.93
Guanylate kinase (EC 2.7.4.8)	Nucleic acid/nucleotide metabolism	*gmk_2*	BN194_21480	K0N9Y7	2.38	-1.55	-2.93
Uncharacterized protein ykuJ	Unknown/uncharacterized	*ykuJ*	BN194_09100	K0N348	0.90	-1.55	-2.93
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	*citD*	BN194_20330	K0N9Q5	3.24	-1.55	-2.94
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB2,pstB*	BN194_10280	K0N6X8	3.24	-1.56	-2.96
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	*fabH*	BN194_22600	K0N7B0	2.79	-1.57	-2.96
Probable glutamine ABC transporter permease protein glnP	ABC-type transporter systems	*glnP*	BN194_21410	K0N6A4	1.31	-1.58	-2.98
Uncharacterized ABC transporter ATP-binding protein YdiF	General prediction only	*ydiF*	BN194_23830	K0NA88	1.21	-1.58	-2.98
DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	DNA replication-related	*dnaX*	BN194_23990	K0MXD3	3.01	-1.58	-2.99
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	*guaB*	BN194_02100	K0N1G3	4.47	-1.60	-3.03
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	*rpoC*	BN194_26330	K0NAN3	2.71	-1.61	-3.05
DNA translocase SftA	Cytokinesis	*sftA*	BN194_18960	K0N5Q1	4.53	-1.61	-3.05
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2_2,lacD*	BN194_27060	K0N7P0	4.52	-1.62	-3.06
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2,lacD*	BN194_07480	K0N6A8	2.83	-1.62	-3.07

Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	*purA*	BN194_01160	K0N1J0	4.95	-1.62	-3.08
50S ribosomal protein L2	Ribosomal proteins	*rplB*	BN194_26190	K0MXU1	3.56	-1.62	-3.08
Predicted acetyltransferase			BN194_11820	K0N9Y9	1.65	-1.63	-3.09
50S ribosomal protein L20	Ribosomal proteins	*rplT*	BN194_18800	K0N5Y4	2.09	-1.63	-3.11
Deoxyguanosine kinase (EC 2.7.1.113)	*Nucleic acid/nucleotide metabolism*		BN194_14000	K0N4M7	1.90	-1.63	-3.11
Transcription termination/antitermination protein NusA	Transcription-associated proteins	*nusA*	BN194_17580	K0N927	3.44	-1.64	-3.11
Uncharacterized protein	Unknown/uncharacterized		BN194_25820	K0NCG9	2.10	-1.64	-3.13
D-lactate dehydrogenase (EC 1.1.1.28)	Carbohydrate-related metabolism	*dld*	BN194_06590	K0MT28	2.42	-1.65	-3.14
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	*guaA*	BN194_21070	K0NBJ2	3.03	-1.65	-3.15
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	*mtlF*	BN194_30410	K0N8N0	2.29	-1.65	-3.15
GCN5-related N-acetyltransferase	General prediction only		BN194_19760	K0N5W1	2.03	-1.66	-3.15
50S ribosomal protein L1	Ribosomal proteins	*rplA*	BN194_24150	K0N7M7	5.44	-1.66	-3.15
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	*hslV*	BN194_16000	K0N542	0.91	-1.67	-3.17
Uncharacterized protein	Unknown/uncharacterized		BN194_24010	K0N715	2.62	-1.67	-3.19
Alkyl hydroperoxide reductase subunit C (EC 1.11.1.15)	Cell defense/detoxification	*ahpC*	BN194_26250	K0N876	1.99	-1.68	-3.20
PTS family mannose/fructose/sorbose porter component IIC	Phosphotransferase systems		BN194_02980	K0N5D0	1.56	-1.69	-3.22
Uncharacterized protein	Signal transduction		BN194_18490	K0MW74	2.20	-1.69	-3.23
Phosphoesterase (EC 3.1.4.-)	General prediction only	*ysnB*	BN194_08650	K0N317	4.13	-1.69	-3.23
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_2*	BN194_03120	K0N7V6	5.03	-1.70	-3.24
Uncharacterized zinc protease ymfH (EC 3.4.24.-)	Amino acid-related metabolism	*ymfH*	BN194_10030	K0N6V9	1.76	-1.70	-3.25
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	*rpoB*	BN194_26340	K0MXV4	3.08	-1.70	-3.26
tRNA N6-adenosine threonylcarbamoyltransferase (EC 2.3.1.234) (N6-L-threonylcarbamoyladenine synthase) (t(6)A37 threonylcarbamoyladenosine biosynthesis protein TsaD) (tRNA threonylcarbamoyladenosine biosynthesis protein TsaD)	General prediction only	*tsaD,gcp*	BN194_23850	K0N7L3	2.02	-1.71	-3.26
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	*patB_2*	BN194_09790	K0MTW3	2.19	-1.71	-3.27

tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	*dus1*	BN194_26390	K0MXV9	2.65	-1.71	-3.27
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	*yuxL*	BN194_19910	K0N5X4	3.73	-1.71	-3.28
Glutathione peroxidase	Cell defense/detoxification	*gpo*	BN194_09780	K0N6T6	2.37	-1.71	-3.28
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA*	BN194_05120	K0N8B5	1.12	-1.72	-3.30
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	*alaS*	BN194_08480	K0N6K2	3.43	-1.72	-3.30
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	*fabK*	BN194_22580	K0NA38	2.63	-1.72	-3.30
Thioredoxin	Posttranslational modification	*trxA_2*	BN194_08570	K0N975	2.96	-1.72	-3.31
30S ribosomal protein S7	Ribosomal proteins	*rpsG*	BN194_26280	K0NAM9	3.79	-1.73	-3.31
5'-nucleotidase (EC 3.1.3.5)	General prediction only		BN194_08220	K0N957	2.36	-1.73	-3.31
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E,P100*	BN194_02180	K0N513	6.22	-1.73	-3.31
Uncharacterized protein MJ1651	General prediction only		BN194_04410	K0N281	3.11	-1.74	-3.33
Acylphosphatase	Carbohydrate-related metabolism	*acyP*	BN194_18620	K0NB65	4.13	-1.75	-3.36
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB_2*	BN194_21970	K0NBP6	1.69	-1.76	-3.39
Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	*ptp3*	BN194_23520	K0NBX6	2.68	-1.76	-3.39
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*asnS*	BN194_16760	K0N569	3.08	-1.77	-3.40
Protein ytsP	Signal transduction	*ytsP*	BN194_14450	K0N4Q9	1.50	-1.77	-3.40
Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	ABC-type transporter systems	*ecfA2, ecfA*	BN194_25920	K0NCI4	3.01	-1.77	-3.41
Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	Carbohydrate-related metabolism	*scrB*	BN194_22440	K0MX27	1.27	-1.77	-3.41
Probable L-serine dehydratase, beta chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAB*	BN194_13940	K0MV34	2.62	-1.77	-3.41
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (ACCase subunit beta) (Acetyl-CoA carboxylase carboxyltransferase subunit beta) (EC 6.4.1.2)	Lipid-related metabolism	*accD*	BN194_22480	K0NA32	1.27	-1.77	-3.41
30S ribosomal protein S4	Ribosomal proteins	*rpsD*	BN194_14440	K0MV63	2.70	-1.77	-3.42
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	*pyrG*	BN194_26790	K0MXZ1	2.87	-1.78	-3.42
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		BN194_08960	K0N387	2.61	-1.78	-3.43
Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase)	Nucleic acid/nucleotide metabolism	*pyrB*	BN194_16480	K0N8N2	2.65	-1.79	-3.47

Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	*ilvE*	BN194_21620	K0NBM4	3.48	-1.80	-3.47
Tyrosine--tRNA ligase (EC 6.1.1.1)		*tyrS*	BN194_21510	K0N6A9	2.95	-1.80	-3.48
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	*pmi*	BN194_02920	K0N7U2	4.10	-1.80	-3.49
Replicative DNA helicase (EC 3.6.4.12)	DNA replication-related	*dnaC*	BN194_01140	K0MRW2	1.00	-1.80	-3.49
30S ribosomal protein S6	Ribosomal proteins	*rpsF*	BN194_00100	K0N0Z1	2.20	-1.81	-3.50
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	*prfB*	BN194_10180	K0N6W9	3.35	-1.81	-3.51
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB_2*	BN194_29110	K0N8A4	2.51	-1.83	-3.56
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	*mhqD*	BN194_18770	K0NB71	1.77	-1.83	-3.56
Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	4.21	-1.83	-3.56
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI*	BN194_07860	K0N327	1.75	-1.84	-3.58
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yutF*	BN194_08910	K0N383	2.54	-1.84	-3.59
Uncharacterized protein ysxB	Ribosomal proteins	*ysxB*	BN194_18280	K0N9A9	2.35	-1.85	-3.60
Septation ring formation regulator EzrA	Cytokinesis	*ezrA*	BN194_14460	K0N4J2	2.76	-1.85	-3.60
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh*	BN194_26560	K0N7J5	4.31	-1.85	-3.61
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)	Nucleic acid/nucleotide metabolism	*ntd*	BN194_24240	K0MXE6	2.38	-1.85	-3.61
Rod shape-determining protein MreB	Cytokinesis	*mreB*	BN194_14550	K0N4R7	3.11	-1.86	-3.63
Methionyl-tRNA formyltransferase (EC 2.1.2.9)	Protein translation (initiation)	*fmt*	BN194_18060	K0N5J2	4.47	-1.87	-3.64
Transcriptional repressor NrdR	Transcriptional regulation	*nrdR*	BN194_18900	K0N5Z5	2.54	-1.87	-3.65
Putative tRNA-binding protein ytpR	General prediction only	*ytpR*	BN194_18970	K0NB80	3.28	-1.87	-3.66
Uncharacterized protein	Unknown/uncharacterized		BN194_20720	K0NBH5	3.10	-1.87	-3.66
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhB*	BN194_15090	K0MVA7	2.93	-1.88	-3.68
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacB*	BN194_07490	K0MTB7	2.20	-1.88	-3.69
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	*mtnN*	BN194_14890	K0MV90	3.91	-1.89	-3.70
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	*map*	BN194_12230	K0N7E0	5.00	-1.89	-3.70
Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	*Steap4*	BN194_01990	K0MS41	3.07	-1.90	-3.73

Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA*	BN194_08450	K0N309	3.15	-1.90	-3.74
tRNA modification GTPase MnmE (EC 3.6.-.-)	tRNA/Ribosome assembly/processing	*mnmE,trmE*	BN194_30600	K0N9F0	2.93	-1.91	-3.75
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	*pepQ*	BN194_08740	K0MTP0	2.84	-1.91	-3.76
Thioredoxin-like protein ytpP	Posttranslational modification	*ytpP*	BN194_18980	K0N9F1	3.20	-1.91	-3.76
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	*glmM*	BN194_11550	K0N3Y7	5.07	-1.91	-3.77
NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	5.37	-1.92	-3.78
Uncharacterized metallophosphoesterase yunD	Nucleic acid/nucleotide metabolism	*yunD*	BN194_08890	K0MTQ0	2.79	-1.93	-3.80
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	*pgk*	BN194_11020	K0N9R1	4.59	-1.94	-3.83
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	*garB*	BN194_27400	K0N8K3	3.42	-1.94	-3.83
Response regulator ArlR	Signal transduction	*arlR*	BN194_18650	K0N5X3	2.23	-1.94	-3.84
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	*zwf*	BN194_08420	K0N966	3.61	-1.94	-3.85
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	*galK*	BN194_07340	K0MTA3	2.90	-1.95	-3.86
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	*pepN*	BN194_05410	K0N2F5	2.99	-1.95	-3.87
30S ribosomal protein S3	Ribosomal proteins	*rpsC*	BN194_26160	K0N7G5	2.89	-1.96	-3.88
Protein QmcA	Unknown/uncharacterized	*qmcA*	BN194_12070	K0NA10	4.13	-1.96	-3.89
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	*npr*	BN194_04740	K0MSP8	2.54	-1.96	-3.90
Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	*phoP*	BN194_10220	K0N9J6	2.59	-1.96	-3.90
Uncharacterized protein IRC4	Unknown/uncharacterized	*IRC4*	BN194_30110	K0N8K0	3.78	-1.97	-3.91
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	*maa*	BN194_30010	K0N8I9	2.68	-1.97	-3.93
Transcriptional regulator, xre family	Transcriptional regulation		BN194_13860	K0N4E8	1.99	-1.98	-3.95
Lipopolysaccharide synthesis sugar transferase	Cell wall biogenesis		BN194_21390	K0MWS4	3.08	-1.98	-3.96
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	*accA*	BN194_22470	K0NBS6	3.39	-2.00	-4.00
Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	*rp2*	BN194_17060	K0N598	2.35	-2.00	-4.01
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP_3*	BN194_21160	K0N682	3.92	-2.01	-4.03
DNA replication protein dnaD	DNA replication-related	*dnaD*	BN194_16750	K0N5B1	1.46	-2.02	-4.06
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	*murI*	BN194_08640	K0MTN4	3.67	-2.02	-4.06

Oligoendopeptidase F homolog (EC 3.4.24.-)	Amino acid-related metabolism	*yjbG*	BN194_02530	K0N560	3.33	-2.03	-4.08
Probable dipeptidase A (EC 3.4.-.-)	Amino acid-related metabolism	*pepDA*	BN194_00410	K0N1E0	4.84	-2.04	-4.10
Transcriptional regulator, xre family	Transcriptional regulation		BN194_23510	K0N6Y7	4.14	-2.04	-4.11
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*gmuB*	BN194_23840	K0MXC7	1.64	-2.04	-4.11
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	*aldB*	BN194_20140	K0MWH5	4.79	-2.04	-4.12
Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase)	Cofactor-related metabolism	*coaA*	BN194_21080	K0N9V9	2.25	-2.05	-4.13
Uncharacterized protein YxeH	General prediction only	*yxeH*	BN194_04750	K0N1Y7	2.54	-2.05	-4.14
TPR repeat-containing protein ypiA	Unknown/uncharacterized	*ypiA*	BN194_15750	K0N517	5.35	-2.06	-4.16
Uncharacterized protein				K0N2Q1;K0MXJ1	4.44	-2.06	-4.17
Uncharacterized protein	General prediction only		BN194_28370	K0NDC5	1.27	-2.08	-4.22
Oligoendopeptidase F	Amino acid-related metabolism	*yjbG_2*	BN194_08130	K0N6H7	2.68	-2.08	-4.24
Threonylcarbamoyl-AMP synthase (TC-AMP synthase) (EC 2.7.7.87) (L-threonylcarbamoyladenylate synthase)	tRNA/Ribosome assembly/processing	*ywlC*	BN194_13530	K0N7S6	2.06	-2.10	-4.28
Uncharacterized protein yjdJ	General prediction only	*yjdJ*	BN194_24650	K0N7R2	1.54	-2.10	-4.28
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	*iscS1*	BN194_14900	K0N4U8	2.61	-2.10	-4.29
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA*	BN194_09090	K0MTR3	4.01	-2.10	-4.29
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	*hslU*	BN194_16010	K0N4Y1	2.31	-2.10	-4.30
L-sorbose 1-phosphate reductase (EC 1.1.1.-)	Carbohydrate-related metabolism	*sorE*	BN194_04300	K0N1W2	0.68	-2.10	-4.30
Probable flavodoxin-1	Membrane bioenergetics	*ykuN_2*	BN194_12220	K0NA19	2.35	-2.11	-4.30
Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Phosphoglucose isomerase) (Phosphohexose isomerase)	Central glycolytic/intermediary pathways	*pgi*	BN194_12580	K0N7I6	3.02	-2.11	-4.32
Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-)		*rsmB*	BN194_18040	K0MW45	2.56	-2.12	-4.35
Alanine racemase (EC 5.1.1.1)	Amino acid-related metabolism	*alr*	BN194_26680	K0NAR1	3.22	-2.12	-4.35
Site-determining protein	Cytokinesis	*minD*	BN194_14590	K0MV70	2.09	-2.13	-4.38
Glucose-1-phosphate thymidylyltransferase		*rmlA*		K0N699;K0MWW4	4.35	-2.13	-4.39
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*ileS*	BN194_14810	K0N4L9	4.62	-2.14	-4.40
Uncharacterized protein yjbK	General prediction only	*yjbK*	BN194_09860	K0N3G6	1.83	-2.14	-4.42

Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	*ykpA*	BN194_07220	K0N8V6	4.86	-2.15	-4.44
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	*msrA_2,msrA*	BN194_15860	K0N4W6	1.39	-2.15	-4.44
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	*iolS*	BN194_29680	K0NB94	5.81	-2.15	-4.45
50S ribosomal protein L33	Ribosomal proteins	*rpmG*	BN194_20200	K0N697	0.40	-2.16	-4.48
Glycolate oxidase subunit glcD	General prediction only	*glcD*	BN194_24440	K0MXF3	1.71	-2.18	-4.54
Uncharacterized protein yxkA	General prediction only	*yxkA*	BN194_27230	K0NAV1	2.57	-2.19	-4.58
Ribosome biogenesis GTPase A	tRNA/Ribosome assembly/processing	*rbgA*	BN194_15940	K0MVH2	0.93	-2.22	-4.65
PhoH-like protein	General prediction only	*phoH*	BN194_17020	K0NAW2	4.00	-2.22	-4.65
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	*pheS*	BN194_18570	K0NB64	5.17	-2.22	-4.67
Glycosyl transferase family protein	Cell wall biogenesis		BN194_02420	K0N7L2	3.50	-2.22	-4.67
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	*agaS*	BN194_02940	K0MSD9	3.87	-2.23	-4.68
Uncharacterized protein yxjH	Amino acid-related metabolism	*yxjH*	BN194_08320	K0N962	1.71	-2.24	-4.73
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	1.65	-2.24	-4.74
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	*rny*	BN194_10100	K0N3E5	1.82	-2.25	-4.75
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	*valS*	BN194_14510	K0N4J6	4.16	-2.26	-4.79
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*pheT*	BN194_18560	K0N5M4	4.73	-2.26	-4.80
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase 2 (EC 5.4.2.1)	Central glycolytic/intermediary pathways	*gpmA2_2*	BN194_27560	K0N7W0	2.65	-2.26	-4.80
50S ribosomal protein L19	Ribosomal proteins	*rplS*	BN194_17770	K0NB12	1.88	-2.26	-4.80
Uncharacterized RNA methyltransferase lp_3226 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_19580	K0N9J4	4.18	-2.27	-4.81
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	*yhaA*	BN194_30550	K0N9E4	2.11	-2.27	-4.83
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC_2*	BN194_24680	K0NAC2	3.76	-2.28	-4.87
Uncharacterized protein YwcC	Carbohydrate-related metabolism	*ywcC*	BN194_09930	K0N6V0	3.17	-2.29	-4.90
Multifunctional protein: 5-nucleotidase 2,3-cyclic-nucleotide 2-phosphodiesterase	Nucleic acid/nucleotide metabolism	*ushA*	BN194_15530	K0N8A9	2.72	-2.30	-4.91

Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	*def*	BN194_15060	K0N4N6	3.20	-2.30	-4.94
Uncharacterized protein	Unknown/uncharacterized		BN194_29450	K0N932	5.56	-2.31	-4.94
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	*galE*	BN194_07350	K0N2R3	4.53	-2.31	-4.97
Heat-inducible transcription repressor HrcA	Transcriptional regulation	*hrcA*	BN194_17480	K0N915	2.79	-2.32	-4.98
Penicillin acylase (EC 3.5.1.11)	Cell defense/detoxification		BN194_04910	K0N2B8	3.45	-2.32	-4.99
Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	General prediction only	*yqiG*	BN194_25330	K0NAG4	1.47	-2.32	-4.99
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	*lplJ*	BN194_16640	K0MVN0	2.43	-2.32	-5.00
Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	2.44	-2.32	-5.00
Glycosyl transferase group 1	Cell wall biogenesis		BN194_09760	K0N3F8	2.01	-2.33	-5.01
S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	*metK*	BN194_09150	K0N352	2.70	-2.33	-5.02
FeS cluster assembly protein sufB	Cofactor-related metabolism	*sufB*	BN194_13810	K0N4E5	3.33	-2.34	-5.06
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*manD*	BN194_02950	K0N1P4	3.12	-2.34	-5.06
Glycosyl transferase family 8	Cell wall biogenesis		BN194_11730	K0N795	2.92	-2.34	-5.07
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrDA, pyrD*	BN194_19150	K0N623	5.01	-2.34	-5.07
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	*cmk*	BN194_15710	K0N4V1	3.28	-2.34	-5.07
Adenosylcobalamin-dependent ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*rtpR*	BN194_24230	K0NAA3	1.76	-2.35	-5.08
ABC-type antimicrobial peptide transport system,ATPase component	*ABC-type transporter systems*		BN194_19940	K0MWG2	2.45	-2.35	-5.09
Fructoselysine kinase (EC 2.7.1.-)	Carbohydrate-related metabolism	*frlD*	BN194_22240	K0MX05	3.91	-2.35	-5.09
Predicted hydrolase of the HAD superfamily	General prediction only	*mtlD*	BN194_30450	K0N9D4	3.88	-2.35	-5.11
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	Cell wall biogenesis	*glmS*	BN194_11560	K0N3V9	3.20	-2.36	-5.12
Predicted Zn-dependent peptidase	*Amino acid-related metabolism*		BN194_10020	K0N9H8	1.84	-2.36	-5.13
Uncharacterized protein	Unknown/uncharacterized		BN194_20160	K0N5Z4	3.83	-2.36	-5.14
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*gnd*	BN194_18660	K0N5N2	3.25	-2.36	-5.15

Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	*proS*	BN194_17610	K0N5E2	5.12	-2.36	-5.15
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	*obg*	BN194_15440	K0MVD3	4.30	-2.37	-5.15
Guanine deaminase (EC 3.5.4.3)	Nucleic acid/nucleotide metabolism	*guaD*	BN194_13320	K0NA96	3.87	-2.37	-5.16
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	*hmgCS1*	BN194_19680	K0N9K3	2.09	-2.37	-5.17
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	*nadE*	BN194_19840	K0MWF6	4.45	-2.39	-5.25
Oligoendopeptidase, pepF/M3 family	*Amino acid-related metabolism*		BN194_11580	K0N779	3.41	-2.40	-5.27
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	*yfeX*	BN194_07170	K0N8U9	4.33	-2.41	-5.33
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	*sph*	BN194_04930	K0N5Q0	3.60	-2.42	-5.34
FeS cluster assembly protein sufD	Cofactor-related metabolism	*sufD*	BN194_13780	K0N7U0	4.41	-2.42	-5.34
CCA-adding enzyme (EC 2.7.7.72) (CCA tRNA nucleotidyltransferase) (tRNA CCA-pyrophosphorylase) (tRNA adenylyl-/cytidylyl-transferase) (tRNA nucleotidyltransferase) (tRNA-NT)	tRNA/Ribosome assembly/processing	*cca*	BN194_15770	K0NAM4	2.56	-2.42	-5.34
Uncharacterized protein	Unknown/uncharacterized		BN194_01870	K0N7D4	3.90	-2.42	-5.34
Sporulation initiation inhibitor protein soj	Cytokinesis	*soj*	BN194_02040	K0MS45	2.96	-2.42	-5.35
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	*pcp*	BN194_01980	K0N4Y4	4.28	-2.42	-5.37
Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	*aspC*	BN194_16770	K0NAU6	3.51	-2.43	-5.38
GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	4.77	-2.43	-5.39
Protein RecA (Recombinase A)	DNA repair/recombination	*recA_2,recA*	BN194_27650	K0N8P0	2.38	-2.44	-5.42
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	*ung*	BN194_11330	K0N758	3.12	-2.44	-5.44
Glucitol operon repressor	Transcriptional regulation	*srlR*	BN194_28690	K0MYG3	5.76	-2.45	-5.48
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA_2*	BN194_22950	K0N7F8	3.23	-2.46	-5.51
30S ribosomal protein S12	Ribosomal proteins	*rpsL*	BN194_26290	K0MXV0	2.22	-2.46	-5.51
Uncharacterized RNA methyltransferase lp_1151 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_11990	K0MUI2	3.57	-2.47	-5.53
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA*	BN194_18520	K0NB62	4.20	-2.47	-5.53
Ribosomal RNA small subunit methyltransferase A (EC 2.1.1.182) (16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase) (16S rRNA dimethyladenosine transferase) (16S	tRNA/Ribosome assembly/processing	*rsmA,ksgA*	BN194_27020	K0NCX3	3.49	-2.47	-5.53

rRNA dimethylase) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase)							
Glutamate--cysteine ligase/gamma-glutamylcysteine synthetase	Cofactor-related metabolism	*gshAB*	BN194_13910	K0N4F0	3.65	-2.47	-5.55
30S ribosomal protein S14 type Z	Ribosomal proteins	*rpsZ,rpsN*	BN194_26090	K0MXS9	0.62	-2.48	-5.58
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	*thyA*	BN194_15800	K0N522	3.40	-2.48	-5.58
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	*glyr1*	BN194_30100	K0N992	1.78	-2.48	-5.59
Spore coat polysaccharide biosynthesis protein spsK				K0N9X8;K0N6D6	5.25	-2.49	-5.62
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	*trpS*	BN194_27360	K0N7S4	4.40	-2.49	-5.63
Uncharacterized protein ynbB	Cell defense/detoxification	*ynbB*	BN194_18380	K0N9B7	3.44	-2.50	-5.65
Uncharacterized protein	RNA degradation		BN194_11250	K0N3V2	2.24	-2.50	-5.66
Primosomal protein DnaI	DNA replication-related	*dnaI*	BN194_18880	K0N9E5	2.86	-2.51	-5.69
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA*	BN194_01620	K0N7B1	1.82	-2.52	-5.74
DNA polymerase III PolC-type (PolIII) (EC 2.7.7.7)	DNA replication-related	*polC*	BN194_17600	K0N5L6	5.71	-2.52	-5.75
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	*gatA*	BN194_11960	K0N3Z6	3.71	-2.52	-5.75
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_27170	K0NCZ6	3.75	-2.53	-5.78
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox_2*	BN194_02850	K0N1N9	5.57	-2.54	-5.81
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ_2*	BN194_20470	K0NBG3	1.95	-2.55	-5.84
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	*aspS*	BN194_17100	K0N5F3	3.55	-2.55	-5.85
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	*pepDB*	BN194_21110	K0N678	3.96	-2.56	-5.89
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatC*	BN194_11950	K0N436	5.87	-2.56	-5.90
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdE2*	BN194_16600	K0N5A1	3.89	-2.57	-5.94
Probable L-serine dehydratase, alpha chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAA*	BN194_13950	K0N4M4	2.56	-2.57	-5.94
Uncharacterized protein ycaC	General prediction only	*ycaC*	BN194_29650	K0N948	2.67	-2.57	-5.95
Uncharacterized protein YdiC	General prediction only	*ydiC_3*	BN194_23870	K0NBZ8	2.55	-2.57	-5.95
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	*serS*	BN194_20080	K0N9N4	3.31	-2.58	-5.96
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	*BN194_21350*	BN194_21780	K0N6Q5	4.58	-2.58	-5.96
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	*pycB*	BN194_20290	K0MWI8	1.81	-2.58	-6.00

Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*leuS*	BN194_09210	K0N3A9	5.45	-2.60	-6.05
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	*thiD_2*	BN194_07650	K0N2U9	2.01	-2.60	-6.06
Ribonuclease Z (RNase Z) (EC 3.1.26.11) (tRNA 3 endonuclease) (tRNase Z)	tRNA/Ribosome assembly/processing	*rnz*	BN194_15470	K0NAK0	1.82	-2.60	-6.07
DNA mismatch repair protein MutL	DNA repair/recombination	*mutL*	BN194_23710	K0N6Z8	2.79	-2.60	-6.08
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_3*	BN194_21990	K0MWY0	1.70	-2.61	-6.09
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	*agl*	BN194_27950	K0N8T1	5.04	-2.61	-6.11
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacA*	BN194_07500	K0N2T4	3.09	-2.61	-6.13
UvrABC system protein B (Protein UvrB) (Excinuclease ABC subunit B)	DNA repair/recombination	*uvrB*	BN194_10440	K0MU09	5.81	-2.62	-6.15
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citF*	BN194_20310	K0N607	3.36	-2.62	-6.16
Peptide chain release factor 3 (RF-3)	Protein translation (peptide release)	*prfC*	BN194_19480	K0N9I7	3.44	-2.62	-6.17
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	*der*	BN194_15730	K0N8E1	1.63	-2.63	-6.17
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatB*	BN194_11970	K0NA01	4.06	-2.63	-6.18
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	*glyA*	BN194_13540	K0MV12	3.14	-2.65	-6.26
Ribosomal RNA small subunit methyltransferase G (EC 2.1.1.-) (16S rRNA 7-methylguanosine methyltransferase)	tRNA/Ribosome assembly/processing	*rsmG*	BN194_02020	K0N7F1	3.90	-2.65	-6.29
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	*mtlD_3mtlD*	BN194_30400	K0N9C8	3.77	-2.66	-6.31
NAD-dependent protein deacetylase (EC 3.5.1.-)	General prediction only	*cobB*	BN194_27190	K0MY36	4.34	-2.68	-6.40
Uncharacterized protein	Unknown/uncharacterized		BN194_16570	K0NAT3	1.78	-2.68	-6.42
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO_2*	BN194_16630	K0N8Q0	6.41	-2.68	-6.42
Hydroxyacid oxidase (EC 1.1.3.15)	Central glycolytic/intermediary pathways	*haox*	BN194_24790	K0MXH5	3.18	-2.68	-6.43
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh1,ldh*	BN194_06970	K0N8S5	3.14	-2.69	-6.44
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	*asd*	BN194_01060	K0N1I5	3.97	-2.69	-6.44
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	2.65	-2.70	-6.50
Probable phosphoketolase (EC 4.1.2.-)	Central glycolytic/intermediary pathways	*xpkA*	BN194_01710	K0N1M9	3.54	-2.71	-6.53
Uncharacterized protein	*Central glycolytic/intermediary pathways*		BN194_04970	K0N8A3	3.77	-2.71	-6.53

Uncharacterized protein yieF	General prediction only	*yieF_2*	BN194_06540	K0MT25	1.48	-2.71	-6.55
Uncharacterized protein	Unknown/uncharacterized		BN194_19530	K0N9J0	2.92	-2.74	-6.70
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA_2*	BN194_29210	K0N8B2	5.96	-2.75	-6.72
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC*	BN194_00080	K0N486	3.20	-2.75	-6.74
Uncharacterized oxidoreductase YbdH (EC 1.1.-.-)	Carbohydrate-related metabolism	*ybdH*	BN194_30540	K0MYX0	4.58	-2.77	-6.80
Cysteine desulfurase (EC 2.8.1.7)	Cofactor-related metabolism	*csd*	BN194_13790	K0MV25	4.38	-2.77	-6.84
Aldose 1-epimerase (EC 5.1.3.3)	*Central glycolytic/intermediary pathways*		BN194_07390	K0MTA8	2.94	-2.78	-6.86
Acid shock protein	Protein folding/turnover		BN194_29440	K0MYM2	2.35	-2.79	-6.91
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI_2*	BN194_16210	K0N508	1.93	-2.79	-6.92
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	*pgcA*	BN194_10370	K0N9K8	7.59	-2.81	-7.00
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	*apbE_3*	BN194_21550	K0N6S8	3.50	-2.83	-7.13
Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	*pox5*	BN194_19670	K0NBB6	2.84	-2.86	-7.28
Phosphoribosylformylglycinamidine synthase subunit PurQ (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit I) (Glutaminase PurQ) (Phosphoribosylformylglycinamidine synthase subunit I)	Nucleic acid/nucleotide metabolism	*purQ*	BN194_19340	K0MWC7	3.79	-2.87	-7.32
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	*accB*	BN194_22530	K0NA35	2.69	-2.87	-7.33
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	3.19	-2.89	-7.43
Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)	Nucleic acid/nucleotide metabolism	*purC*	BN194_19360	K0N5S8	3.57	-2.92	-7.54
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	*dnaK*	BN194_17460	K0N5C7	5.03	-2.95	-7.71
Histidinol-phosphatase	General prediction only		BN194_14010	K0N4F8	2.11	-2.96	-7.77
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citE*	BN194_20320	K0NBF4	3.57	-2.96	-7.77
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*lacC*	BN194_07470	K0N8Y4	5.12	-2.97	-7.84
UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.3.1.98) (UDP-N-acetylmuramate dehydrogenase)	Cell wall biogenesis	*murB*	BN194_11400	K0N3X0	5.21	-2.99	-7.93
1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157)	Cell wall biogenesis		BN194_09040	K0MTQ9	2.94	-3.00	-7.97

Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	Nucleic acid/nucleotide metabolism	*purD*	BN194_19290	K0MWC4	3.46	-3.00	-8.01
Uncharacterized protein	Unknown/uncharacterized		BN194_17360	K0N5B9	2.36	-3.01	-8.06
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC*	BN194_24670	K0NC50	4.52	-3.01	-8.06
Esterase/lipase	General prediction only		BN194_30390	K0MYV7	2.68	-3.02	-8.12
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*glyS*	BN194_16950	K0N5D3	3.55	-3.03	-8.19
Uncharacterized protein			BN194_22500	K0N788	1.06	-3.03	-8.19
NAD-dependent epimerase/dehydratase:3-beta hydroxysteroid dehydrogenase/isomerase:NmrA-like	General prediction only		BN194_25520	K0NCC8	4.43	-3.05	-8.26
ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	DNA repair/recombination	*addA*	BN194_16800	K0N5B6	2.62	-3.08	-8.46
Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	Nucleic acid/nucleotide metabolism	*add*	BN194_23440	K0MXB1	3.35	-3.10	-8.57
Uncharacterized protein	General prediction only	*gpm1*	BN194_13960	K0N4F5	4.24	-3.10	-8.59
Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		BN194_20000	K0N684	2.99	-3.11	-8.61
Pyridoxine 5'-phosphate oxidase V related favin-nucleotide-binding protein	Cofactor-related metabolism		BN194_01900	K0N1E7	2.37	-3.12	-8.72
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	*hpt*	BN194_26470	K0NCR2	4.11	-3.13	-8.74
Uncharacterized protein	Unknown/uncharacterized		BN194_25890	K0MXR4	1.60	-3.14	-8.82
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		BN194_21400	K0N6R1	3.63	-3.16	-8.92
Esterase/lipase	General prediction only	*yneB*	BN194_20230	K0N9P7	3.63	-3.17	-8.98
Uncharacterized protein ybxB	tRNA/Ribosome assembly/processing	*ybxB*	BN194_24020	K0NC08	3.61	-3.17	-9.00
Uridine phosphorylase (EC 2.4.2.3)	Nucleic acid/nucleotide metabolism	*udp*	BN194_24830	K0NAD0	2.24	-3.18	-9.07
Uncharacterized protein YPL245W	Unknown/uncharacterized		BN194_25000	K0N7U3	2.88	-3.18	-9.08
Uncharacterized protein	Unknown/uncharacterized		BN194_22290	K0MX11	4.35	-3.18	-9.08
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*pip_2*	BN194_27140	K0MY30	4.51	-3.19	-9.10
Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	*fhs*	BN194_16520	K0NAT0	4.11	-3.19	-9.11
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_23190	K0MXA1	2.87	-3.19	-9.12
Uncharacterized protein yaaQ	Unknown/uncharacterized	*yaaQ*	BN194_23940	K0MXD1	3.31	-3.19	-9.14

Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE*	BN194_13710	K0N4D8	3.07	-3.19	-9.14
Putative carboxypeptidase SCO6489 (EC 3.4.16.-)			BN194_01370	K0N787	3.97	-3.19	-9.14
Probable calcium-transporting ATPase (EC 3.6.3.8)	Other transporter proteins	*pacL*	BN194_11490	K0MUB1	3.57	-3.21	-9.26
Phosphoribosylformylglycinamidine synthase subunit PurL (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit II) (Glutamine amidotransferase PurL) (Phosphoribosylformylglycinamidine synthase subunit II)	Nucleic acid/nucleotide metabolism	*purL*	BN194_19330	K0N9H6	6.25	-3.24	-9.42
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB*	BN194_19860	K0N5X0	6.81	-3.27	-9.65
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	*treA*	BN194_06930	K0N662	1.71	-3.28	-9.68
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP*	BN194_08180	K0N6I0	2.17	-3.29	-9.79
UvrABC system protein A	DNA repair/recombination	*uvrA_3*	BN194_27500	K0N8M1	7.43	-3.30	-9.87
Dihydrofolate reductase (EC 1.5.1.3)	Cofactor-related metabolism	*folA*	BN194_15810	K0N4W0	2.15	-3.31	-9.93
Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	*nfo*	BN194_17070	K0NAW5	3.07	-3.33	-10.03
Uncharacterized protein	Unknown/uncharacterized		BN194_30140	K0MYT6	3.05	-3.33	-10.03
Uncharacterized protein	General prediction only		BN194_26820	K0NCV9	2.63	-3.36	-10.26
Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase)	Cofactor-related metabolism	*coaE*	BN194_18910	K0N5P8	2.92	-3.46	-11.03
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	2.67	-3.48	-11.13
3'-5' exoribonuclease yhaM (EC 3.1.-.-)	RNA degradation	*yhaM*	BN194_19070	K0NB84	1.85	-3.50	-11.34
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	*deoB*	BN194_02800	K0N1N0	3.67	-3.51	-11.36
DNA mismatch repair protein MutS	DNA repair/recombination	*mutS*	BN194_23720	K0NBY9	4.05	-3.51	-11.42
Phage capsid protein	Prophage genome		BN194_30330	K0NBD3	2.66	-3.52	-11.48
Glutamate dehydrogenase	Amino acid-related metabolism	*gdh*	BN194_06980	K0N666	2.61	-3.57	-11.89
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	*carB*	BN194_16450	K0N587	4.49	-3.58	-11.99
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	*nagB*	BN194_30440	K0MYW0	3.81	-3.59	-12.03
Chromosome partition protein Smc	Cytokinesis	*smc*	BN194_17860	K0N5H9	2.83	-3.65	-12.55
GTPase HflX (GTP-binding protein HflX)	tRNA/Ribosome assembly/processing	*hflX*	BN194_21260	K0N689	4.07	-3.65	-12.57

LexA repressor (EC 3.4.21.-) (EC 3.4.21.88)	DNA repair/recombination	*lexA*	BN194_07970	K0N944	3.88	-3.66	-12.64
Uncharacterized ABC transporter ATP-binding protein YdbJ	ABC-type transporter systems	*ydbJ*	BN194_24600	K0N7Q8	2.59	-3.68	-12.84
NADH-dependent butanol dehydrogenase A (EC 1.1.1.-)	Carbohydrate-related metabolism	*bdhA*	BN194_22640	K0MX50	2.04	-3.69	-12.91
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA1, greA*	BN194_02150	K0N1G7	1.92	-3.69	-12.95
Kinase, putative	General prediction only		BN194_29890	K0MYR0	3.32	-3.72	-13.17
Type I restriction enzyme EcoR124II M protein (EC 2.1.1.72)	IS elements/foreign DNA defense	*hsdM*	BN194_22340	K0MX17	2.10	-3.73	-13.24
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	*pepS*	BN194_12180	K0N7D5	2.68	-3.75	-13.45
Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase)	Nucleic acid/nucleotide metabolism	*purM*	BN194_19320	K0NB95	4.48	-3.79	-13.84
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_13380	K0N7S0	4.07	-3.80	-13.96
Zinc-type alcohol dehydrogenase-like protein SE_1777	General prediction only		BN194_07910	K0N329	4.14	-3.81	-14.04
Probable phosphoketolase (EC 4.1.2.-)	*Central glycolytic/intermediary pathways*		BN194_28700	K0N8X7	5.62	-3.83	-14.26
Uncharacterized protein	Unknown/uncharacterized		BN194_23650	K0N7J8	5.60	-3.85	-14.40
Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain)	Nucleic acid/nucleotide metabolism	*carA*	BN194_16460	K0N535	4.37	-3.90	-14.89
Uncharacterized protein yeaE	General prediction only	*yeaE*	BN194_07040	K0MT72	5.07	-3.90	-14.98
Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) (Peptide-methionine (R)-S-oxide reductase)	Posttranslational modification	*msrB*	BN194_17090	K0MVR6	2.23	-3.93	-15.21
Uncharacterized protein	General prediction only		BN194_30000	K0N979	5.41	-3.93	-15.23
Transcriptional regulator	*Posttranslational modification*		BN194_29310	K0N8C2	2.25	-3.93	-15.26
Chromosomal replication initiator protein DnaA	DNA replication-related	*dnaA*	BN194_00010	K0N1B5	4.26	-3.98	-15.76
Elongation factor 4 (EF-4) (EC 3.6.5.n1) (Ribosomal back-translocase LepA)	Protein translation (elongation)	*lepA*	BN194_17440	K0MVU5	5.05	-4.03	-16.31
Peptidase T (EC 3.-.-.-) (EC 3.4.11.-) (EC 3.4.11.4)	Amino acid-related metabolism	*pepT*	BN194_03110	K0N213	4.93	-4.04	-16.50
Uncharacterized protein ywfO	General prediction only	*ywfO*	BN194_26840	K0MXZ5	4.37	-4.06	-16.63
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	*mhqA_3*	BN194_18760	K0N5N7	3.41	-4.07	-16.85
L-asparaginase (EC 3.5.1.1)	Amino acid-related metabolism	*ansA*	BN194_23900	K0N7L6	3.45	-4.10	-17.14
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO*	BN194_12030	K0N7B7	4.19	-4.11	-17.27

Acyl-ACP thioesterase	Lipid-related metabolism		BN194_23910	K0N709	4.73	-4.16	-17.84
Uncharacterized protein	Unknown/uncharacterized		BN194_21450	K0N6R7	3.60	-4.17	-18.00
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E_2,P100*	BN194_05160	K0N2D7	4.02	-4.29	-19.52
Uncharacterized protein			BN194_19420	K0NB98	0.94	-4.29	-19.62
Uncharacterized protein ypgQ	General prediction only	*ypgQ*	BN194_27480	K0NAX0	3.73	-4.30	-19.65
Uncharacterized protein			BN194_21520	K0NBL8	6.32	-4.34	-20.23
Monooxygenase	General prediction only		BN194_07600	K0N2U5	3.84	-4.41	-21.31
Folate transporter FolT	Unknown/uncharacterized	*folT*	BN194_23890	K0MXC9	2.19	-4.47	-22.22
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		BN194_24180	K0NAA2	3.28	-4.52	-22.91
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	*mnmA*	BN194_14930	K0N844	3.15	-4.58	-23.95
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_2*	BN194_04490	K0MSM9	2.43	-4.60	-24.17
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	*mco*	BN194_25410	K0N7A4	3.81	-4.60	-24.18
Microcin C7 self-immunity protein mccF			BN194_01360	K0N1K5	3.63	-4.61	-24.47
UvrABC system protein A	DNA repair/recombination	*uvrA_2*	BN194_14920	K0NAH3	2.68	-4.73	-26.56
Uncharacterized ABC transporter ATP-binding protein YfmR (EC 3.6.3.-)	ABC-type transporter systems	*yfmR*	BN194_15790	K0MVF8	5.95	-4.80	-27.77
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	*alsS*	BN194_20150	K0N695	2.60	-4.96	-31.21
ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease RexB)	DNA repair/recombination	*rexB*	BN194_16810	K0N573	4.28	-5.01	-32.15
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	*polA*	BN194_18930	K0N9E7	5.06	-5.02	-32.44
Uncharacterized aminotransferase SSO0104 (EC 2.6.1.-)	*Amino acid-related metabolism*		BN194_27600	K0N8N4	2.29	-5.26	-38.31
Beta-galactosidase 17 (EC 3.2.1.23)	Carbohydrate-related metabolism	*BGAL17*	BN194_02960	K0N204	2.39	-5.37	-41.29
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	*cysS*	BN194_24430	K0NAB2	5.22	-5.43	-43.16
Dumpy	Cell surface proteins/internalins	*dp*	BN194_05390	K0MSV0	4.00	-5.61	-48.91
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB*	BN194_21340	K0MWS0	3.18	-8.36	-329.14

(7f)Protein FC LiCL pH 6.5 Vs CFE pH 6.5

Protein names	Functional Class	Gene	Gene locus	Protein IDs	-Log t-test p-value	t-test difference	Fold change
Uncharacterized protein yitL	General prediction only	*yitL*	BN194_15600	K0N505	3.83	6.71	104.98
50S ribosomal protein L32	Ribosomal proteins	*rpmF*	BN194_15510	K0N4T0	1.50	6.54	93.17
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*rluB*	BN194_15650	K0N509	3.02	5.85	57.68
Uncharacterized protein	Unknown/uncharacterized (signal sequence, MW 13.7)		BN194_01080	K0N4J7	4.33	5.74	53.58
Uncharacterized protein	Unknown/uncharacterized		BN194_16650	K0N5A4	3.93	5.70	51.93
Uncharacterized protein	Unknown/uncharacterized		BN194_15370	K0NAJ2	4.71	5.51	45.47
Uncharacterized protein yaaA	General prediction only	*yaaA*	BN194_00040	K0MRL5	5.17	5.47	44.33
Uncharacterized protein	Unknown/uncharacterized, MW 38.3; Sig Seq; cell wall associated hydrolase, surface and ECF		BN194_23630	K0NA78	5.49	5.34	40.47
Arginine repressor	Transcriptional regulation	*argR1,argR*	BN194_19110	K0N5R1	1.97	5.18	36.28
Ribonuclease P protein component (RNase P protein) (RNaseP protein) (EC 3.1.26.5) (Protein C5)	tRNA/Ribosome assembly/processing	*rnpA*	BN194_30620	K0NDS2	2.26	5.10	34.20
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	*yabO*	BN194_26520	K0NCR8	4.02	5.09	34.13
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	*yabR*	BN194_26500	K0N8A7	4.73	5.07	33.60
Uncharacterized protein	Unknown/uncharacterized		BN194_21380	K0N9Y1	4.43	4.77	27.29
SsrA-binding protein (Small protein B)	Posttranslational modification	*smpB*	BN194_11110	K0N3S3	2.92	4.68	25.59
Uncharacterized protein	Unknown/uncharacterized		BN194_05550	K0N257	2.60	4.63	24.73
Putative secreted protein	cell wall biogenesis		BN194_02820	K0N7S8	2.63	4.54	23.28
Nucleoid occlusion protein	Cytokinesis	*noc*	BN194_02030	K0N4Z1	3.62	4.46	22.03

Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP*	BN194_17930	K0N988	2.09	4.41	21.19
Alternansucrase	Cell wall biogenesis		BN194_02430	K0N547	5.67	4.37	20.67
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB*	BN194_17900	K0N5S3	2.28	4.36	20.50
50S ribosomal protein L33	Ribosomal proteins	*rpmG2,rpmG*	BN194_24280	K0NAA5	2.77	4.16	17.87
Ribonuclease H (EC 3.1.26.4)	DNA repair/recombination	*rnhA*	BN194_27580	K0NAX8	2.91	4.13	17.57
Uncharacterized protein RP368	*ABC-type transporter systems*		BN194_07720	K0N914	3.62	4.11	17.28
HTH-type transcriptional regulator galR	Transcriptional regulation	*galR*	BN194_03780	K0N5G9	2.38	4.10	17.21
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ysgA*	BN194_18610	K0N5M8	3.63	4.10	17.09
50S ribosomal protein L21	Ribosomal proteins	*rplU*	BN194_18290	K0MW61	4.95	4.02	16.20
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	*dut*	BN194_24640	K0MXG3	5.24	4.01	16.09
Uncharacterized protein yeaO	Unknown/uncharacterized	*yeaO*	BN194_08040	K0MTJ2	2.69	3.93	15.24
50S ribosomal protein L33	Ribosomal proteins	*rpmG*	BN194_20200	K0N697	0.91	3.89	14.84
HTH-type transcriptional repressor yvoA	Transcriptional regulation	*yvoA_2*	BN194_19880	K0N9L8	4.65	3.88	14.75
Putative sporulation transcription regulator WhiA	Transcriptional regulation	*whiA*	BN194_10490	K0MU14	3.26	3.84	14.28
Ribosome maturation factor RimP	tRNA/Ribosome assembly/processing	*rimP*	BN194_17590	K0MVW3	3.55	3.82	14.15
Xre-like DNA-binding protein	Transcriptional regulation		BN194_10050	K0N3E1	3.06	3.71	13.12
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*ytzG*	BN194_09230	K0N6P7	2.97	3.64	12.49
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	4.99	3.64	12.48
30S ribosomal protein S21	Ribosomal proteins	*rpsU*	BN194_17050	K0N5E5	3.11	3.63	12.38
Sortase	Cell wall biogenesis		BN194_22780	K0NA48	4.70	3.63	12.38
Uncharacterized protein	Cell wall biogenesis		BN194_02360	K0N1U1	1.86	3.58	11.98
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	2.47	3.56	11.79

UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227) (Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase)	Cell wall biogenesis	*murG*	BN194_14730	K0N819	5.36	3.43	10.79
Putative N-acetylmuramoyl-L-alanine amidase YrvJ (EC 3.5.1.28)	Cytokinesis	*yrvJ*	BN194_17200	K0N5G4	4.54	3.41	10.66
Isoprenyl transferase (EC 2.5.1.-)	Lipid-related metabolism	*uppS*	BN194_17640	K0MVX1	2.02	3.41	10.62
Translation initiation factor IF-3	Protein translation (initiation)	*infC*	BN194_18820	K0NB73	5.99	3.40	10.56
ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136) (ADP-dependent NAD(P)HX dehydratase)	Cofactor-related metabolism	*nnrD*	BN194_09250	K0N360	3.81	3.29	9.81
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	*htrA*	BN194_29460	K0N8D9	4.06	3.27	9.68
NAD kinase (EC 2.7.1.23) (ATP-dependent NAD kinase)		*nadK*	ppnK	K0N6U5	2.67	3.19	9.10
Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase (EC 4.2.-.-)	*tRNA/Ribosome assembly/processing*		BN194_17370	K0NAY4	5.50	3.16	8.94
Uncharacterized protein	Unknown/uncharacterized		BN194_02900	K0N1P1	5.78	3.14	8.84
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	5.48	3.12	8.70
30S ribosomal protein S9	Ribosomal proteins	*rpsI*	BN194_25840	K0MXR0	0.51	3.05	8.30
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*bglP*	BN194_06940	K0MT60	4.92	3.03	8.17
50S ribosomal protein L35	Ribosomal proteins	*rpmI*	BN194_18810	K0N5P1	3.44	2.99	7.97
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshB*	BN194_08460	K0N356	5.13	2.93	7.62
Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	DNA repair/recombination	*recJ*	BN194_17390	K0MVT7	2.82	2.92	7.58
Carboxy-terminal processing protease CtpA (EC 3.4.21.102)	Protein folding/turnover	*ctpA*	BN194_15880	K0N8G1	5.46	2.90	7.46
RNA polymerase sigma factor SigA	RNA polymerase	*rpoD,sigA*	BN194_16920	K0NAV6	3.89	2.88	7.39
Transcriptional regulatory protein YycF	Signal transduction	*yycF_2*	BN194_29510	K0N8E4	1.05	2.87	7.33
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ*	BN194_14610	K0N4K4	4.52	2.87	7.29
30S ribosomal protein S17	Ribosomal proteins	*rpsQ*	BN194_26130	K0NAL6	4.61	2.82	7.06

Transcriptional regulator lytR	Transcriptional regulation	*lytR*	BN194_02540	K0MS94	5.69	2.78	6.86
Adapter protein MecA	Competence (DNA uptake)	*mecA*	BN194_19170	K0NB89	1.34	2.68	6.41
Protein veg	Unknown/uncharacterized	*veg*	BN194_27010	K0N7N4	4.11	2.60	6.05
Translation initiation factor IF-2	Protein translation (initiation)	*infB*	BN194_17550	K0N5K7	4.82	2.55	5.87
Transcriptional repressor smtB homolog	Transcriptional regulation	*ziaR*	BN194_01180	K0N4L0	2.40	2.54	5.83
50S ribosomal protein L16	Ribosomal proteins	*rplP*	BN194_26150	K0N863	2.99	2.53	5.78
D-alanine--poly(phosphoribitol) ligase subunit 2 (EC 6.1.1.13) (D-alanyl carrier protein)	Cell wall biogenesis	*dltC*	BN194_08610	K0N361	2.54	2.51	5.71
Segregation and condensation protein B	Cytokinesis	*scpB*	BN194_15640	K0MVE6	2.64	2.43	5.38
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	*bkr4*	BN194_22550	K0N799	3.25	2.39	5.25
Uncharacterized oxidoreductase YcsN (EC 1.-.-.-)	General prediction only	*ycsN*	BN194_27290	K0MY45	2.54	2.38	5.22
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB_2*	BN194_20630	K0N9S5	1.29	2.37	5.16
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*manX_5*	BN194_29720	K0NDL4	3.71	2.33	5.04
Uncharacterized protein	Unknown/uncharacterized	*yvcC*	BN194_05260	K0N2E5	5.07	2.33	5.01
50S ribosomal protein L24	Ribosomal proteins	*rplX*	BN194_26110	K0N7F9	3.80	2.31	4.96
50S ribosomal protein L30	Ribosomal proteins	*rpmD*	BN194_26040	K0MXS6	3.71	2.30	4.93
30S ribosomal protein S1 homolog	Ribosomal proteins	*ypfD*	BN194_15720	K0NAL9	7.46	2.29	4.89
MarR family transcriptional regulator	Transcriptional regulation		BN194_22610	K0N6N9	1.37	2.25	4.76
ABC transporter, ATP-binding protein	*Cell surface proteins/internalins*		BN194_15700	K0N514	2.26	2.25	4.75
Transcriptional regulator lytR	Transcriptional regulation	*lytR_4*	BN194_23780	K0NA85	4.51	2.23	4.69
50S ribosomal protein L15	Ribosomal proteins	*rplO*	BN194_26030	K0NAK7	4.17	2.21	4.63
Uncharacterized ABC transporter ATP-binding protein TM_0288	*ABC-type transporter systems*		BN194_06900	K0N2K4	1.41	2.19	4.56
Predicted ORF			BN194_P0560	K0MZ29	3.06	2.19	4.56

DNA-binding protein HU	DNA replication-related	*hup*	BN194_15740	K0MVF4	5.86	2.19	4.55
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_2*	BN194_15390	K0MVD0	1.81	2.18	4.53
CBS domain-containing protein	Unknown/uncharacterized		BN194_26610	K0N7J7	3.77	2.16	4.46
30S ribosomal protein S16	Ribosomal proteins	*rpsP*	BN194_17810	K0N5H1	4.37	2.14	4.40
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	*HBN1*	BN194_16550	K0N597	3.34	2.13	4.37
DNA topoisomerase 1 (EC 5.99.1.2) (DNA topoisomerase I)	DNA replication-related	*topA*	BN194_15970	K0NAP0	3.74	2.11	4.31
Possible TrsG protein	Unknown/uncharacterized		BN194_00240	K0MRM8	1.69	2.10	4.29
Transcriptional repressor CcpN	Transcriptional regulation	*ccpN*	BN194_24740	K0MXH2	2.56	2.04	4.12
50S ribosomal protein L9	Ribosomal proteins	*rplI*	BN194_01130	K0N4K3	3.70	2.02	4.05
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	*murF*	BN194_26720	K0NCU5	4.23	2.00	4.01
TPR repeat-containing protein ypiA	Unknown/uncharacterized	*ypiA*	BN194_15750	K0N517	4.31	2.00	4.01
Ribosomal RNA small subunit methyltransferase F (EC 2.1.1.178)	tRNA/Ribosome assembly/processing	*rsmF*	BN194_16850	K0N5C0	2.71	1.99	3.97
DNA topoisomerase 4 subunit A (EC 5.99.1.-)		*parC*	BN194_16070	K0NAP8	3.88	1.93	3.80
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*yacO*	BN194_24420	K0NC34	3.37	1.92	3.78
50S ribosomal protein L7/L12	Ribosomal proteins	*rplL*	BN194_24080	K0NA98	4.81	1.91	3.76
Uncharacterized protein			BN194_16060	K0N4Y8	1.89	1.91	3.76
HTH-type transcriptional repressor glcR	Transcriptional regulation	*glcR*	BN194_02570	K0N7M8	3.51	1.89	3.72
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	*hslO*	BN194_26400	K0N893	3.12	1.89	3.72
Uncharacterized MscS family protein YkuT	Other transporter proteins	*ykuT*	BN194_08700	K0N322	2.24	1.86	3.63
Uncharacterized protein	Unknown/uncharacterized		BN194_25540	K0MXN3	1.08	1.85	3.61
Queuosine transporter QueT	General prediction only	*queT*	BN194_21930	K0NA07	1.36	1.85	3.60
50S ribosomal protein L27	Ribosomal proteins	*rpmA*	BN194_18270	K0NB51	3.68	1.84	3.59

Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	*bceA_2*	BN194_21230	K0N9X1	3.55	1.84	3.58
Putative RNA-binding protein ylmH	General prediction only	*ylmH*	BN194_14790	K0MV84	3.16	1.84	3.58
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*yfmL*	BN194_12120	K0NA13	3.94	1.81	3.51
Surface antigen	Cell wall biogenesis		BN194_21500	K0N6S2	4.37	1.80	3.49
41 kDa protein		*repA*	BN194_P0550	K0NBI6	2.79	1.79	3.46
Ribosome maturation factor RimM	tRNA/Ribosome assembly/processing	*rimM*	BN194_17790	K0MVZ6	5.09	1.78	3.44
Cadmium efflux system accessory protein	Other transporter proteins	*cadC*	BN194_21540	K0MWU0	3.32	1.76	3.39
30S ribosomal protein S8	Ribosomal proteins	*rpsH*	BN194_26080	K0NAL1	4.38	1.74	3.35
Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	*lysS*	BN194_26380	K0NAN7	4.16	1.74	3.35
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB_2*	BN194_21770	K0NBN4	4.14	1.74	3.33
Acyltransferase 3			BN194_15460	K0N4S6	1.53	1.72	3.30
Uncharacterized protein	Unknown/uncharacterized		BN194_28350	K0N8V3	3.38	1.71	3.28
Uncharacterized protein MJ0282	Cofactor-related metabolism		BN194_03700	K0N1T2	4.75	1.71	3.27
Putative transcriptional regulator, MarR family	Transcriptional regulation		BN194_27490	K0MY64	3.07	1.71	3.26
Translation initiation factor IF-1	Protein translation (initiation)	*infA*	BN194_26000	K0N847	3.46	1.70	3.26
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_07710	K0N2Z3	4.96	1.70	3.25
Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)	Nucleic acid/nucleotide metabolism	*pyrF*	BN194_16430	K0N8M7	2.23	1.65	3.14
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	*fabG*	BN194_22560	K0N6N3	3.53	1.64	3.12
Uncharacterized protein	Unknown/uncharacterized		BN194_20240	K0MWI3	0.72	1.63	3.10
Sorbose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*sorB_2*	BN194_29180	K0NB63	4.19	1.63	3.09
UPF0337 protein lp_1708	General prediction only		BN194_05810	K0N2J8	1.84	1.60	3.03
Probable transcription repressor NiaR	Transcriptional regulation	*niaR*	BN194_08730	K0N6L8	4.68	1.59	3.01

Cell wall surface anchor family protein	*Cell surface proteins/internalins*		BN194_05290	K0MSU3	3.38	1.57	2.97
Endonuclease MutS2 (EC 3.1.-.-)	DNA repair/recombination	*mutS2*	BN194_08560	K0N359	2.34	1.55	2.92
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	4.09	1.54	2.90
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF*	BN194_08770	K0N987	4.78	1.53	2.90
50S ribosomal protein L6	Ribosomal proteins	*rplF*	BN194_26070	K0NCK5	5.48	1.52	2.87
Uncharacterized protein	Unknown/uncharacterized		BN194_11770	K0N9Y6	1.65	1.51	2.85
30S ribosomal protein S13	Ribosomal proteins	*rpsM*	BN194_25980	K0NAK3	2.22	1.50	2.84
Probable GTP-binding protein EngB	tRNA/Ribosome assembly/processing	*engB*	BN194_15350	K0N4Y5	0.97	1.50	2.83
tRNA-specific adenosine deaminase (EC 3.5.4.33)	tRNA/Ribosome assembly/processing	*tadA*	BN194_24000	K0N7M1	2.41	1.50	2.83
Uncharacterized protein	Unknown/uncharacterized		BN194_19470	K0NBA0	2.08	1.50	2.82
Uncharacterized protein	Prophage genome		BN194_09330	K0N6Q4	3.77	1.49	2.80
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE*	BN194_02970	K0N7U7	3.77	1.48	2.79
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	*rnjA*	BN194_15020	K0NAH6	4.15	1.48	2.78
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	3.21	1.46	2.76
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	*fabZ*	BN194_22520	K0NBS8	4.15	1.44	2.70
Uncharacterized protein	Unknown/uncharacterized		BN194_19210	K0N5R7	0.92	1.42	2.67
Uncharacterized protein ylxR	General prediction only	*ylxR*	BN194_17570	K0NAZ6	3.15	1.40	2.64
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF_2*	BN194_19090	K0MWB2	3.02	1.38	2.60
Xanthine permease	Other transporter proteins	*pbuX*	BN194_12500	K0N490	0.78	1.34	2.53
50S ribosomal protein L23	Ribosomal proteins	*rplW*	BN194_26200	K0N869	2.87	1.34	2.53
D-2-hydroxyacid dehydrogenase (EC 1.1.1.-)	General prediction only	*ddh*	BN194_16660	K0N557	3.45	1.34	2.53
50S ribosomal protein L13	Ribosomal proteins	*rplM*	BN194_25850	K0N828	3.94	1.34	2.53

50S ribosomal protein L29	Ribosomal proteins	*rpmC*	BN194_26140	K0MXT6	5.40	1.33	2.51
Uncharacterized protein	General prediction only		BN194_01300	K0N194	2.38	1.33	2.51
50S ribosomal protein L22	Ribosomal proteins	*rplV*	BN194_26170	K0NCM1	3.44	1.32	2.50
ErfK family protein	Cell wall biogenesis		BN194_26570	K0NCS1	3.19	1.31	2.48
Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	*upp*	BN194_13550	K0N4J8	3.99	1.30	2.46
Uncharacterized protein ybbP	Unknown/uncharacterized	*ybbP*	BN194_11530	K0N776	0.55	1.29	2.44
Chaperone protein DnaJ	Protein folding/turnover	*dnaJ*	BN194_17450	K0N5J4	3.55	1.28	2.43
HTH-type transcriptional regulator yodB	Transcriptional regulation	*yodB*	BN194_18590	K0MW80	2.71	1.28	2.42
Gluconate 5-dehydrogenase (EC 1.1.1.69)	General prediction only	*idnO*	BN194_08150	K0N2Z5	1.02	1.24	2.35
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	*accA*	BN194_22470	K0NBS6	2.98	1.23	2.34
Membrane protein insertase YidC 1	Protein export	*yidC1*	BN194_18630	K0N9D1	0.98	1.23	2.34
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	*rpoE*	BN194_26810	K0N7L4	2.50	1.22	2.33
Uncharacterized protein	Transcriptional regulation		BN194_22670	K0NBT5	3.00	1.22	2.32
50S ribosomal protein L10	Ribosomal proteins	*rplJ*	BN194_24090	K0MXD8	2.97	1.21	2.31
UPF0337 protein yhjA	General prediction only	*yhjA*	BN194_24800	K0N7S1	0.21	1.20	2.30
Uncharacterized protein YqhY	Unknown/uncharacterized	*yqhY*	BN194_18230	K0N9A7	1.49	1.19	2.28
Uncharacterized protein	Lipid-related metabolism		BN194_11980	K0N7B3	3.51	1.18	2.26
Polyphosphate kinase (EC 2.7.4.1) (ATP-polyphosphate phosphotransferase) (Polyphosphoric acid kinase)	Membrane bioenergetics	*ppk*	BN194_27270	K0ND10	2.27	1.18	2.26
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	3.48	1.16	2.24
Ferredoxin--NADP reductase (FNR) (Fd-NADP(+) reductase) (EC 1.18.1.2)	Membrane bioenergetics		BN194_08950	K0N337	3.62	1.16	2.23
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (ACCase subunit beta) (Acetyl-CoA carboxylase carboxyltransferase subunit beta) (EC 6.4.1.2)	Lipid-related metabolism	*accD*	BN194_22480	K0NA32	0.75	1.16	2.23

Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*fruK*	BN194_15420	K0NAJ6	2.50	1.15	2.22
Protein translocase subunit SecY	Protein export	*secY*	BN194_26020	K0NCJ6	1.38	1.13	2.18
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*fruA_3*	BN194_15410	K0N4S1	0.99	1.10	2.15
Elongation factor P	Protein translation (elongation)	*efp*	BN194_18240	K0MW57	2.39	1.09	2.13
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	*clpC*	BN194_21680	K0N9Z7	3.78	1.08	2.12
Putative RNA methyltransferase YpsC (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ypsC*	BN194_16670	K0NAU0	3.36	1.08	2.12
ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_19800	K0N670	2.41	1.08	2.12
30S ribosomal protein S20	Ribosomal proteins	*rpsT*	BN194_15250	K0N4X9	1.60	1.08	2.11
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_4*	BN194_29900	K0N971	2.92	1.08	2.11
Uncharacterized protein	Unknown/uncharacterized	*FNV1452*	BN194_18830	K0N9E3	0.98	1.08	2.11
30S ribosomal protein S19	Ribosomal proteins	*rpsS*	BN194_26180	K0NAM1	3.00	1.06	2.08
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	*yqeL,rsfS*	BN194_18710	K0N5N6	3.25	1.06	2.08
30S ribosomal protein S2	Ribosomal proteins	*rpsB*	BN194_17680	K0N936	5.05	1.06	2.08
Acid shock protein	Protein folding/turnover		BN194_29440	K0MYM2	2.44	1.04	2.06
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC_2*	BN194_20620	K0NBH0	0.83	1.00	2.00
Nucleotide-binding protein BN194_10470	General prediction only		BN194_10470	K0N9L7	3.89	1.00	1.99
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	3.29	0.99	1.99
4-hydroxy-tetrahydrodipicolinate synthase (HTPA synthase) (EC 4.3.3.7)	Amino acid-related metabolism	*dapA*	BN194_01010	K0N1I2	2.26	0.99	1.98
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	3.63	0.97	1.95
30S ribosomal protein S15	Ribosomal proteins	*rpsO*	BN194_15260	K0N4Q6	1.90	0.97	1.95
Transcriptional regulator	Transcriptional regulation		BN194_08230	K0N6I4	3.92	0.96	1.95
Stage 0 sporulation protein J	Cytokinesis	*spo0J*	BN194_02050	K0N1F9	3.42	0.95	1.93

Uncharacterized amino acid permease YfnA	Other transporter proteins	*yfnA*	BN194_06960	K0N2T0	1.01	0.95	1.93
30S ribosomal protein S7	Ribosomal proteins	*rpsG*	BN194_26280	K0NAM9	4.31	0.94	1.92
Diphosphomevalonate decarboxylase (EC 4.1.1.33)	Lipid-related metabolism	*mvd1*	BN194_16830	K0N8S2	1.24	0.94	1.92
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	*cysK*	BN194_05520	K0N8E6	3.03	0.94	1.92
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	*cap4C*	BN194_12280	K0N7E3	3.99	0.94	1.92
Uncharacterized protein	Unknown/uncharacterized		BN194_01790	K0MS25	2.73	0.93	1.91
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_3*	BN194_21440	K0MWS9	3.07	0.93	1.90
50S ribosomal protein L11	Ribosomal proteins	*rplK*	BN194_24160	K0N724	2.03	0.92	1.90
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	*atpH*	BN194_13590	K0MV16	2.44	0.92	1.89
50S ribosomal protein L14	Ribosomal proteins	*rplN*	BN194_26120	K0NCL3	3.79	0.92	1.89
50S ribosomal protein L17	Ribosomal proteins	*rplQ*	BN194_25950	K0N841	2.14	0.90	1.87
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA*	BN194_11290	K0MU90	2.30	0.89	1.86
UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	3.22	0.87	1.83
Glycine cleavage system H protein	Amino acid-related metabolism	*gcvH*	BN194_13700	K0N4K8	2.33	0.87	1.82
Lipoprotein	ABC-type transporter systems	*metQ_2*	BN194_13740	K0MV23	4.30	0.86	1.81
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	3.71	0.85	1.81
Single-stranded DNA-binding protein (SSB)	DNA replication-related	*ssb*	BN194_00110	K0N1C2	3.05	0.85	1.81
Hex regulon repressor	Transcriptional regulation		BN194_02320	K0N7J9	1.01	0.84	1.79
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	2.37	0.84	1.79
Transcriptional regulator, XRE family	Transcriptional regulation		BN194_30170	K0NDP4	3.32	0.82	1.77
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	*ppaC*	BN194_16110	K0N4Z4	2.77	0.82	1.76
Transcriptional regulator, xre family	Transcriptional regulation		BN194_05600	K0N260	2.69	0.81	1.75

ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_07700	K0N2V5	3.46	0.79	1.73
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	*ybeY*	BN194_17010	K0N594	1.18	0.78	1.72
LexA repressor (EC 3.4.21.-) (EC 3.4.21.88)	DNA repair/recombination	*lexA*	BN194_07970	K0N944	0.18	0.78	1.72
Cell growth regulatory protein	*IS elements/foreign DNA defense*		BN194_00940	K0MRU4	0.95	0.77	1.70
Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	0.39	0.76	1.69
Uncharacterized protein	Unknown/uncharacterized		BN194_00400	K0N116	2.35	0.75	1.68
Uncharacterized protein	Unknown/uncharacterized		BN194_27210	K0N7Q6	2.60	0.74	1.67
Penicillin-binding protein 1A	Cell wall biogenesis	*ponA*	BN194_16720	K0NAU3	3.88	0.73	1.66
Phosphate-binding protein pstS 1	ABC-type transporter systems	*pstS1*	BN194_10240	K0MTZ5	3.24	0.72	1.65
Glutathione peroxidase	Cell defense/detoxification	*gpo*	BN194_09780	K0N6T6	2.72	0.70	1.62
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	*gltX*	BN194_24470	K0NC38	3.37	0.66	1.58
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC_2,deoC*	BN194_02790	K0MSB5	1.86	0.66	1.58
Cell division protein FtsX	Cytokinesis	*ftsX*	BN194_10200	K0N3G0	2.89	0.66	1.58
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	1.36	0.65	1.57
Uridine kinase (EC 2.7.1.48)		*udk*	BN194_18540	K0MW76	0.39	0.64	1.56
Transcriptional regulator GltC	Transcriptional regulation	*nac*	BN194_16620	K0NAT7	2.48	0.63	1.55
Probable fatty acid methyltransferase (EC 2.1.1.-)	Lipid-related metabolism		BN194_22460	K0N6M0	4.25	0.62	1.54
Glycine betaine/carnitine/choline transport ATP-binding protein OpuCA	ABC-type transporter systems	*opuCA*	BN194_00680	K0N4E4	3.68	0.62	1.54
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	*glcK*	BN194_18420	K0NB57	2.37	0.62	1.53
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	*hslV*	BN194_16000	K0N542	1.93	0.61	1.52
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	*tsf*	BN194_17670	K0NB01	3.30	0.60	1.51

Cytochrome d ubiquinol oxidase subunit 1 (EC 1.10.3.-)	Membrane bioenergetics	*cydA_2*	BN194_23410	K0N6Y2	0.34	0.60	1.51
UPF0473 protein BN194_08530	Unknown/uncharacterized		BN194_08530	K0N6K6	2.11	0.59	1.51
Uncharacterized lipoprotein yerH	General prediction only	*yerH*	BN194_11940	K0MUH2	2.77	0.59	1.50
Chaperone protein ClpB	Protein folding/turnover	*clpB*	BN194_15500	K0N4Z8	1.42	0.58	1.50
Fumarate hydratase class II (Fumarase C) (EC 4.2.1.2)	Tricarboxylic acid pathway	*fumC*	BN194_25340	K0MXL5	3.00	0.58	1.49
Uncharacterized protein	Unknown/uncharacterized		BN194_12110	K0N410	0.95	0.56	1.47
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	*pta*	BN194_11340	K0MU95	3.02	0.55	1.46
Cytidine deaminase (EC 3.5.4.5)	Nucleic acid/nucleotide metabolism	*cdd*	BN194_17000	K0N5D8	1.49	0.54	1.46
Manganese ABC transporter substrate-binding lipoprotein	ABC-type transporter systems	*fimA*	BN194_25450	K0N7Y2	1.73	0.54	1.46
Putative thiamine pyrophosphate-containing protein ydaP	Carbohydrate-related metabolism	*ydaP*	BN194_05070	K0N8B1	0.34	0.53	1.44
UPF0346 protein BN194_15870	Unknown/uncharacterized		BN194_15870	K0NAN2	0.48	0.53	1.44
Transcriptional regulator	Transcriptional regulation		BN194_16100	K0N551	1.78	0.53	1.44
Penicillin acylase (EC 3.5.1.11)	Cell defense/detoxification		BN194_04910	K0N2B8	1.33	0.52	1.43
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_3*	BN194_29920	K0NDN0	1.43	0.51	1.42
FemAB family protein	General prediction only		BN194_22880	K0NA57	2.08	0.50	1.41
Double-stranded beta-helix related protein	Transcriptional regulation		BN194_11420	K0N9U8	1.88	0.49	1.41
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	*ohrR*	BN194_10500	K0N3J7	0.74	0.49	1.40
Uncharacterized protein	*Nucleic acid/nucleotide metabolism*		BN194_27260	K0N7R1	0.91	0.49	1.40
FMN-binding domain protein	General prediction only		BN194_24320	K0NC29	3.20	0.48	1.39
Uncharacterized protein YneR	General prediction only	*yneR*	BN194_18480	K0N9C1	0.41	0.48	1.39
Probable flavodoxin-1	General prediction only	*ykuN*	BN194_01860	K0N1P2	0.51	0.47	1.38
Uncharacterized protein	Unknown/uncharacterized		BN194_15520	K0NAK2	0.53	0.47	1.38

Uncharacterized protein ypuA	Unknown/uncharacterized	*ypuA*	BN194_27250	K0N8I3	1.50	0.46	1.38
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	*xpt*	BN194_12490	K0MUR6	1.94	0.46	1.37
Membrane protein	Unknown/uncharacterized		BN194_22700	K0N7C6	0.57	0.45	1.36
Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	*gpsB*	BN194_16690	K0MVN5	1.67	0.44	1.36
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	*hprK*	BN194_10330	K0N6Y3	2.94	0.44	1.36
Nod factor export ATP-binding protein I (EC 3.6.3.-)	ABC-type transporter systems	*nodI*	BN194_06850	K0N2J7	0.54	0.44	1.36
Probable dipeptidase A (EC 3.4.-.-)	Amino acid-related metabolism	*pepDA*	BN194_00410	K0N1E0	0.46	0.43	1.34
Uncharacterized ABC transporter ATP-binding protein YfiB	ABC-type transporter systems	*yfiB*	BN194_06890	K0MT56	0.96	0.42	1.33
Uncharacterized protein yqgF	Cell wall biogenesis	*yqgF*	BN194_18440	K0MW71	1.01	0.40	1.32
Uncharacterized protein	Unknown/uncharacterized		BN194_12200	K0N464	0.16	0.40	1.32
Bifunctional protein BirA (EC 6.3.4.15)	Lipid-related metabolism	*birA*	BN194_08790	K0MTP3	1.38	0.39	1.31
Acetyltransferase	General prediction only		BN194_08200	K0N2Z8	1.36	0.39	1.31
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	*atpG*	BN194_13610	K0N4D3	2.67	0.39	1.31
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	*rbfA*	BN194_17540	K0MVV7	1.66	0.38	1.31
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*yqeC*	BN194_02330	K0N532	0.20	0.38	1.30
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	*rpoA*	BN194_25960	K0N7E5	3.70	0.38	1.30
Methionine import ATP-binding protein MetN (EC 3.6.3.-)	ABC-type transporter systems	*metN*	BN194_13750	K0N4L1	3.93	0.38	1.30
Uncharacterized protein	Unknown/uncharacterized		BN194_17360	K0N5B9	0.17	0.37	1.29
Uncharacterized protein yeaC		*yeaC*	BN194_29960	K0N8I6	1.37	0.37	1.29
NifU-like protein	Cofactor-related metabolism	*nifU*	BN194_13800	K0N4L4	0.84	0.36	1.29
N5-carboxyaminoimidazole ribonucleotide mutase (N5-CAIR mutase) (EC 5.4.99.18) (5-(carboxyamino)imidazole ribonucleotide mutase)	Nucleic acid/nucleotide metabolism	*purE*	BN194_19380	K0N9H9	1.23	0.36	1.28

Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03000	K0N1P6	0.54	0.35	1.28
Transcription termination/antitermination protein NusA	Transcription-associated proteins	*nusA*	BN194_17580	K0N927	1.57	0.35	1.28
Cell division ATP-binding protein FtsE	Cytokinesis	*ftsE*	BN194_10190	K0MTZ2	2.11	0.35	1.28
Archaeal fructose-1,6-bisphosphatase related enzyme of inositol monophosphatase family	*Carbohydrate-related metabolism*		BN194_15140	K0MVB0	1.54	0.34	1.26
Uncharacterized protein yjdJ	General prediction only	*yjdJ*	BN194_24650	K0N7R2	0.45	0.34	1.26
Protein dedA	Unknown/uncharacterized	*dedA*	BN194_08930	K0N6M9	0.12	0.33	1.26
Integral membrane protein	Unknown/uncharacterized		BN194_07890	K0MTI0	0.20	0.33	1.25
Serine/threonine-protein kinase PrkC (EC 2.7.11.1)	Posttranslational modification	*prkC*	BN194_18020	K0NB40	0.31	0.32	1.25
Exopolyphosphatase	Membrane bioenergetics		BN194_27280	K0NAV4	0.15	0.31	1.24
Uncharacterized protein	Unknown/uncharacterized		BN194_23540	K0MXB4	1.22	0.30	1.23
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_2*	BN194_29910	K0N8I1	1.98	0.30	1.23
Exodeoxyribonuclease (EC 3.1.11.2)	DNA repair/recombination	*exoA*	BN194_11390	K0MUA0	0.40	0.28	1.22
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	*proC*	BN194_19900	K0N677	1.45	0.27	1.21
30S ribosomal protein S10	Ribosomal proteins	*rpsJ*	BN194_26230	K0NAM5	0.77	0.27	1.21
Uncharacterized protein ACIAD3023	Cell defense/detoxification		BN194_07010	K0N2T5	0.09	0.25	1.19
GTPase Era	tRNA/Ribosome assembly/processing	*era*	BN194_16990	K0MVQ8	0.34	0.25	1.19
Chaperone protein ClpB	Protein folding/turnover	*clpB_2*	BN194_26350	K0N887	1.16	0.25	1.19
DegV domain-containing protein SP_1112	Unknown/uncharacterized		BN194_15830	K0N8F3	1.35	0.25	1.19
GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*relA*	BN194_17230	K0N8Y0	0.52	0.24	1.18
Protein RibT (EC 2.3.1.-)	Cofactor-related metabolism	*ribT*	BN194_15620	K0NAL0	0.47	0.24	1.18
Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	*plsX*	BN194_17940	K0MW37	0.30	0.23	1.17

CBS domain-containing protein ykuL	Unknown/uncharacterized	*ykuL*	BN194_08670	K0N981	0.57	0.23	1.17
Uncharacterized protein ykuJ	Unknown/uncharacterized	*ykuJ*	BN194_09100	K0N348	0.35	0.22	1.17
Ribosomal RNA small subunit methyltransferase H (EC 2.1.1.199) (16S rRNA m(4)C1402 methyltransferase) (rRNA (cytosine-N(4)-)-methyltransferase RsmH)	tRNA/Ribosome assembly/processing	*rsmH*	BN194_14680	K0N814	0.39	0.22	1.16
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	*rnr*	BN194_11100	K0N3S4	1.93	0.22	1.16
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	*tpiA*	BN194_11030	K0N736	0.66	0.21	1.16
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	*prfA*	BN194_13510	K0N4C6	0.61	0.21	1.15
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	*ftsY*	BN194_17850	K0N5R8	1.15	0.19	1.14
30S ribosomal protein S14 type Z	Ribosomal proteins	*rpsZ,rpsN*	BN194_26090	K0MXS9	0.39	0.19	1.14
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	*dnaN*	BN194_00020	K0N6S3	1.46	0.19	1.14
30S ribosomal protein S18	Ribosomal proteins	*rpsR*	BN194_00120	K0N6T2	0.17	0.18	1.14
Zinc metalloprotease (EC 3.4.24.-)	General prediction only	*eep*	BN194_17620	K0NAZ9	0.55	0.17	1.12
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	0.90	0.17	1.12
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	*ispA*	BN194_18180	K0N9A2	0.10	0.16	1.12
Uncharacterized protein	Unknown/uncharacterized		BN194_21170	K0NBJ9	0.21	0.16	1.12
Uncharacterized protein			BN194_02080	K0N4Z7	0.24	0.16	1.11
Transcriptional regulator, xre family	Transcriptional regulation		BN194_23510	K0N6Y7	0.96	0.15	1.11
Uncharacterized protein	Unknown/uncharacterized		BN194_20190	K0MWI0	0.41	0.15	1.11
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	0.24	0.15	1.11
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Cobalamin-independent methionine synthase) (Methionine synthase, vitamin-B12 independent isozyme)	Amino acid-related metabolism	*metE*	BN194_06880	K0N658	0.62	0.15	1.11

Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	*prfB*	BN194_10180	K0N6W9	0.96	0.15	1.11
Septum site-determining protein DivIVA	Cytokinesis	*divIVA*	BN194_14800	K0N4T8	0.57	0.14	1.10
MFS permease-like protein	Other transporter proteins		BN194_06910	K0N2S6	0.26	0.14	1.10
tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA (guanine(46)-N(7))-methyltransferase) (tRNA(m7G46)-methyltransferase)	tRNA/Ribosome assembly/processing	*trmB*	BN194_19000	K0N606	0.22	0.13	1.09
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	*atpD*	BN194_13620	K0NAB3	0.61	0.13	1.09
Putative nrdI-like protein	*Nucleic acid/nucleotide metabolism*		BN194_08250	K0N300	0.37	0.12	1.09
Cold shock protein 1	Transcription-associated proteins	*csp*	BN194_06990	K0MT67	0.21	0.11	1.08
3-keto-L-gulonate-6-phosphate decarboxylase sgbH (EC 4.1.1.85)	Carbohydrate-related metabolism	*sgbH*	BN194_28550	K0N8W6	0.05	0.11	1.08
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25570	K0NCD4	0.59	0.10	1.08
30S ribosomal protein S11	Ribosomal proteins	*rpsK*	BN194_25970	K0NCJ0	0.20	0.09	1.07
50S ribosomal protein L1	Ribosomal proteins	*rplA*	BN194_24150	K0N7M7	0.79	0.08	1.06
50S ribosomal protein L5	Ribosomal proteins	*rplE*	BN194_26100	K0N859	0.53	0.08	1.06
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	*nusB*	BN194_18220	K0NB49	0.09	0.07	1.05
Coenzyme A biosynthesis bifunctional protein CoaBC (EC 4.1.1.36) (EC 6.3.2.5)		*coaBC*	BN194_18090	K0MW49	0.20	0.07	1.05
Phage capsid protein	Prophage genome		BN194_30330	K0NBD3	0.07	0.06	1.04
Protein hit	tRNA aminoacyl synthesis	*hit*	BN194_19040	K0MWA8	0.13	0.06	1.04
6-phospho-beta-galactosidase (EC 3.2.1.85) (Beta-D-phosphogalactoside galactohydrolase) (P-beta-Gal)	Carbohydrate-related metabolism	*lacG*	BN194_07320	K0N8W7	0.03	0.06	1.04
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	0.58	0.06	1.04
Probable transcriptional regulatory protein BN194_11600	Transcriptional regulation		BN194_11600	K0N3Z3	0.07	0.05	1.03
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB*	BN194_13410	K0N4C0	0.03	0.05	1.03
Aldose 1-epimerase	*Central glycolytic/intermediary pathways*		BN194_16020	K0NAP4	0.18	0.04	1.03

Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	0.06	0.04	1.03
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	*clpE*	BN194_19450	K0N644	0.22	0.03	1.02
Bifunctional protein GlmU	Cell wall biogenesis	*glmU*	BN194_26940	K0MY10	0.11	0.02	1.02
Diaminopimelate decarboxylase (DAP decarboxylase) (DAPDC) (EC 4.1.1.20)	Amino acid-related metabolism	*lysA*	BN194_01030	K0N4I7	0.01	0.02	1.01
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	*tig*	BN194_15330	K0N884	0.06	0.02	1.01
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	*ptsH*	BN194_19430	K0N9I2	0.04	0.01	1.01
Uncharacterized protein	Unknown/uncharacterized		BN194_29560	K0N8E9	0.00	0.01	1.01
ABC-type phosphate/phosphonate transport system,periplasmic component	*ABC-type transporter systems*		BN194_25680	K0NAI1	0.02	0.00	1.00
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	*pth*	BN194_26550	K0N8B3	0.02	-0.01	-1.01
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	*pyrC*	BN194_16470	K0NAS6	0.02	-0.01	-1.01
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB1,pstB*	BN194_10270	K0N9K1	0.02	-0.02	-1.01
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD*	BN194_17920	K0NB35	0.07	-0.02	-1.01
DNA topoisomerase 4 subunit B (EC 5.99.1.3) (Topoisomerase IV subunit B)	DNA replication-related	*parE*	BN194_16050	K0N545	0.47	-0.04	-1.03
Septum formation inhibitor MinC, C-terminal domain family	Cytokinesis	*minC*	BN194_14580	K0N805	0.16	-0.04	-1.03
Integral membrane protein	Unknown/uncharacterized		BN194_02590	K0MS97	0.06	-0.05	-1.03
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrD*	BN194_16440	K0MVL3	0.17	-0.05	-1.03
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	*yclJ*	BN194_11790	K0MUE5	0.14	-0.05	-1.03
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	*pepV*	BN194_08800	K0N324	0.17	-0.05	-1.04
Uncharacterized protein	Unknown/uncharacterized		BN194_08020	K0N947	0.50	-0.05	-1.04
Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	*adk*	BN194_26010	K0N7F0	0.15	-0.06	-1.04
Uncharacterized protein	Protein folding/turnover		BN194_19460	K0N5T8	0.56	-0.07	-1.05
Uncharacterized protein Lin2081	Cell defense/detoxification		BN194_14850	K0N4U3	0.37	-0.07	-1.05

GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	0.24	-0.08	-1.05
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP_2, acpP*	BN194_22590	K0MX45	0.09	-0.08	-1.06
Uncharacterized protein	General prediction only		BN194_21910	K0N6F1	0.14	-0.08	-1.06
Uncharacterized protein	Unknown/uncharacterized		BN194_29850	K0N968	0.34	-0.09	-1.06
Putative transcriptional regulator (DtxR family)	Transcriptional regulation		BN194_08410	K0N354	0.34	-0.10	-1.07
4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase) (EC 1.17.1.8)	Amino acid-related metabolism	*dapB*	BN194_01000	K0N166	0.12	-0.10	-1.07
Probable tRNA sulfurtransferase (EC 2.8.1.4) (Sulfur carrier protein ThiS sulfurtransferase) (Thiamine biosynthesis protein ThiI) (tRNA 4-thiouridine synthase)	Cofactor-related metabolism	*thiI*	BN194_14480	K0N7Z7	0.55	-0.11	-1.08
Pur operon repressor	Transcriptional regulation	*purR_2*	BN194_26960	K0N7M9	1.12	-0.11	-1.08
Uncharacterized protein	Posttranslational modification	*pp2C*	BN194_18030	K0N993	0.05	-0.12	-1.08
Uncharacterized protein yslB	Unknown/uncharacterized	*yslB*	BN194_08630	K0N6L4	0.55	-0.12	-1.09
Transport protein	Other transporter proteins		BN194_00630	K0N4D9	0.08	-0.13	-1.09
Nucleoid-associated protein BN194_23980	General prediction only		BN194_23980	K0NA95	0.14	-0.13	-1.09
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	*eno*	BN194_11040	K0MU67	0.48	-0.13	-1.09
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	*rex_2,rex*	BN194_23820	K0NBZ5	0.75	-0.13	-1.09
Penicillin-binding protein 2B	Cytokinesis	*pbpB*	BN194_14700	K0N4S9	0.63	-0.13	-1.10
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	*dacA*	BN194_02140	K0MS53	1.97	-0.13	-1.10
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	*queA*	BN194_08370	K0N965	1.50	-0.14	-1.10
tRNA pseudouridine synthase B (EC 5.4.99.25) (tRNA pseudouridine(55) synthase) (tRNA pseudouridylate synthase) (tRNA-uridine isomerase)	tRNA/Ribosome assembly/processing	*truB*	BN194_17520	K0NAZ5	0.08	-0.14	-1.10
CutC-like protein M6_Spy0363	Cell defense/detoxification		BN194_09910	K0N3H0	0.60	-0.16	-1.11
Xanthine/uracil/vitamin C permease	Other transporter proteins		BN194_01470	K0N796	2.27	-0.16	-1.12

GNAT family acetyltransferase	General prediction only		BN194_01510	K0N1L8	0.29	-0.16	-1.12
Sorbitol PTS, EIIA	Phosphotransferase systems		BN194_09940	K0MTX4	0.47	-0.17	-1.12
Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (EC 5.3.3.2) (Isopentenyl diphosphate:dimethylallyl diphosphate isomerase) (Isopentenyl pyrophosphate isomerase) (Type 2 isopentenyl diphosphate isomerase)	Lipid-related metabolism	*fni*	BN194_16840	K0MVP7	0.15	-0.17	-1.12
Uncharacterized protein	Unknown/uncharacterized		BN194_19810	K0N5W5	1.05	-0.17	-1.13
Putative gluconeogenesis factor	General prediction only	*yjiF*	BN194_10480	K0N6Z4	0.07	-0.17	-1.13
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	*tuf*	BN194_15310	K0N4R1	1.82	-0.18	-1.14
ABC transporter glutamine-binding protein glnH	ABC-type transporter systems	*glnH*	BN194_21430	K0N9Y4	0.67	-0.19	-1.14
Uncharacterized protein	Unknown/uncharacterized		BN194_01870	K0N7D4	0.74	-0.21	-1.15
50S ribosomal protein L3	Ribosomal proteins	*rplC*	BN194_26220	K0NCN1	0.81	-0.21	-1.16
Uncharacterized protein SE_0534	*tRNA/Ribosome assembly/processing*		BN194_10150	K0N3F2	0.53	-0.22	-1.16
Recombination protein RecR	DNA repair/recombination	*recR*	BN194_23970	K0NC03	0.45	-0.22	-1.17
30S ribosomal protein S5	Ribosomal proteins	*rpsE*	BN194_26050	K0N853	1.42	-0.22	-1.17
Cell shape-determining protein MreC (Cell shape protein MreC)	Cytokinesis	*mreC*	BN194_14560	K0N4K0	0.93	-0.23	-1.17
Ribonuclease Z (RNase Z) (EC 3.1.26.11) (tRNA 3 endonuclease) (tRNase Z)	tRNA/Ribosome assembly/processing	*rnz*	BN194_15470	K0NAK0	0.08	-0.23	-1.18
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	*gyrA*	BN194_00070	K0N6S7	0.24	-0.24	-1.18
Regulatory protein vanR	Signal transduction	*vanR*	BN194_02120	K0N7G4	1.39	-0.24	-1.18
Mannose permease IID component	Phosphotransferase systems	*manZ*	BN194_02990	K0MSE1	1.10	-0.25	-1.19
Uncharacterized protein ytoI	Transcriptional regulation	*ytoI*	BN194_08440	K0MTM0	0.34	-0.25	-1.19
Probable glutamine ABC transporter permease protein glnP	ABC-type transporter systems	*glnP*	BN194_21410	K0N6A4	0.10	-0.26	-1.20
Mannose permease IID component	Phosphotransferase systems	*manZ_9*	BN194_29700	K0N954	1.39	-0.27	-1.20
Spermidine/putrescine-binding periplasmic protein	ABC-type transporter systems	*potD*	BN194_11460	K0N3U9	0.72	-0.27	-1.20

Transcriptional regulator lytR	Transcriptional regulation	*lytR_3*	BN194_21700	K0N6U3	2.83	-0.27	-1.21
Uncharacterized protein	Unknown/uncharacterized		BN194_15540	K0MVD8	0.41	-0.28	-1.21
UPF0755 protein yrrL	Unknown/uncharacterized	*yrrL*	BN194_18550	K0N5W7	1.21	-0.28	-1.22
Probable amino-acid ABC transporter-binding protein HI_1080	*ABC-type transporter systems*		BN194_06710	K0N2R6	2.21	-0.29	-1.22
Transcription termination/antitermination protein NusG	Transcription-associated proteins	*nusG*	BN194_24260	K0N730	0.71	-0.31	-1.24
Probable catabolite control protein A	Transcriptional regulation	*ccpA*	BN194_08750	K0N323	1.43	-0.31	-1.24
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	*groS,grES*	BN194_23760	K0N700	0.97	-0.31	-1.24
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25510	K0N7B2	0.80	-0.31	-1.24
Transaldolase (EC 2.2.1.2)	Central glycolytic/intermediary pathways	*fsa*	BN194_28440	K0MYF0	0.32	-0.32	-1.25
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	Protein folding/turnover		BN194_08960	K0N387	1.18	-0.33	-1.26
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	*guaB*	BN194_02100	K0N1G3	1.66	-0.34	-1.27
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	*atpA*	BN194_13600	K0N4K1	2.76	-0.35	-1.27
Cysteine desulfurase (EC 2.8.1.7)	Cofactor-related metabolism	*csd*	BN194_13790	K0MV25	0.74	-0.35	-1.28
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	*yqjQ*	BN194_15480	K0N8A1	1.10	-0.35	-1.28
Uncharacterized protein	Transcriptional regulation		BN194_22710	K0N6Q3	0.16	-0.36	-1.28
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	*phoU*	BN194_10290	K0MTZ9	1.26	-0.37	-1.29
Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	*fba_2*	BN194_05060	K0N2C9	1.16	-0.37	-1.29
Uncharacterized protein MJ1445	General prediction only		BN194_08880	K0N6M7	0.85	-0.38	-1.30
Protein translocase subunit SecA	Protein export	*secA*	BN194_10170	K0N9J2	1.96	-0.39	-1.31
Uncharacterized protein	Cell wall biogenesis		BN194_21890	K0MWX1	0.74	-0.39	-1.31
Uncharacterized metallophosphoesterase yunD	Nucleic acid/nucleotide metabolism	*yunD*	BN194_08890	K0MTQ0	1.78	-0.39	-1.31

DNA replication protein dnaD	DNA replication-related	*dnaD*	BN194_16750	K0N5B1	0.70	-0.40	-1.32
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	*fabZ_2*	BN194_22620	K0NBT3	1.42	-0.40	-1.32
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	*yqeH*	BN194_18740	K0MW90	0.94	-0.40	-1.32
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA*	BN194_17880	K0N983	1.73	-0.40	-1.32
Uncharacterized protein	Unknown/uncharacterized		BN194_12100	K0N456	0.25	-0.40	-1.32
DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	1.96	-0.41	-1.32
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	*murD*	BN194_14720	K0NAG5	1.88	-0.41	-1.33
Uncharacterized protein yqhL	General prediction only	*yqhL*	BN194_18410	K0N5L5	1.30	-0.42	-1.34
Glycine betaine/carnitine/choline-binding protein OpuCC	ABC-type transporter systems	*opuCC*	BN194_00670	K0N6Z3	1.88	-0.42	-1.34
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA*	BN194_18520	K0NB62	1.99	-0.43	-1.34
Cold shock-like protein CspLA	Transcription-associated proteins	*cspLA*	BN194_12460	K0N438	0.43	-0.44	-1.36
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA_2*	BN194_20640	K0MWL6	2.18	-0.45	-1.36
Phosphohydrolase (MutT/nudix family protein)	General prediction only		BN194_27160	K0N7P9	0.39	-0.45	-1.37
Uncharacterized aminotransferase SSO0104 (EC 2.6.1.-)	*Amino acid-related metabolism*		BN194_27600	K0N8N4	0.18	-0.46	-1.38
Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	0.99	-0.48	-1.40
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	3.70	-0.48	-1.40
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	2.50	-0.49	-1.41
Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-)	Nucleic acid/nucleotide metabolism	*purK*	BN194_12510	K0N441	1.82	-0.49	-1.41
Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase)	Nucleic acid/nucleotide metabolism	*pyrB*	BN194_16480	K0N8N2	1.98	-0.49	-1.41
Uncharacterized protein	*ABC-type transporter systems*		BN194_21220	K0NBK2	2.97	-0.50	-1.41
Transcriptional regulator, TetR family	Transcriptional regulation		BN194_12190	K0MUM1	0.70	-0.50	-1.41
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	*prsA*	BN194_19060	K0N5Q8	2.61	-0.51	-1.42

Sensory transduction protein BceR	Signal transduction	*bceR_2*	BN194_19250	K0N630	1.79	-0.51	-1.42
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	*ndk*	BN194_08160	K0N340	1.95	-0.51	-1.43
Aspartate racemase (EC 5.1.1.13)	*Amino acid-related metabolism*		BN194_02170	K0N7H2	1.66	-0.52	-1.43
SPFH/Band 7/PHB domain protein	Unknown/uncharacterized		BN194_29820	K0NDM1	0.52	-0.56	-1.47
3-hydroxy-3-methylglutaryl coenzyme A reductase (HMG-CoA reductase) (EC 1.1.1.88)	Lipid-related metabolism	*mvaA*	BN194_19690	K0MWE8	0.80	-0.56	-1.47
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	*pdhD*	BN194_15110	K0N4P1	2.05	-0.57	-1.48
Uncharacterized protein	Unknown/uncharacterized		BN194_27530	K0NAX5	2.13	-0.57	-1.48
Calcium-transporting ATPase lmo0841 (EC 3.6.3.8)	Other transporter proteins		BN194_19820	K0NBC5	2.60	-0.57	-1.49
UPF0659 protein YMR090W	General prediction only	*ylbE*	BN194_07030	K0N671	3.44	-0.57	-1.49
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1_2*	BN194_12550	K0N496	2.48	-0.58	-1.50
UPF0237 protein BN194_09820	Unknown/uncharacterized		BN194_09820	K0N9F9	1.18	-0.59	-1.50
Uncharacterized protein	Unknown/uncharacterized		BN194_24220	K0NC21	0.54	-0.60	-1.51
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC*	BN194_17890	K0MW34	1.64	-0.60	-1.51
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	*fabH*	BN194_22600	K0N7B0	2.33	-0.60	-1.52
Uncharacterized protein ytxK	DNA repair/recombination	*ytxK*	BN194_11680	K0N791	1.95	-0.60	-1.52
Signal recognition particle protein (Fifty-four homolog)	Protein export	*ffh*	BN194_17820	K0NB27	1.05	-0.60	-1.52
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	2.94	-0.60	-1.52
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	*metG*	BN194_27130	K0NAU5	2.98	-0.60	-1.52
Uncharacterized protein yueI	Unknown/uncharacterized	*yueI*	BN194_13920	K0NAC7	0.89	-0.61	-1.52
Deoxyguanosine kinase (EC 2.7.1.113)	*Nucleic acid/nucleotide metabolism*		BN194_14000	K0N4M7	0.53	-0.61	-1.53
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	*rpe*	BN194_18000	K0N5T1	1.87	-0.61	-1.53

UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	3.16	-0.61	-1.53
ABC-type Na+ efflux pump permease component-like protein	*ABC-type transporter systems*		BN194_11370	K0N9U5	1.92	-0.61	-1.53
Transcriptional repressor NrdR	Transcriptional regulation	*nrdR*	BN194_18900	K0N5Z5	1.95	-0.61	-1.53
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_3*	BN194_14020	K0NAD1	2.42	-0.62	-1.53
ABC-type uncharacterized transport system, ATPase component	*ABC-type transporter systems*		BN194_07730	K0N6C9	3.00	-0.62	-1.53
30S ribosomal protein S6	Ribosomal proteins	*rpsF*	BN194_00100	K0N0Z1	3.18	-0.62	-1.54
Uncharacterized protein	Unknown/uncharacterized		BN194_01600	K0N1B9	1.63	-0.63	-1.55
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI*	BN194_07860	K0N327	0.60	-0.63	-1.55
Dehydrogenase	General prediction only		BN194_24480	K0NAB4	0.64	-0.63	-1.55
Elongation factor G (EF-G)	Protein translation (elongation)	*fusA*	BN194_26270	K0NCN8	2.29	-0.64	-1.55
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	*dltA*	BN194_08590	K0MTN0	3.28	-0.64	-1.56
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	*pyrH*	BN194_17660	K0N5E6	2.31	-0.65	-1.57
50S ribosomal protein L18	Ribosomal proteins	*rplR*	BN194_26060	K0N7F4	1.76	-0.66	-1.58
PspC domain-containing protein	Unknown/uncharacterized	*ythC*	BN194_10300	K0N3H5	2.92	-0.66	-1.58
Glycerol-3-phosphate ABC transporter substrate-binding protein	*ABC-type transporter systems*		BN194_11260	K0N3T6	4.75	-0.66	-1.58
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	*yjlD*	BN194_24330	K0NAA7	2.59	-0.66	-1.58
Uncharacterized protein	Unknown/uncharacterized		BN194_02470	K0N7L7	4.36	-0.67	-1.59
Sorbose permease IIC component	Phosphotransferase systems	*sorA_4*	BN194_29710	K0N8G4	1.43	-0.67	-1.59
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1*	BN194_09110	K0N399	2.83	-0.67	-1.59
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	Nucleic acid/nucleotide metabolism	*tmk*	BN194_23950	K0N7L9	2.09	-0.67	-1.59
UPF0092 membrane protein yrbF	Protein export	*yrbF*	BN194_08390	K0MTL6	2.14	-0.68	-1.60
Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	*ung*	BN194_11330	K0N758	1.09	-0.68	-1.61

Response regulator ArlR	Signal transduction	*arlR*	BN194_18650	K0N5X3	0.88	-0.68	-1.61
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	*pmi*	BN194_02920	K0N7U2	3.57	-0.69	-1.61
ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	*atpF*	BN194_13580	K0N7S9	2.42	-0.69	-1.61
Predicted hydrolase of HD superfamily	General prediction only		BN194_10430	K0N6Z0	3.00	-0.69	-1.62
tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	*dus1*	BN194_26390	K0MXV9	3.19	-0.70	-1.63
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_01410	K0N1L0	3.03	-0.70	-1.63
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ*	BN194_11360	K0N3U2	1.66	-0.71	-1.64
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*pip_2*	BN194_27140	K0MY30	1.48	-0.73	-1.66
Phosphoesterase (EC 3.1.4.-)	General prediction only	*ysnB*	BN194_08650	K0N317	1.71	-0.73	-1.66
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	*grpE*	BN194_17470	K0NAZ2	1.35	-0.73	-1.66
Signal peptidase I (EC 3.4.21.89)	Protein export	*lepB*	BN194_02610	K0N1V9	1.66	-0.74	-1.67
Uncharacterized protein	Unknown/uncharacterized		BN194_16570	K0NAT3	0.48	-0.75	-1.68
Elongation factor P	Protein translation (elongation)	*efp_2*	BN194_22050	K0N712	1.50	-0.76	-1.69
Uncharacterized protein ypmR	General prediction only	*ypmR*	BN194_15840	K0MVG3	0.88	-0.76	-1.69
Uncharacterized protein	General prediction only		BN194_28370	K0NDC5	0.64	-0.76	-1.69
Uncharacterized protein	Unknown/uncharacterized		BN194_07460	K0N2W9	1.18	-0.77	-1.70
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	*maa*	BN194_30010	K0N8I9	2.30	-0.77	-1.70
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	2.58	-0.77	-1.70
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_02890	K0MSD4	1.91	-0.78	-1.72
50S ribosomal protein L31 type B	Ribosomal proteins	*rpmE2*	BN194_26770	K0NCV4	1.58	-0.78	-1.72
Oligo-1,6-glucosidase (EC 3.2.1.10)	Carbohydrate-related metabolism	*malL*	BN194_04830	K0N5P4	0.53	-0.78	-1.72
Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)	Nucleic acid/nucleotide metabolism	*pdp*	BN194_23430	K0NA73	3.06	-0.78	-1.72

Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*asnS*	BN194_16760	K0N569	5.37	-0.78	-1.72
Esterase/lipase	General prediction only	*yneB*	BN194_20230	K0N9P7	1.13	-0.79	-1.73
Uncharacterized protein	Unknown/uncharacterized		BN194_15850	K0N527	3.00	-0.80	-1.74
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB_2*	BN194_21970	K0NBP6	0.98	-0.80	-1.74
Mevalonate kinase (EC 2.7.1.36)	Lipid-related metabolism	*mvk*	BN194_12270	K0NA23	3.89	-0.80	-1.74
Thioredoxin	Posttranslational modification	*trxA_2*	BN194_08570	K0N975	1.89	-0.81	-1.75
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	*citD*	BN194_20330	K0N9Q5	0.75	-0.81	-1.76
Large-conductance mechanosensitive channel	Other transporter proteins	*mscL*	BN194_26890	K0MY02	0.98	-0.82	-1.76
Uncharacterized protein	Unknown/uncharacterized		BN194_08270	K0N959	2.08	-0.82	-1.76
DltD protein	Cell wall biogenesis		BN194_08620	K0N978	3.04	-0.82	-1.77
Thymidine kinase (EC 2.7.1.21)	Nucleic acid/nucleotide metabolism	*tdk*	BN194_13500	K0N4J4	1.62	-0.83	-1.77
Uncharacterized protein	Unknown/uncharacterized		BN194_07550	K0N2T9	0.23	-0.85	-1.80
Putative tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207) (tRNA (cytidine/uridine-2'-O-)-methyltransferase)	*tRNA/Ribosome assembly/processing*		BN194_09990	K0MTX9	2.20	-0.86	-1.81
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	*prs1_2*	BN194_30370	K0NDQ5	1.36	-0.86	-1.82
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_29810	K0N8H4	4.39	-0.87	-1.82
Protein lacX, plasmid	Carbohydrate-related metabolism	*lacX*	BN194_27070	K0NCY0	2.32	-0.87	-1.82
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	*aldB*	BN194_20140	K0MWH5	2.09	-0.87	-1.83
Glycolate oxidase subunit glcD	General prediction only	*glcD*	BN194_24440	K0MXF3	2.04	-0.87	-1.83
Probable cation-transporting ATPase exp7 (EC 3.6.3.-)	Other transporter proteins	*exp7*	BN194_08170	K0N955	3.28	-0.87	-1.83
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	*hisS*	BN194_17110	K0N5A0	3.59	-0.87	-1.83
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	*trxB*	BN194_10360	K0N3L1	3.37	-0.88	-1.84
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	*dkgB*	BN194_08260	K0N347	2.47	-0.89	-1.85

Exodeoxyribonuclease 7 small subunit (EC 3.1.11.6) (Exodeoxyribonuclease VII small subunit)	DNA repair/recombination	*xseB*	BN194_18190	K0MW55	0.89	-0.91	-1.88
Uncharacterized protein yxjH	Amino acid-related metabolism	*yxjH*	BN194_08320	K0N962	0.95	-0.93	-1.91
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	*deoD*	BN194_02810	K0N1Z0	2.43	-0.94	-1.92
Uncharacterized protein	Unknown/uncharacterized		BN194_29450	K0N932	2.94	-0.94	-1.92
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	*ddl*	BN194_01390	K0MRY4	2.80	-0.94	-1.92
tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	tRNA/Ribosome assembly/processing	*mnmG,gidA*	BN194_30590	K0MYX4	1.83	-0.94	-1.92
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	*tpx*	BN194_08090	K0MTJ5	2.64	-0.95	-1.94
Uncharacterized protein			BN194_21520	K0NBL8	0.32	-0.96	-1.94
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	*murA2,murA*	BN194_26780	K0NAR9	1.31	-0.96	-1.94
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdF*	BN194_16610	K0N552	2.87	-0.96	-1.95
50S ribosomal protein L4	Ribosomal proteins	*rplD*	BN194_26210	K0N7H0	3.72	-0.96	-1.95
Uncharacterized protein	General prediction only		BN194_17420	K0NAY8	2.41	-0.96	-1.95
Cell division protein FtsA	Cytokinesis	*ftsA*	BN194_14750	K0N4T3	3.21	-0.96	-1.95
Replicative DNA helicase (EC 3.6.4.12)	DNA replication-related	*dnaC*	BN194_01140	K0MRW2	2.18	-0.99	-1.98
Anaerobic ribonucleoside-triphosphate reductase-activating protein (EC 1.97.1.-)	Nucleic acid/nucleotide metabolism	*nrdG*	BN194_19270	K0NB93	2.38	-0.99	-1.99
ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	*clpX*	BN194_15340	K0MVC6	3.19	-0.99	-1.99
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	*fabK*	BN194_22580	K0NA38	2.64	-1.00	-2.00
Cell division protein DivIB	Cytokinesis	*divIB*	BN194_14740	K0MV80	1.26	-1.00	-2.00
Probable copper-transporting P-type ATPase B (EC 3.6.3.-)	Other transporter proteins	*copB*	BN194_19280	K0N9H1	1.45	-1.01	-2.01
Uncharacterized RNA pseudouridine synthase YhcT (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*yhcT_2*	BN194_20220	K0NBE7	0.55	-1.02	-2.03
Uncharacterized protein				K0N2Q1;K0MXJ1	1.90	-1.03	-2.04

Uncharacterized protein ywnB	General prediction only	*ywnB_2*	BN194_20050	K0N687	2.92	-1.03	-2.05
Uncharacterized protein	Unknown/uncharacterized		BN194_13400	K0N4I9	0.58	-1.03	-2.05
tRNA (Adenine(22)-N(1))-methyltransferase (EC 2.1.1.217)	tRNA/Ribosome assembly/processing	*trmK*	BN194_16910	K0N584	2.01	-1.04	-2.05
Inner membrane amino-acid ABC transporter permease protein yecS	ABC-type transporter systems	*yecS_3*	BN194_29780	K0NB99	1.94	-1.04	-2.05
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	*clpP_2, clpP*	BN194_10510	K0N3M4	3.03	-1.04	-2.05
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	*zwf*	BN194_08420	K0N966	3.76	-1.04	-2.05
Uncharacterized protein	Unknown/uncharacterized		BN194_01150	K0N181	2.16	-1.04	-2.06
Phosphoenolpyruvate-dependent sugar phosphotransferase system EIIA, galactitol/fructose specific	Phosphotransferase systems		BN194_27050	K0N8F9	3.06	-1.04	-2.06
Uncharacterized isochorismatase family protein pncA (EC 3.-.-.-)	General prediction only	*pncA*	BN194_29120	K0NDH8	0.72	-1.05	-2.07
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	*uvrA*	BN194_10450	K0N3J2	3.95	-1.05	-2.07
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	*fabD*	BN194_22570	K0NBT1	3.54	-1.05	-2.08
Uncharacterized protein	Unknown/uncharacterized		BN194_13840	K0MV29	1.11	-1.06	-2.08
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	*apt*	BN194_17380	K0N902	3.38	-1.07	-2.10
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	*yhfP*	BN194_07740	K0MTE1	3.44	-1.07	-2.10
UPF0342 protein yheA	Unknown/uncharacterized	*yheA*	BN194_19080	K0N9F7	2.45	-1.08	-2.11
Zinc-transporting ATPase (EC 3.6.3.5)	Other transporter proteins	*zosA_2*	BN194_29430	K0NB79	3.49	-1.08	-2.12
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	4.03	-1.09	-2.13
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	Central glycolytic/intermediary pathways	*gap*	BN194_11010	K0N3R3	3.76	-1.10	-2.14
Uncharacterized protein ybfG	General prediction only	*ybfG*	BN194_00330	K0N4B3	3.82	-1.12	-2.17
Uncharacterized protein	Unknown/uncharacterized		BN194_11890	K0MUG0	3.06	-1.12	-2.17

Glucose 1-dehydrogenase 2 (EC 1.1.1.47)	Central glycolytic/intermediary pathways	*gdhII*	BN194_23130	K0NA64	0.87	-1.13	-2.18
Phosphatase YidA (EC 3.1.3.-)	General prediction only	*yidA*	BN194_28520	K0NDD5	4.10	-1.13	-2.18
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*ileS*	BN194_14810	K0N4L9	4.82	-1.13	-2.18
PTS family mannose/fructose/sorbose porter component IIC	Phosphotransferase systems		BN194_02980	K0N5D0	4.16	-1.13	-2.19
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_2*	BN194_20600	K0N6C6	4.96	-1.14	-2.20
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF*	BN194_17910	K0N5I3	2.74	-1.14	-2.20
Transcriptional regulator, PadR-like family	Transcriptional regulation		BN194_26580	K0NAQ3	0.35	-1.14	-2.20
Hydrolase of the alpha/beta superfamily	General prediction only		BN194_08240	K0MTK6	2.63	-1.14	-2.21
Predicted pyrophosphatase	General prediction only		BN194_15360	K0N4R6	0.81	-1.15	-2.21
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*pcrA*	BN194_11920	K0N9Z6	2.34	-1.15	-2.21
Uncharacterized protein	Unknown/uncharacterized		BN194_08190	K0MTK3	0.47	-1.15	-2.21
Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	*nfo*	BN194_17070	K0NAW5	3.77	-1.15	-2.22
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2,lacD*	BN194_07480	K0N6A8	3.33	-1.15	-2.23
Virulence factor mviM	General prediction only	*mviM*	BN194_13310	K0N4B2	2.82	-1.15	-2.23
DegV domain-containing protein CPE0026	Unknown/uncharacterized		BN194_12060	K0N405	3.01	-1.16	-2.24
Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*leuS*	BN194_09210	K0N3A9	3.91	-1.17	-2.25
Uncharacterized protein yxkA	General prediction only	*yxkA*	BN194_27230	K0NAV1	3.26	-1.18	-2.26
YbbR-like domain-containing protein ybbR	Unknown/uncharacterized	*ybbR*	BN194_11540	K0MUB6	3.47	-1.18	-2.27
Probable ABC transporter ATP-binding protein spyM18_0273	Cofactor-related metabolism		BN194_13770	K0NAC0	2.61	-1.19	-2.28
CCA-adding enzyme (EC 2.7.7.72) (CCA tRNA nucleotidyltransferase) (tRNA CCA-pyrophosphorylase) (tRNA adenylyl-/cytidylyl-transferase) (tRNA nucleotidyltransferase) (tRNA-NT)	tRNA/Ribosome assembly/processing	*cca*	BN194_15770	K0NAM4	0.48	-1.20	-2.29

Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	*pepDB*	BN194_21110	K0N678	2.99	-1.20	-2.30
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	*typA*	BN194_15150	K0N4W9	4.39	-1.21	-2.31
HTH-type transcriptional regulator iolR	Transcriptional regulation	*iolR*	BN194_02190	K0MS58	1.91	-1.22	-2.33
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*lacC*	BN194_07470	K0N8Y4	3.76	-1.22	-2.33
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	*dnaK*	BN194_17460	K0N5C7	3.56	-1.22	-2.33
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	*pepS*	BN194_12180	K0N7D5	1.59	-1.23	-2.34
Oligoendopeptidase F homolog (EC 3.4.24.-)	Amino acid-related metabolism	*yjbG*	BN194_02530	K0N560	6.15	-1.23	-2.35
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	*asnB*	BN194_22990	K0MX90	3.68	-1.24	-2.36
Uncharacterized protein yghZ	General prediction only	*yghZ*	BN194_27510	K0N7U8	3.98	-1.24	-2.37
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	*glgC*	BN194_21600	K0N6T3	2.12	-1.25	-2.38
Multifunctional protein: 5-nucleotidase 2,3-cyclic-nucleotide 2-phosphodiesterase	Nucleic acid/nucleotide metabolism	*ushA*	BN194_15530	K0N8A9	3.55	-1.25	-2.38
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E_2,P100*	BN194_05160	K0N2D7	0.71	-1.26	-2.39
Ribosome-binding ATPase YchF	Protein translation (peptide release)	*engD,ychF*	BN194_02070	K0N7F7	4.80	-1.26	-2.40
Phosphoribosylformylglycinamidine synthase subunit PurS (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit III) (Phosphoribosylformylglycinamidine synthase subunit III)	Nucleic acid/nucleotide metabolism	*yexA,purS*	BN194_19350	K0N638	2.63	-1.27	-2.41
30S ribosomal protein S14	Ribosomal proteins	*rpsN*	BN194_09950	K0N3D1	0.65	-1.27	-2.41
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox_2*	BN194_02850	K0N1N9	3.78	-1.27	-2.42
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	*luxS*	BN194_08330	K0N6J0	2.97	-1.28	-2.43
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E,P100*	BN194_02180	K0N513	6.06	-1.29	-2.44
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE*	BN194_01720	K0N7C1	5.10	-1.29	-2.45
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA*	BN194_05120	K0N8B5	1.52	-1.29	-2.45

Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_3*	BN194_04780	K0N5N9	4.23	-1.30	-2.46
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	*fabF*	BN194_22540	K0MX40	2.76	-1.31	-2.47
Oxidoreductase YdhF (EC 1.-.-.-)	General prediction only	*ydhF*	BN194_25320	K0NCA1	3.57	-1.31	-2.47
Thioredoxin-like protein ytpP	Posttranslational modification	*ytpP*	BN194_18980	K0N9F1	2.82	-1.31	-2.47
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	*ywpJ*	BN194_11320	K0N9U2	3.49	-1.31	-2.47
Uncharacterized protein	Signal transduction		BN194_18490	K0MW74	3.54	-1.31	-2.48
Uncharacterized protein	General prediction only		BN194_14990	K0MV99	2.37	-1.31	-2.48
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD(+)])	DNA replication-related	*ligA*	BN194_11930	K0N7A9	2.16	-1.31	-2.49
Maf-like protein maf	General prediction only	*maf*	BN194_23700	K0N7K3	0.78	-1.32	-2.49
Uncharacterized protein ysxB	Ribosomal proteins	*ysxB*	BN194_18280	K0N9A9	0.74	-1.32	-2.50
Uncharacterized RNA methyltransferase lp_3226 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_19580	K0N9J4	0.71	-1.33	-2.51
Uncharacterized protein	General prediction only		BN194_21200	K0N6M8	3.07	-1.33	-2.52
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	*pdhC*	BN194_15100	K0N4W5	3.26	-1.33	-2.52
UbiE/COQ5 family methyltransferase	General prediction only		BN194_23620	K0NBY4	1.52	-1.34	-2.53
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.-)	Lipid-related metabolism	*plsC*	BN194_17710	K0N5F1	2.38	-1.34	-2.53
Putative ribosome biogenesis GTPase RsgA (EC 3.6.1.-)	tRNA/Ribosome assembly/processing	*rsgA*	BN194_18010	K0N5J0	1.08	-1.34	-2.53
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	*guaA*	BN194_21070	K0NBJ2	3.89	-1.34	-2.54
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_4*	BN194_22020	K0NBQ1	4.45	-1.35	-2.55
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	Membrane bioenergetics		BN194_18780	K0N9E0	0.97	-1.35	-2.55
UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.3.1.98) (UDP-N-acetylmuramate dehydrogenase)	Cell wall biogenesis	*murB*	BN194_11400	K0N3X0	3.57	-1.36	-2.57
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	3.70	-1.36	-2.57
Lipopolysaccharide synthesis sugar transferase	Cell wall biogenesis		BN194_21390	K0MWS4	2.34	-1.36	-2.57

GMP reductase (EC 1.7.1.7) (Guanosine 5'-monophosphate oxidoreductase)	Nucleic acid/nucleotide metabolism	*guaC*	BN194_09960	K0N3H4	4.87	-1.37	-2.58
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	*ftsH*	BN194_26460	K0N7I8	4.42	-1.37	-2.59
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	*glmM*	BN194_11550	K0N3Y7	5.79	-1.38	-2.59
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	*pgk*	BN194_11020	K0N9R1	4.28	-1.38	-2.60
Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	Nucleic acid/nucleotide metabolism	*purD*	BN194_19290	K0MWC4	3.49	-1.38	-2.61
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	*murC*	BN194_18950	K0N600	4.62	-1.39	-2.63
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	*dhaM*	BN194_04960	K0N2C2	3.77	-1.39	-2.63
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	*def*	BN194_15060	K0N4N6	2.54	-1.40	-2.64
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2_2,lacD*	BN194_27060	K0N7P0	4.62	-1.40	-2.65
Acylphosphatase	Carbohydrate-related metabolism	*acyP*	BN194_18620	K0NB65	2.76	-1.40	-2.65
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA*	BN194_08450	K0N309	6.39	-1.41	-2.65
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	*alaS*	BN194_08480	K0N6K2	3.84	-1.41	-2.67
Uncharacterized protein	Phosphotransferase systems		BN194_04820	K0N885	2.30	-1.42	-2.68
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	5.17	-1.43	-2.69
Pyridoxine 5'-phosphate oxidase V related favin-nucleotide-binding protein	Cofactor-related metabolism		BN194_01900	K0N1E7	1.85	-1.43	-2.70
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA1, greA*	BN194_02150	K0N1G7	2.24	-1.43	-2.70
Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	*phoP*	BN194_10220	K0N9J6	5.08	-1.44	-2.71
GCN5-related N-acetyltransferase	General prediction only		BN194_19760	K0N5W1	1.36	-1.44	-2.72
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrDA, pyrD*	BN194_19150	K0N623	4.79	-1.45	-2.73
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacB*	BN194_07490	K0MTB7	2.32	-1.45	-2.73

L-sorbose 1-phosphate reductase (EC 1.1.1.-)	Carbohydrate-related metabolism	*sorE*	BN194_04300	K0N1W2	2.98	-1.49	-2.81
tRNA modification GTPase MnmE (EC 3.6.-.-)	tRNA/Ribosome assembly/processing	*mnmE,trmE*	BN194_30600	K0N9F0	1.63	-1.49	-2.81
50S ribosomal protein L19	Ribosomal proteins	*rplS*	BN194_17770	K0NB12	3.99	-1.50	-2.82
NAD-dependent protein deacetylase (EC 3.5.1.-)	General prediction only	*cobB*	BN194_27190	K0MY36	1.95	-1.50	-2.83
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	*yuxL*	BN194_19910	K0N5X4	4.61	-1.52	-2.86
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*argS*	BN194_19120	K0NB86	4.91	-1.52	-2.88
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	*proS*	BN194_17610	K0N5E2	4.39	-1.52	-2.88
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*helD*	BN194_21130	K0N9W3	5.11	-1.53	-2.88
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA2,gpmA*	BN194_22740	K0MX58	3.77	-1.53	-2.89
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ_2*	BN194_20470	K0NBG3	1.11	-1.53	-2.90
Site-determining protein	Cytokinesis	*minD*	BN194_14590	K0MV70	2.80	-1.53	-2.90
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	*obg*	BN194_15440	K0MVD3	4.90	-1.54	-2.91
30S ribosomal protein S4	Ribosomal proteins	*rpsD*	BN194_14440	K0MV63	4.23	-1.54	-2.91
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	*garB*	BN194_27400	K0N8K3	5.14	-1.55	-2.93
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	*fbp*	BN194_21660	K0N6C3	2.91	-1.56	-2.94
Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	*rpiA_2, ripA*	BN194_28600	K0N8W9	3.34	-1.56	-2.94
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	*pcp*	BN194_01980	K0N4Y4	3.96	-1.56	-2.95
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP_3*	BN194_21160	K0N682	3.27	-1.58	-2.99
Protein LemA	Unknown/uncharacterized	*lemA*	BN194_27350	K0N8J7	3.96	-1.59	-3.02
Protein ytsP	Signal transduction	*ytsP*	BN194_14450	K0N4Q9	1.06	-1.60	-3.04

Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	*pyk*	BN194_15580	K0N8B6	5.16	-1.61	-3.06
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	*groL,groEL*	BN194_23750	K0N7K7	5.11	-1.62	-3.06
Type I restriction enzyme EcoR124II M protein (EC 2.1.1.72)	IS elements/foreign DNA defense	*hsdM*	BN194_22340	K0MX17	3.96	-1.62	-3.07
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification		BN194_25280	K0NAG2	1.34	-1.62	-3.07
Uncharacterized protein	Unknown/uncharacterized		BN194_01760	K0N1N3	1.67	-1.63	-3.09
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	*rnc*	BN194_17870	K0NB31	3.23	-1.63	-3.10
Uncharacterized protein YwcC	Carbohydrate-related metabolism	*ywcC*	BN194_09930	K0N6V0	3.41	-1.63	-3.10
Alanine racemase (EC 5.1.1.1)	Amino acid-related metabolism	*alr*	BN194_26680	K0NAR1	3.48	-1.63	-3.10
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	*patB_2*	BN194_09790	K0MTW3	4.13	-1.63	-3.10
Uncharacterized protein ydcI	General prediction only	*ydcI*	BN194_14310	K0N4I1	1.27	-1.64	-3.11
Uncharacterized protein	Unknown/uncharacterized		BN194_24010	K0N715	3.72	-1.64	-3.11
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	*ykwC*	BN194_02520	K0N7M3	4.48	-1.64	-3.12
Dihydrofolate reductase (EC 1.5.1.3)	Cofactor-related metabolism	*folA*	BN194_15810	K0N4W0	2.93	-1.64	-3.12
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA_2, potA*	BN194_11430	K0N765	3.88	-1.65	-3.14
18 kDa heat shock protein	Protein folding/turnover	*hsp18*	BN194_07570	K0N8Z3	0.94	-1.65	-3.15
Penicillin-binding protein 3	Cell wall biogenesis	*pbpC*	BN194_03320	K0N7W9	3.78	-1.66	-3.16
Ribosomal RNA small subunit methyltransferase G (EC 2.1.1.-) (16S rRNA 7-methylguanosine methyltransferase)	tRNA/Ribosome assembly/processing	*rsmG*	BN194_02020	K0N7F1	2.52	-1.66	-3.17
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	*mtlF*	BN194_30410	K0N8N0	3.60	-1.67	-3.18
Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Phosphotransferase system, enzyme I)		*ptsI*	BN194_19410	K0N5T2	4.15	-1.68	-3.21
Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	*gntK*	BN194_02340	K0MS76	2.24	-1.70	-3.25
Nuclease sbcCD subunit D	DNA repair/recombination	*sbcD*	BN194_07530	K0N6B1	1.26	-1.70	-3.25

50S ribosomal protein L20	Ribosomal proteins	*rplT*	BN194_18800	K0N5Y4	4.47	-1.71	-3.26
Probable L-serine dehydratase, beta chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAB*	BN194_13940	K0MV34	2.40	-1.71	-3.27
Glycosyltransferase	Cell wall biogenesis		BN194_09050	K0N346	1.47	-1.72	-3.30
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	*murE*	BN194_02160	K0N1S5	5.67	-1.73	-3.31
Uncharacterized protein yloA	Cell surface proteins/internalins	*yloA*	BN194_16340	K0MVK5	4.30	-1.73	-3.32
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*nagA*	BN194_19890	K0MWF9	4.55	-1.74	-3.34
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	*thrS*	BN194_18860	K0N5P5	7.24	-1.75	-3.36
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*manD*	BN194_02950	K0N1P4	4.59	-1.75	-3.37
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	*agaS*	BN194_02940	K0MSD9	4.99	-1.76	-3.39
Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	*rbsK*	BN194_03300	K0N1R2	3.90	-1.78	-3.43
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF_2*	BN194_20590	K0MWL1	3.54	-1.79	-3.46
Uncharacterized protein	General prediction only		BN194_26820	K0NCV9	3.21	-1.79	-3.46
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	*mhqD*	BN194_18770	K0NB71	1.56	-1.80	-3.48
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	*rny*	BN194_10100	K0N3E5	3.02	-1.82	-3.54
Putative pre-16S rRNA nuclease (EC 3.1.-.-)	DNA repair/recombination		BN194_08520	K0N972	4.21	-1.83	-3.54
Uncharacterized protein	Unknown/uncharacterized		BN194_05660	K0N2I2	1.05	-1.83	-3.55
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_3*	BN194_21990	K0MWY0	2.02	-1.83	-3.56
Glycosyl transferase family 8	Cell wall biogenesis		BN194_11730	K0N795	3.14	-1.83	-3.56
Mannose permease IID component	Phosphotransferase systems	*manZ_4*	BN194_04510	K0N287	1.86	-1.83	-3.57
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE*	BN194_13710	K0N4D8	1.77	-1.84	-3.57
Uncharacterized protein	Unknown/uncharacterized		BN194_20720	K0NBH5	4.86	-1.84	-3.58
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	*msmK*	BN194_11180	K0N747	3.34	-1.85	-3.61

Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	*ycnE*	BN194_13230	K0N7R3	2.24	-1.85	-3.61
S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	*metK*	BN194_09150	K0N352	4.44	-1.87	-3.64
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	*frr*	BN194_17650	K0N5M3	3.96	-1.87	-3.66
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	*pepQ*	BN194_08740	K0MTP0	3.86	-1.88	-3.67
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	*galE*	BN194_07350	K0N2R3	3.90	-1.88	-3.68
D-ribose-binding protein	ABC-type transporter systems	*rbsB*	BN194_03290	K0MSF6	3.99	-1.88	-3.69
DNA polymerase III subunit delta (EC 2.7.7.7)	DNA replication-related	*holB*	BN194_23930	K0NA93	1.62	-1.90	-3.73
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	*serS*	BN194_20080	K0N9N4	5.77	-1.91	-3.76
Fructoselysine kinase (EC 2.7.1.-)	Carbohydrate-related metabolism	*frlD*	BN194_22240	K0MX05	2.28	-1.93	-3.81
Probable phosphoketolase (EC 4.1.2.-)	Central glycolytic/intermediary pathways	*xpkA*	BN194_01710	K0N1M9	4.71	-1.94	-3.83
Uncharacterized protein	*Cell surface proteins/internalins*		BN194_20060	K0N5Y7	1.25	-1.95	-3.85
Uncharacterized protein	Unknown/uncharacterized		BN194_25820	K0NCG9	2.41	-1.97	-3.91
Hydroxyacid oxidase (EC 1.1.3.15)	Central glycolytic/intermediary pathways	*haox*	BN194_24790	K0MXH5	1.59	-1.97	-3.92
Beta-galactosidase 17 (EC 3.2.1.23)	Carbohydrate-related metabolism	*BGAL17*	BN194_02960	K0N204	0.69	-1.97	-3.92
Uncharacterized protein	General prediction only		BN194_30000	K0N979	1.78	-1.98	-3.94
Hypothetical lipoprotein	Unknown/uncharacterized		BN194_12440	K0MUR1	5.01	-1.98	-3.94
50S ribosomal protein L2	Ribosomal proteins	*rplB*	BN194_26190	K0MXU1	5.13	-1.98	-3.94
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhB*	BN194_15090	K0MVA7	4.88	-2.00	-4.01
Uncharacterized protein MJ1651	General prediction only		BN194_04410	K0N281	2.74	-2.00	-4.01
Uncharacterized protein	Unknown/uncharacterized		BN194_20070	K0NBE0	4.18	-2.01	-4.01
Putative competence-damage inducible protein	General prediction only	*cinA*	BN194_10070	K0N9I3	3.09	-2.02	-4.04

Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	*valS*	BN194_14510	K0N4J6	5.87	-2.03	-4.08
D-lactate dehydrogenase (EC 1.1.1.28)	Carbohydrate-related metabolism	*dld*	BN194_06590	K0MT28	3.72	-2.05	-4.14
NifS/IcsS protein homolog	Cofactor-related metabolism		BN194_14470	K0NAF3	4.31	-2.06	-4.16
GNAT family acetyltransferase	General prediction only		BN194_29620	K0NDL0	1.32	-2.06	-4.18
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE_2*	BN194_19740	K0MWF1	4.25	-2.07	-4.19
LPXTG-motif cell wall anchor domain protein			BN194_26300	K0N883	3.77	-2.08	-4.23
Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) (Peptide-methionine (R)-S-oxide reductase)	Posttranslational modification	*msrB*	BN194_17090	K0MVR6	1.00	-2.09	-4.25
Uncharacterized protein HI_0912	General prediction only	*thiF3*	BN194_05090	K0MSS8	2.72	-2.09	-4.25
Glucitol operon repressor	Transcriptional regulation	*srlR*	BN194_28690	K0MYG3	3.07	-2.09	-4.27
5-bromo-4-chloroindolyl phosphate hydrolysis protein	General prediction only		BN194_14860	K0N4M3	4.38	-2.10	-4.28
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhA*	BN194_15080	K0N860	3.95	-2.10	-4.29
N5-carboxyaminoimidazole ribonucleotide synthase (N5-CAIR synthase) (EC 6.3.4.18) (5-(carboxyamino)imidazole ribonucleotide synthetase)	Nucleic acid/nucleotide metabolism	*purK_2, purK*	BN194_19370	K0NB96	4.30	-2.11	-4.30
Glycosyl transferase family protein	Cell wall biogenesis		BN194_02420	K0N7L2	3.81	-2.11	-4.31
MerR family transcriptional regulator	Transcriptional regulation		BN194_25900	K0N833	2.52	-2.11	-4.32
Zinc-type alcohol dehydrogenase-like protein SE_1777	General prediction only		BN194_07910	K0N329	3.32	-2.11	-4.33
UvrABC system protein B (Protein UvrB) (Excinuclease ABC subunit B)	DNA repair/recombination	*uvrB*	BN194_10440	K0MU09	2.11	-2.13	-4.39
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	*map*	BN194_12230	K0N7E0	4.93	-2.14	-4.40
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	*ssdA*	BN194_24140	K0MXE0	5.81	-2.14	-4.42
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	*purB*	BN194_12520	K0NA41	5.18	-2.16	-4.46
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)		*accC*	BN194_22510	K0N6M5	3.65	-2.16	-4.46
UPF0478 protein SAOUHSC_01855	Signal transduction		BN194_08710	K0N365	3.94	-2.17	-4.49

Probable L-serine dehydratase, alpha chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAA*	BN194_13950	K0N4M4	3.89	-2.17	-4.50
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yutF*	BN194_08910	K0N383	4.30	-2.17	-4.52
Uncharacterized glycosyltransferase HI_0868 (EC 2.4.-.-)	Cell wall biogenesis		BN194_02410	K0N1U3	1.33	-2.18	-4.53
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)	Amino acid-related metabolism	*mtnN*	BN194_14890	K0MV90	4.18	-2.19	-4.56
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	*act*	BN194_16090	K0MVI3	2.05	-2.19	-4.57
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*gmuB*	BN194_23840	K0MXC7	1.67	-2.20	-4.60
Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	*Steap4*	BN194_01990	K0MS41	6.08	-2.20	-4.60
Guanine deaminase (EC 3.5.4.3)	Nucleic acid/nucleotide metabolism	*guaD*	BN194_13320	K0NA96	4.82	-2.21	-4.64
Putative ADP-ribose pyrophosphatase yjhB (EC 3.6.1.-)	General prediction only	*yjhB*	BN194_25530	K0NAH4	1.85	-2.22	-4.66
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh*	BN194_26560	K0N7J5	4.48	-2.23	-4.70
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshA*	BN194_26700	K0N8C7	5.92	-2.23	-4.70
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	*asd*	BN194_01060	K0N1I5	4.90	-2.23	-4.70
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*pheT*	BN194_18560	K0N5M4	4.06	-2.25	-4.74
Malolactic enzyme (EC 1.-.-.-)	Tricarboxylic acid pathway	*mleA*	BN194_08070	K0N949	3.24	-2.25	-4.76
Transcriptional regulator, xre family	Transcriptional regulation		BN194_13860	K0N4E8	2.62	-2.26	-4.78
Tyrosine--tRNA ligase (EC 6.1.1.1)		*tyrS*	BN194_21510	K0N6A9	5.14	-2.26	-4.80
Phosphonates import ATP-binding protein PhnC (EC 3.6.3.28)	ABC-type transporter systems	*phnC_2,phnC*	BN194_25690	K0MXP5	4.59	-2.26	-4.80
PhoH-like protein	General prediction only	*phoH*	BN194_17020	K0NAW2	5.23	-2.29	-4.88
Predicted hydrolase of the HAD superfamily	General prediction only	*mtlD*	BN194_30450	K0N9D4	2.22	-2.29	-4.88
Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	*ADH2*	BN194_08400	K0N307	6.18	-2.29	-4.89

TPR repeats containing protein	Unknown/uncharacterized		BN194_14960	K0N4M8	3.67	-2.29	-4.89
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	*BN194_21350*	BN194_21780	K0N6Q5	4.12	-2.30	-4.94
Uncharacterized protein			BN194_19420	K0NB98	3.50	-2.31	-4.94
DNA translocase SftA	Cytokinesis	*sftA*	BN194_18960	K0N5Q1	2.13	-2.31	-4.95
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	*glpK_2,glpK*	BN194_27720	K0ND65	2.64	-2.31	-4.95
Uncharacterized protein	Cofactor-related metabolism		BN194_18720	K0NB69	2.89	-2.32	-4.99
Cof protein	General prediction only		BN194_12010	K0N401	2.01	-2.32	-5.00
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	*npr*	BN194_04740	K0MSP8	5.31	-2.32	-5.01
Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase)	Cofactor-related metabolism	*coaA*	BN194_21080	K0N9V9	2.80	-2.33	-5.03
Uncharacterized protein yqeY	Unknown/uncharacterized	*yqeY*	BN194_17040	K0MVR2	2.78	-2.35	-5.09
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*glyS*	BN194_16950	K0N5D3	5.10	-2.35	-5.10
Septation ring formation regulator EzrA	Cytokinesis	*ezrA*	BN194_14460	K0N4J2	4.93	-2.36	-5.13
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	*aspS*	BN194_17100	K0N5F3	5.53	-2.36	-5.14
FeS cluster assembly protein sufD	Cofactor-related metabolism	*sufD*	BN194_13780	K0N7U0	4.16	-2.37	-5.17
Uncharacterized protein yutG	Lipid-related metabolism	*yutG*	BN194_08940	K0MTQ3	4.04	-2.38	-5.21
MreB-like protein	Cytokinesis	*mbl*	BN194_13650	K0N4K5	5.23	-2.38	-5.22
Uncharacterized protein	Unknown/uncharacterized		BN194_19050	K0N613	1.71	-2.40	-5.29
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_23190	K0MXA1	5.22	-2.40	-5.30
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	*iolS*	BN194_29680	K0NB94	4.60	-2.41	-5.31
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	*msrA_2,msrA*	BN194_15860	K0N4W6	0.81	-2.42	-5.37
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	*alsS*	BN194_20150	K0N695	2.05	-2.43	-5.38
30S ribosomal protein S12	Ribosomal proteins	*rpsL*	BN194_26290	K0MXV0	4.20	-2.45	-5.46

Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacA*	BN194_07500	K0N2T4	4.21	-2.45	-5.47
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	*sph*	BN194_04930	K0N5Q0	4.81	-2.46	-5.51
30S ribosomal protein S3	Ribosomal proteins	*rpsC*	BN194_26160	K0N7G5	5.03	-2.46	-5.52
Putative tRNA-binding protein ytpR	General prediction only	*ytpR*	BN194_18970	K0NB80	5.68	-2.46	-5.52
L-asparaginase (EC 3.5.1.1)	Amino acid-related metabolism	*ansA*	BN194_23900	K0N7L6	3.67	-2.46	-5.52
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	*pepN*	BN194_05410	K0N2F5	5.63	-2.47	-5.53
Probable flavodoxin-1	Membrane bioenergetics	*ykuN_2*	BN194_12220	K0NA19	1.09	-2.47	-5.55
Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	4.04	-2.47	-5.56
Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	2.56	-2.48	-5.58
Uncharacterized protein	Unknown/uncharacterized		BN194_19530	K0N9J0	2.94	-2.49	-5.60
DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	DNA replication-related	*dnaX*	BN194_23990	K0MXD3	1.26	-2.49	-5.61
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA_2*	BN194_29210	K0N8B2	3.55	-2.49	-5.61
Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	ABC-type transporter systems	*ecfA2, ecfA*	BN194_25920	K0NCI4	2.68	-2.50	-5.64
Uncharacterized protein	RNA degradation		BN194_11250	K0N3V2	5.20	-2.51	-5.69
Ribosomal RNA small subunit methyltransferase A (EC 2.1.1.182) (16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase) (16S rRNA dimethyladenosine transferase) (16S rRNA dimethylase) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase)	tRNA/Ribosome assembly/processing	*rsmA,ksgA*	BN194_27020	K0NCX3	3.99	-2.52	-5.72
Putative PTS system mannose-specific EIIAB component	Phosphotransferase systems		BN194_03940	K0MSJ3	2.79	-2.53	-5.76
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB2,pstB*	BN194_10280	K0N6X8	1.22	-2.53	-5.79
Uncharacterized zinc protease ymfH (EC 3.4.24.-)	Amino acid-related metabolism	*ymfH*	BN194_10030	K0N6V9	2.37	-2.53	-5.79
Cell division protein FtsZ	Cytokinesis	*ftsZ*	BN194_14760	K0N4L6	5.43	-2.54	-5.80

Methionyl-tRNA formyltransferase (EC 2.1.2.9)	Protein translation (initiation)	*fmt*	BN194_18060	K0N5J2	5.32	-2.54	-5.81
Uncharacterized protein	Unknown/uncharacterized		BN194_30140	K0MYT6	2.34	-2.54	-5.82
DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	*rpoB*	BN194_26340	K0MXV4	5.47	-2.54	-5.82
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)	Cell wall biogenesis	*glmS*	BN194_11560	K0N3V9	5.53	-2.54	-5.83
Ribosome biogenesis GTPase A	tRNA/Ribosome assembly/processing	*rbgA*	BN194_15940	K0MVH2	2.32	-2.55	-5.84
Holo-[acyl-carrier-protein] synthase (Holo-ACP synthase) (EC 2.7.8.7) (4'-phosphopantetheinyl transferase AcpS)	Cofactor-related metabolism	*acpS*	BN194_26690	K0MXY2	4.83	-2.55	-5.87
Peptide chain release factor 3 (RF-3)	Protein translation (peptide release)	*prfC*	BN194_19480	K0N9I7	4.45	-2.56	-5.90
Protein QmcA	Unknown/uncharacterized	*qmcA*	BN194_12070	K0NA10	5.39	-2.56	-5.91
Uncharacterized protein	General prediction only		BN194_13850	K0N4L8	2.54	-2.57	-5.96
Primosomal protein DnaI	DNA replication-related	*dnaI*	BN194_18880	K0N9E5	1.70	-2.58	-5.98
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	*prs1,prs*	BN194_26930	K0NAT2	4.79	-2.59	-6.02
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	*nagB*	BN194_30440	K0MYW0	4.89	-2.60	-6.05
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA_2*	BN194_22950	K0N7F8	5.03	-2.60	-6.06
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO_2*	BN194_16630	K0N8Q0	5.30	-2.60	-6.08
Bifunctional protein FolD	Cofactor-related metabolism	*folD*	BN194_18210	K0N5K0	1.89	-2.61	-6.10
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	*dhaK_2*	BN194_04980	K0N5Q3	4.73	-2.61	-6.11
Uncharacterized protein	Unknown/uncharacterized		BN194_22290	K0MX11	3.04	-2.61	-6.12
Uncharacterized protein yjbK	General prediction only	*yjbK*	BN194_09860	K0N3G6	2.71	-2.62	-6.16

Putative HAD-hydrolase yfnB (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yfnB*	BN194_08780	K0N6M1	1.76	-2.63	-6.18
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO*	BN194_12030	K0N7B7	2.82	-2.63	-6.18
Oligoendopeptidase, pepF/M3 family	*Amino acid-related metabolism*		BN194_11580	K0N779	5.17	-2.64	-6.23
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	*accB*	BN194_22530	K0NA35	2.28	-2.64	-6.25
5'-nucleotidase (EC 3.1.3.5)	General prediction only		BN194_08220	K0N957	6.45	-2.64	-6.25
Adenosylcobalamin-dependent ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*rtpR*	BN194_24230	K0NAA3	2.50	-2.65	-6.26
Uridine phosphorylase (EC 2.4.2.3)	Nucleic acid/nucleotide metabolism	*udp*	BN194_24830	K0NAD0	2.09	-2.65	-6.27
Putative beta-phosphoglucomutase (EC 5.4.2.6)	Central glycolytic/intermediary pathways	*yvdM*	BN194_11170	K0N9S7	2.61	-2.65	-6.27
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	*cmk*	BN194_15710	K0N4V1	6.42	-2.66	-6.33
Bifunctional purine biosynthesis protein PurH	Nucleic acid/nucleotide metabolism	*purH*	BN194_19300	K0N634	6.77	-2.66	-6.34
Alkyl hydroperoxide reductase subunit C (EC 1.11.1.15)	Cell defense/detoxification	*ahpC*	BN194_26250	K0N876	1.44	-2.67	-6.36
Putative 2-hydroxyacid dehydrogenase SH0752 (EC 1.1.1.-)	General prediction only		BN194_01890	K0MS33	3.91	-2.68	-6.41
3'-5' exoribonuclease yhaM (EC 3.1.-.-)	RNA degradation	*yhaM*	BN194_19070	K0NB84	5.69	-2.68	-6.43
Ribosomal protein L11 methyltransferase (L11 Mtase) (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*prmA*	BN194_17260	K0N5B0	1.96	-2.69	-6.45
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	*yfeX*	BN194_07170	K0N8U9	4.85	-2.71	-6.53
Uncharacterized protein YdiC	General prediction only	*ydiC_3*	BN194_23870	K0NBZ8	2.45	-2.71	-6.55
1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157)	Cell wall biogenesis		BN194_09040	K0MTQ9	4.64	-2.71	-6.56
Rod shape-determining protein MreB	Cytokinesis	*mreB*	BN194_14550	K0N4R7	5.37	-2.73	-6.63
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)	Nucleic acid/nucleotide metabolism	*ntd*	BN194_24240	K0MXE6	4.25	-2.73	-6.66
Spore coat polysaccharide biosynthesis protein spsK				K0N9X8;K0N6D6	4.71	-2.75	-6.71
Predicted acetyltransferase			BN194_11820	K0N9Y9	4.09	-2.75	-6.74
Dumpy	Cell surface proteins/internalins	*dp*	BN194_05390	K0MSV0	0.67	-2.75	-6.75

DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	*rpoC*	BN194_26330	K0NAN3	6.45	-2.76	-6.77
Uncharacterized protein	General prediction only	*gpm1*	BN194_13960	K0N4F5	1.16	-2.77	-6.83
Putative integral membrane protein	Unknown/uncharacterized		BN194_01660	K0N1M7	4.87	-2.78	-6.88
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	*nadE*	BN194_19840	K0MWF6	5.01	-2.80	-6.96
Uncharacterized protein IRC4	Unknown/uncharacterized	*IRC4*	BN194_30110	K0N8K0	2.07	-2.81	-7.03
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA_2*	BN194_18340	K0MW64	5.87	-2.82	-7.05
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	*pfkA*	BN194_15570	K0NAK6	4.65	-2.82	-7.06
Uncharacterized protein ycaC	General prediction only	*ycaC*	BN194_29650	K0N948	5.62	-2.83	-7.13
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	*trpS*	BN194_27360	K0N7S4	5.04	-2.84	-7.15
Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-)		*rsmB*	BN194_18040	K0MW45	4.62	-2.84	-7.17
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	*carB*	BN194_16450	K0N587	6.40	-2.87	-7.32
Phosphatase YbjI (EC 3.1.3.-)	General prediction only	*ybjI*	BN194_30020	K0NDN5	2.15	-2.88	-7.38
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	*der*	BN194_15730	K0N8E1	4.82	-2.89	-7.42
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	*citX*	BN194_20300	K0N6A3	2.06	-2.90	-7.45
Manganese transport system ATP-binding protein MntB	ABC-type transporter systems	*mntB*	BN194_25460	K0N7A8	2.84	-2.90	-7.47
Uncharacterized protein ynbB	Cell defense/detoxification	*ynbB*	BN194_18380	K0N9B7	4.36	-2.90	-7.48
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	*gpsA*	BN194_10350	K0N3I2	4.59	-2.91	-7.54
GTPase HflX (GTP-binding protein HflX)	tRNA/Ribosome assembly/processing	*hflX*	BN194_21260	K0N689	3.17	-2.92	-7.56
NAD-dependent epimerase/dehydratase:3-beta hydroxysteroid dehydrogenase/isomerase:NmrA-like	General prediction only		BN194_25520	K0NCC8	3.38	-2.92	-7.57
Lactose phosphotransferase system repressor	Transcriptional regulation	*lacR*	BN194_07510	K0N2X5	3.80	-2.94	-7.68
Oligoendopeptidase F	Amino acid-related metabolism	*yjbG_2*	BN194_08130	K0N6H7	5.66	-2.95	-7.70

Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*nrdD*	BN194_01250	K0N190	2.91	-2.95	-7.74
tRNA pseudouridine synthase A (EC 5.4.99.12) (tRNA pseudouridine(38-40) synthase) (tRNA pseudouridylate synthase I) (tRNA-uridine isomerase I)	tRNA/Ribosome assembly/processing	*truA*	BN194_25910	K0N7E2	2.54	-2.97	-7.83
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB_2*	BN194_29110	K0N8A4	4.83	-2.98	-7.87
Uncharacterized protein			BN194_07360	K0N2W3	4.47	-2.98	-7.89
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA_2,ackA*	BN194_23060	K0N6W4	4.00	-2.99	-7.94
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_2*	BN194_03120	K0N7V6	2.70	-2.99	-7.95
Uncharacterized RNA methyltransferase lp_1151 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_11990	K0MUI2	4.67	-2.99	-7.96
CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	*pyrG*	BN194_26790	K0MXZ1	4.63	-3.00	-7.98
tRNA N6-adenosine threonylcarbamoyltransferase (EC 2.3.1.234) (N6-L-threonylcarbamoyladenine synthase) (t(6)A37 threonylcarbamoyladenosine biosynthesis protein TsaD) (tRNA threonylcarbamoyladenosine biosynthesis protein TsaD)	General prediction only	*tsaD,gcp*	BN194_23850	K0N7L3	2.51	-3.00	-7.99
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	*mhqA_3*	BN194_18760	K0N5N7	3.70	-3.01	-8.03
Uncharacterized N-acetyltransferase ycf52-like (EC 2.3.1.-)	General prediction only	*speE1*	BN194_21490	K0MWT4	2.54	-3.02	-8.09
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	*treA*	BN194_06930	K0N662	2.12	-3.02	-8.13
Phosphoribosylformylglycinamidine synthase subunit PurQ (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit I) (Glutaminase PurQ) (Phosphoribosylformylglycinamidine synthase subunit I)	Nucleic acid/nucleotide metabolism	*purQ*	BN194_19340	K0MWC7	4.60	-3.02	-8.13
Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	*rp2*	BN194_17060	K0N598	2.68	-3.04	-8.24
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	*gmk*	BN194_18110	K0N5J6	4.06	-3.05	-8.30
Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.193)	tRNA/Ribosome assembly/processing	*rsmE*	BN194_17250	K0N5G8	2.36	-3.06	-8.36

Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain)	Nucleic acid/nucleotide metabolism	*carA*	BN194_16460	K0N535	3.83	-3.07	-8.37
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	*yhaA*	BN194_30550	K0N9E4	1.81	-3.08	-8.43
Uncharacterized protein	Unknown/uncharacterized		BN194_21450	K0N6R7	2.34	-3.08	-8.47
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	*mco*	BN194_25410	K0N7A4	5.31	-3.08	-8.48
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC_2*	BN194_24680	K0NAC2	5.84	-3.09	-8.49
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox*	BN194_01780	K0N4U4	1.80	-3.11	-8.64
Uncharacterized peptidase yqhT (EC 3.4.-.-)	Amino acid-related metabolism	*yqhT*	BN194_18260	K0N5K4	5.25	-3.11	-8.65
Kinase, putative	General prediction only		BN194_29890	K0MYR0	2.50	-3.12	-8.66
Uncharacterized protein	Unknown/uncharacterized		BN194_20160	K0N5Z4	5.58	-3.12	-8.71
Glycosyl transferase family 2	Cell wall biogenesis		BN194_02460	K0N1U7	0.93	-3.16	-8.92
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	*iscS1*	BN194_14900	K0N4U8	5.05	-3.17	-8.98
Glutathione reductase, chloroplastic (EC 1.8.1.7)	Cofactor-related metabolism	*GOR*	BN194_23200	K0N7H3	5.29	-3.17	-9.00
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdE2*	BN194_16600	K0N5A1	5.48	-3.19	-9.12
Uncharacterized protein ypgQ	General prediction only	*ypgQ*	BN194_27480	K0NAX0	2.09	-3.20	-9.17
Uncharacterized protein YPL245W	Unknown/uncharacterized		BN194_25000	K0N7U3	3.00	-3.20	-9.22
Peptidase T (EC 3.-.-.-) (EC 3.4.11.-) (EC 3.4.11.4)	Amino acid-related metabolism	*pepT*	BN194_03110	K0N213	3.52	-3.21	-9.22
Uncharacterized oxidoreductase YbdH (EC 1.1.-.-)	Carbohydrate-related metabolism	*ybdH*	BN194_30540	K0MYX0	2.89	-3.21	-9.24
Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	General prediction only	*yqiG*	BN194_25330	K0NAG4	2.80	-3.21	-9.28
Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Phosphoglucose isomerase) (Phosphohexose isomerase)	Central glycolytic/intermediary pathways	*pgi*	BN194_12580	K0N7I6	6.37	-3.22	-9.29
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	*hpt*	BN194_26470	K0NCR2	5.11	-3.22	-9.35
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP*	BN194_08180	K0N6I0	2.12	-3.22	-9.35

DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	*gyrB*	BN194_00060	K0N1B8	4.21	-3.23	-9.40
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	*galK*	BN194_07340	K0MTA3	5.58	-3.25	-9.52
ABC-type antimicrobial peptide transport system,ATPase component	*ABC-type transporter systems*		BN194_19940	K0MWG2	3.36	-3.26	-9.60
Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	*aspC*	BN194_16770	K0NAU6	4.98	-3.26	-9.61
Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	*ptp3*	BN194_23520	K0NBX6	2.44	-3.28	-9.70
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	*pyc*	BN194_15170	K0NAI2	4.55	-3.30	-9.86
Probable calcium-transporting ATPase (EC 3.6.3.8)	Other transporter proteins	*pacL*	BN194_11490	K0MUB1	3.70	-3.31	-9.92
Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	*fhs*	BN194_16520	K0NAT0	6.15	-3.31	-9.95
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	*lplJ*	BN194_16640	K0MVN0	4.27	-3.32	-9.96
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	*ykpA*	BN194_07220	K0N8V6	6.19	-3.32	-9.96
Glucose-1-phosphate thymidylyltransferase		*rmlA*		K0N699;K0MWW4	5.10	-3.34	-10.12
Uncharacterized protein ywfO	General prediction only	*ywfO*	BN194_26840	K0MXZ5	3.20	-3.37	-10.35
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	*agl*	BN194_27950	K0N8T1	5.38	-3.40	-10.59
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase 2 (EC 5.4.2.1)	Central glycolytic/intermediary pathways	*gpmA2_2*	BN194_27560	K0N7W0	3.73	-3.41	-10.64
Transcription-repair-coupling factor (TRCF) (EC 3.6.4.-)	DNA repair/recombination	*mfd*	BN194_26540	K0MXW9	3.48	-3.42	-10.71
Putative carboxypeptidase SCO6489 (EC 3.4.16.-)			BN194_01370	K0N787	3.96	-3.43	-10.75
Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (EC 2.7.7.12) (UDP-glucose--hexose-1-phosphate uridylyltransferase)		*galT*	BN194_07370	K0N8X1	3.28	-3.44	-10.82
Protein RecA (Recombinase A)	DNA repair/recombination	*recA_2,recA*	BN194_27650	K0N8P0	3.28	-3.45	-10.93
FeS cluster assembly protein sufB	Cofactor-related metabolism	*sufB*	BN194_13810	K0N4E5	5.29	-3.45	-10.93
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	*pheS*	BN194_18570	K0NB64	4.59	-3.46	-10.98
Threonylcarbamoyl-AMP synthase (TC-AMP synthase) (EC 2.7.7.87) (L-threonylcarbamoyladenylate synthase)	tRNA/Ribosome assembly/processing	*ywlC*	BN194_13530	K0N7S6	2.53	-3.49	-11.23

Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	Nucleic acid/nucleotide metabolism	*purN*	BN194_19310	K0N5S4	2.27	-3.50	-11.30
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	*glyr1*	BN194_30100	K0N992	2.38	-3.52	-11.48
Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	Nucleic acid/nucleotide metabolism	*add*	BN194_23440	K0MXB1	3.95	-3.52	-11.51
Heat-inducible transcription repressor HrcA	Transcriptional regulation	*hrcA*	BN194_17480	K0N915	5.50	-3.53	-11.57
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	3.42	-3.54	-11.67
DNA polymerase III PolC-type (PolIII) (EC 2.7.7.7)	DNA replication-related	*polC*	BN194_17600	K0N5L6	2.23	-3.55	-11.69
Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase)	Cofactor-related metabolism	*coaE*	BN194_18910	K0N5P8	2.42	-3.59	-12.08
ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	DNA repair/recombination	*addA*	BN194_16800	K0N5B6	2.65	-3.61	-12.18
Uncharacterized protein ybxB	tRNA/Ribosome assembly/processing	*ybxB*	BN194_24020	K0NC08	1.68	-3.61	-12.22
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citE*	BN194_20320	K0NBF4	4.78	-3.61	-12.24
Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	*thyA*	BN194_15800	K0N522	5.90	-3.62	-12.28
Transcriptional regulator	*Posttranslational modification*		BN194_29310	K0N8C2	3.18	-3.62	-12.33
Uncharacterized protein yuaG	Unknown/uncharacterized	*yuaG*	BN194_22920	K0NBV0	1.50	-3.64	-12.47
UvrABC system protein A	DNA repair/recombination	*uvrA_3*	BN194_27500	K0N8M1	3.36	-3.65	-12.56
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	*hmgCS1*	BN194_19680	K0N9K3	6.08	-3.65	-12.57
Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	Carbohydrate-related metabolism	*scrB*	BN194_22440	K0MX27	2.83	-3.66	-12.67
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*gnd*	BN194_18660	K0N5N2	5.94	-3.67	-12.71
Histidinol-phosphatase	General prediction only		BN194_14010	K0N4F8	4.74	-3.69	-12.92
Aldose 1-epimerase (EC 5.1.3.3)	*Central glycolytic/intermediary pathways*		BN194_07390	K0MTA8	4.83	-3.70	-13.02
Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase)	Nucleic acid/nucleotide metabolism	*purM*	BN194_19320	K0NB95	5.28	-3.71	-13.06
Chromosomal replication initiator protein DnaA	DNA replication-related	*dnaA*	BN194_00010	K0N1B5	2.79	-3.75	-13.42

L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh1,ldh*	BN194_06970	K0N8S5	2.25	-3.75	-13.44
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	*rpoZ*	BN194_18100	K0N5T7	2.81	-3.76	-13.58
Probable phosphoketolase (EC 4.1.2.-)	*Central glycolytic/intermediary pathways*		BN194_28700	K0N8X7	1.62	-3.78	-13.69
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	*coaD*	BN194_15200	K0N4X3	5.56	-3.79	-13.84
Uncharacterized protein in fgs 3'region	General prediction only		BN194_14530	K0N802	3.27	-3.80	-13.97
Folate transporter FolT	Unknown/uncharacterized	*folT*	BN194_23890	K0MXC9	4.26	-3.84	-14.30
Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	*purA*	BN194_01160	K0N1J0	7.06	-3.84	-14.31
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	*hslU*	BN194_16010	K0N4Y1	3.77	-3.88	-14.77
UPF0039 protein SAR1027	General prediction only		BN194_19510	K0N5U0	3.44	-3.88	-14.77
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	*deoB*	BN194_02800	K0N1N0	5.11	-3.91	-15.04
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA*	BN194_09090	K0MTR3	6.17	-3.92	-15.09
UvrABC system protein A	DNA repair/recombination	*uvrA_2*	BN194_14920	K0NAH3	4.47	-3.94	-15.38
GTP pyrophosphokinase yjbM (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*yjbM*	BN194_09870	K0N9G5	5.92	-3.96	-15.55
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	*cysS*	BN194_24430	K0NAB2	2.25	-3.96	-15.60
Chromosome partition protein Smc	Cytokinesis	*smc*	BN194_17860	K0N5H9	2.92	-3.97	-15.67
Maltose ABC transporter, periplasmic maltose-binding protein	*ABC-type transporter systems*		BN194_11200	K0N3U4	4.69	-3.98	-15.73
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_2*	BN194_04490	K0MSM9	5.38	-3.98	-15.75
Uncharacterized protein yaaQ	Unknown/uncharacterized	*yaaQ*	BN194_23940	K0MXD1	3.35	-3.99	-15.90
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	*gatA*	BN194_11960	K0N3Z6	7.31	-3.99	-15.93
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatB*	BN194_11970	K0NA01	6.47	-4.00	-15.97
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	*pgcA*	BN194_10370	K0N9K8	7.07	-4.01	-16.15

Predicted Zn-dependent peptidase	*Amino acid-related metabolism*		BN194_10020	K0N9H8	2.22	-4.03	-16.28
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_27170	K0NCZ6	4.96	-4.03	-16.31
NADH-dependent butanol dehydrogenase A (EC 1.1.1.-)	Carbohydrate-related metabolism	*bdhA*	BN194_22640	K0MX50	4.99	-4.03	-16.38
Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)	Nucleic acid/nucleotide metabolism	*purC*	BN194_19360	K0N5S8	5.83	-4.05	-16.52
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatC*	BN194_11950	K0N436	6.83	-4.07	-16.76
Esterase/lipase	General prediction only		BN194_30390	K0MYV7	5.65	-4.07	-16.82
Uncharacterized protein	*Central glycolytic/intermediary pathways*		BN194_04970	K0N8A3	6.17	-4.07	-16.85
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	*thiD_2*	BN194_07650	K0N2U9	5.17	-4.10	-17.12
Uncharacterized protein	Unknown/uncharacterized		BN194_25890	K0MXR4	4.09	-4.10	-17.20
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	*glgD*	BN194_21590	K0MWU4	4.19	-4.11	-17.25
Elongation factor 4 (EF-4) (EC 3.6.5.n1) (Ribosomal back-translocase LepA)	Protein translation (elongation)	*lepA*	BN194_17440	K0MVU5	2.46	-4.14	-17.58
DNA mismatch repair protein MutL	DNA repair/recombination	*mutL*	BN194_23710	K0N6Z8	4.34	-4.15	-17.72
Glutamate dehydrogenase	Amino acid-related metabolism	*gdh*	BN194_06980	K0N666	5.78	-4.16	-17.82
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	2.49	-4.18	-18.10
Guanylate kinase (EC 2.7.4.8)	Nucleic acid/nucleotide metabolism	*gmk_2*	BN194_21480	K0N9Y7	3.16	-4.18	-18.11
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis		BN194_21400	K0N6R1	5.88	-4.18	-18.12
Uncharacterized ABC transporter ATP-binding protein YdbJ	ABC-type transporter systems	*ydbJ*	BN194_24600	K0N7Q8	3.06	-4.19	-18.19
Uncharacterized protein yhfI	General prediction only	*yhfI*	BN194_19200	K0N627	3.88	-4.22	-18.59
Alpha-galactosidase 2 (EC 3.2.1.22)	Carbohydrate-related metabolism	*agaS_2*	BN194_22160	K0N6I2	1.01	-4.25	-19.00
Uncharacterized protein yeaE	General prediction only	*yeaE*	BN194_07040	K0MT72	3.30	-4.29	-19.60
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citF*	BN194_20310	K0N607	7.69	-4.32	-19.93
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_13380	K0N7S0	6.02	-4.34	-20.20

Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI_2*	BN194_16210	K0N508	5.11	-4.35	-20.42
Glutamate--cysteine ligase/gamma-glutamylcysteine synthetase	Cofactor-related metabolism	*gshAB*	BN194_13910	K0N4F0	4.75	-4.37	-20.73
Glycosyl transferase group 1	Cell wall biogenesis		BN194_09760	K0N3F8	1.93	-4.38	-20.75
Phosphoribosylformylglycinamidine synthase subunit PurL (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit II) (Glutamine amidotransferase PurL) (Phosphoribosylformylglycinamidine synthase subunit II)	Nucleic acid/nucleotide metabolism	*purL*	BN194_19330	K0N9H6	3.58	-4.38	-20.77
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	General prediction only		BN194_03130	K0N5D9	3.98	-4.46	-22.01
Uncharacterized protein yieF	General prediction only	*yieF_2*	BN194_06540	K0MT25	4.35	-4.49	-22.51
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	*mtlD_3mtlD*	BN194_30400	K0N9C8	6.04	-4.51	-22.74
SMC domain protein	DNA repair/recombination		BN194_07540	K0MTC3	3.97	-4.54	-23.27
6-aminohexanoate-cyclic-dimer hydrolase	General prediction only		BN194_24180	K0NAA2	3.98	-4.54	-23.29
Sporulation initiation inhibitor protein soj	Cytokinesis	*soj*	BN194_02040	K0MS45	5.59	-4.56	-23.51
Uncharacterized ABC transporter ATP-binding protein YdiF	General prediction only	*ydiF*	BN194_23830	K0NA88	3.92	-4.59	-24.04
DNA mismatch repair protein MutS	DNA repair/recombination	*mutS*	BN194_23720	K0NBY9	2.01	-4.59	-24.11
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	*murI*	BN194_08640	K0MTN4	5.42	-4.60	-24.27
Uncharacterized protein			BN194_22500	K0N788	2.61	-4.61	-24.34
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	*ilvE*	BN194_21620	K0NBM4	6.11	-4.64	-24.96
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA1,gpmA*	BN194_24750	K0N7R7	4.31	-4.69	-25.81
Uncharacterized protein	Unknown/uncharacterized		BN194_23650	K0N7J8	5.41	-4.69	-25.88
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB*	BN194_19860	K0N5X0	6.24	-4.73	-26.45
Acyl-ACP thioesterase	Lipid-related metabolism		BN194_23910	K0N709	4.58	-4.73	-26.61

ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease RexB)	DNA repair/recombination	*rexB*	BN194_16810	K0N573	2.31	-4.90	-29.77
Monooxygenase	General prediction only		BN194_07600	K0N2U5	1.68	-4.94	-30.68
Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	*pox5*	BN194_19670	K0NBB6	3.21	-5.04	-32.94
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC*	BN194_00080	K0N486	3.17	-5.05	-33.20
Uncharacterized ABC transporter ATP-binding protein YfmR (EC 3.6.3.-)	ABC-type transporter systems	*yfmR*	BN194_15790	K0MVF8	4.97	-5.18	-36.30
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC*	BN194_24670	K0NC50	5.14	-5.25	-37.98
Uncharacterized protein YxeH	General prediction only	*yxeH*	BN194_04750	K0N1Y7	3.78	-5.27	-38.47
Microcin C7 self-immunity protein mccF			BN194_01360	K0N1K5	4.05	-5.31	-39.76
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	*mnmA*	BN194_14930	K0N844	3.92	-5.32	-39.88
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	*glyA*	BN194_13540	K0MV12	5.95	-5.33	-40.17
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA*	BN194_01620	K0N7B1	2.82	-5.41	-42.39
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	*polA*	BN194_18930	K0N9E7	3.90	-5.56	-47.04
Phosphoenolpyruvate carboxykinase (ATP)	Tricarboxylic acid pathway		BN194_20000	K0N684	5.05	-5.71	-52.18
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	*pycB*	BN194_20290	K0MWI8	5.71	-6.25	-76.21
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	*apbE_3*	BN194_21550	K0N6S8	2.90	-6.36	-82.21
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	*pflB*	BN194_16080	K0N8I5	6.63	-6.66	-101.00
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB*	BN194_21340	K0MWS0	2.97	-9.37	-660.76

Annexure 8: Cumulative FC comparison (acid stress experiment), functional class sorted

Protein names	Functional Class	Gene	Gene Locus	Protein ID	Log ratioCFE 4.5 Vs CFE6.5	FC CFE 4.5 Vs	Log ratio UC pH	FC UC pH Vs	Log ratio UC pH	FC UC pH Vs	Log ratio LiCL pH	FC LiCL Ph4.5 Vs	Log ratio LiCL pH4.5	FC LiC Ph

						CFE 6.5	Vs CFE 6.5	CFE 6.5	Vs CFE 4.5	CFE 4.5	4.5 Vs LiCL pH	LiCL Ph 6.5	Vs CFE pH 4.5	Vs Ph
D-alanine--D-alanine ligase (EC 6.3.2.4) (D-Ala-D-Ala ligase) (D-alanylalanine synthetase)	Cell wall biogenesis	*ddl*	BN194_01390	K0MRY4	-0.1	0.9	0.9	1.8	1.0	2.0	0.2	1.1	-0.6	0.7
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	*dacA*	BN194_02140	K0MS53	-0.8	0.6	-0.5	0.7	0.3	1.2	0.4	1.3	1.1	2.1
UDP-N-acetylmuramyl-tripeptide synthetase (EC 6.3.2.-)	Cell wall biogenesis	*murE*	BN194_02160	K0N1S5	-2.6	0.2	-7.2	0.0	-4.6	0.0	-0.5	0.7	0.3	1.3
Uncharacterized protein	*Cell wall biogenesis*		BN194_02360	K0N1U1	0.3	1.3	-1.4	0.4	-1.8	0.3	0.7	1.6	3.9	15
Uncharacterized glycosyltransferase HI_0868 (EC 2.4.-.-)	*Cell wall biogenesis*		BN194_02410	K0N1U3	0.1	1.1	-0.2	0.8	-0.3	0.8	1.7	3.2	-0.6	0.7
Glycosyl transferase family protein	*Cell wall biogenesis*		BN194_02420	K0N7L2	0.3	1.3	-0.5	0.7	-0.9	0.5	0.2	1.2	-2.2	0.2
Alternansucrase	*Cell wall biogenesis*		BN194_02430	K0N547	-2.7	0.2	-4.6	0.0	-1.9	0.3	1.2	2.3	8.2	30
Glycosyl transferase family 2	*Cell wall biogenesis*		BN194_02460	K0N1U7	-0.4	0.7	-1.2	0.4	-0.7	0.6	2.0	4.0	-0.7	0.6
Putative secreted protein	cell wall biogenesis		BN194_02820	K0N7S8	2.5	5.7	4.0	15.9	1.5	2.8	4.2	18.2	6.2	74
Penicillin-binding protein 3	Cell wall biogenesis	*pbpC*	BN194_03320	K0N7W9	-0.1	0.9	-0.4	0.8	-0.3	0.8	3.1	8.8	1.6	3.6
UDP-glucose 4-epimerase (EC 5.1.3.2)	Cell wall biogenesis	*galE*	BN194_07350	K0N2R3	0.9	1.9	3.4	10.7	2.5	5.7	0.5	1.4	-2.3	0.2
D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13) (D-alanine-D-alanyl carrier protein ligase) (D-alanine-activating enzyme)	Cell wall biogenesis	*dltA*	BN194_08590	K0MTN0	1.6	3.0	0.6	1.5	-1.0	0.5	0.9	1.9	-1.3	0.4
D-alanine--poly(phosphoribitol) ligase subunit 2 (EC 6.1.1.13) (D-alanyl carrier protein)	Cell wall biogenesis	*dltC*	BN194_08610	K0N361	3.7	12.9	5.8	55.6	2.1	4.3	1.7	3.1	0.5	1.4
DltD protein	*Cell wall biogenesis*		BN194_08620	K0N978	1.7	3.3	1.4	2.7	-0.3	0.8	2.0	4.0	-0.5	0.7
Glutamate racemase (EC 5.1.1.-) (EC 5.1.1.3)	Cell wall biogenesis	*murI*	BN194_08640	K0MTN4	-1.9	0.3	-3.9	0.1	-2.1	0.2	0.7	1.6	-2.0	0.2
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF*	BN194_08770	K0N987	-0.7	0.6	-1.2	0.4	-0.5	0.7	0.8	1.8	3.1	8.5
1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157)	*Cell wall biogenesis*		BN194_09040	K0MTQ9	-0.7	0.6	-6.1	0.0	-5.4	0.0	-0.9	0.5	-3.0	0.1
Glycosyltransferase	*Cell wall biogenesis*		BN194_09050	K0N346	-0.4	0.7	-1.0	0.5	-0.6	0.7	0.1	1.0	-1.2	0.4
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1*	BN194_09110	K0N399	0.1	1.0	-0.2	0.9	-0.2	0.8	0.8	1.7	0.1	1.0
Glycosyl transferase group 1	*Cell wall biogenesis*		BN194_09760	K0N3F8	-0.2	0.9	-2.4	0.2	-2.3	0.2	1.9	3.7	-2.3	0.2
UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.3.1.98) (UDP-N-acetylmuramate dehydrogenase)	Cell wall biogenesis	*murB*	BN194_11400	K0N3X0	1.1	2.1	-3.5	0.1	-4.6	0.0	-0.6	0.7	-3.0	0.1
Phosphoglucosamine mutase (EC 5.4.2.10)	Cell wall biogenesis	*glmM*	BN194_11550	K0N3Y7	-0.1	1.0	1.1	2.1	1.1	2.2	-0.6	0.7	-1.9	0.3
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16) (D-fructose-6-phosphate	Cell wall biogenesis	*glmS*	BN194_11560	K0N3V9	0.0	1.0	-2.4	0.2	-2.4	0.2	0.2	1.1	-2.4	0.2

amidotransferase) (GFAT) (Glucosamine-6-phosphate synthase) (Hexosephosphate aminotransferase) (L-glutamine--D-fructose-6-phosphate amidotransferase)														
Glycosyl transferase family 8	*Cell wall biogenesis*		BN194_11730	K0N795	0.9	1.8	-1.3	0.4	-2.1	0.2	0.4	1.3	-2.3	0.
UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase)	Cell wall biogenesis	*cap4C*	BN194_12280	K0N7E3	-1.0	0.5	-4.5	0.0	-3.5	0.1	0.0	1.0	1.9	3.
Lipoteichoic acid synthase 1 (EC 2.7.8.-)	Cell wall biogenesis	*ltaS1_2*	BN194_12550	K0N496	0.5	1.4	2.0	4.0	1.5	2.7	1.4	2.6	0.3	1.
UDP-N-acetylmuramoylalanine--D-glutamate ligase (EC 6.3.2.9) (D-glutamic acid-adding enzyme) (UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase)	Cell wall biogenesis	*murD*	BN194_14720	K0NAG5	0.3	1.2	-3.5	0.1	-3.9	0.1	0.2	1.2	-0.5	0.
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227) (Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase)	Cell wall biogenesis	*murG*	BN194_14730	K0N819	0.5	1.4	-1.2	0.4	-1.7	0.3	-1.6	0.3	1.4	2.
Penicillin-binding protein 1A	Cell wall biogenesis	*ponA*	BN194_16720	K0NAU3	0.2	1.1	0.0	1.0	-0.2	0.9	2.6	5.9	3.1	8.
Uncharacterized protein yqgF	Cell wall biogenesis	*yqgF*	BN194_18440	K0MW71	1.1	2.2	0.3	1.3	-0.8	0.6	0.5	1.5	-0.2	0.
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase)	Cell wall biogenesis	*murC*	BN194_18950	K0N600	0.7	1.6	-1.3	0.4	-2.0	0.3	1.4	2.6	-0.6	0.
Penicillin-binding protein 1F	Cell wall biogenesis	*pbpF_2*	BN194_19090	K0MWB2	-0.5	0.7	-3.4	0.1	-2.8	0.1	3.3	9.7	5.2	35
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB*	BN194_21340	K0MWS0	-0.5	0.7	0.7	1.7	1.3	2.4	0.5	1.4	-8.4	0.
Lipopolysaccharide synthesis sugar transferase	*Cell wall biogenesis*		BN194_21390	K0MWS4	-0.1	0.9	-0.7	0.6	-0.6	0.7	-0.8	0.6	-2.0	0.
Putative UDP-glucose 4-epimerase (EC 5.1.3.2)	*Cell wall biogenesis*		BN194_21400	K0N6R1	-0.4	0.8	1.8	3.4	2.1	4.4	0.7	1.6	-3.2	0.
Surface antigen	*Cell wall biogenesis*		BN194_21500	K0N6S2	1.3	2.5	1.5	2.9	0.2	1.1	4.3	19.0	4.7	26
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	*rmlB_2*	BN194_21770	K0NBN4	-0.9	0.5	0.1	1.1	1.0	2.1	0.4	1.3	3.1	8.
dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)	Cell wall biogenesis	*BN194_21350*	BN194_21780	K0N6Q5	2.0	4.0	4.4	21.8	2.4	5.4	1.7	3.3	-2.6	0.
Uncharacterized protein	*Cell wall biogenesis*		BN194_21890	K0MWX1	-0.2	0.9	-1.2	0.4	-1.0	0.5	-0.2	0.9	-0.4	0.
Sortase	*Cell wall biogenesis*		BN194_22780	K0NA48	0.5	1.5	-0.1	0.9	-0.6	0.7	-0.8	0.6	2.3	5.
ErfK family protein	*Cell wall biogenesis*		BN194_26570	K0NCS1	1.1	2.2	-0.9	0.6	-2.0	0.3	2.0	4.0	2.2	4.
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	*murF*	BN194_26720	K0NCU5	-0.7	0.6	-0.5	0.7	0.2	1.2	-0.5	0.7	2.2	4.
UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7) (Enoylpyruvate transferase) (UDP-N-acetylglucosamine enolpyruvyl transferase)	Cell wall biogenesis	*murA2,murA*	BN194_26780	K0NAR9	-0.2	0.9	-2.2	0.2	-2.0	0.3	-0.7	0.6	-1.5	0.

Bifunctional protein GlmU	Cell wall biogenesis	*glmU*	BN194_26940	K0MY10	-0.6	0.7	-4.7	0.0	-4.2	0.1	-0.9	0.5	-0.3	0.8
Regulatory protein vanR	Signal transduction	*vanR*	BN194_02120	K0N7G4	-0.1	1.0	-5.5	0.0	-5.5	0.0	-0.8	0.6	-1.0	0.9
UPF0478 protein SAOUHSC_01855	Signal transduction		BN194_08710	K0N365	-0.7	0.6	-3.2	0.1	-2.5	0.2	0.7	1.6	-0.8	0.6
Alkaline phosphatase synthesis transcriptional regulatory protein phoP	Signal transduction	*phoP*	BN194_10220	K0N9J6	-0.8	0.6	-5.3	0.0	-4.5	0.0	-1.4	0.4	-2.0	0.3
Uncharacterized transcriptional regulatory protein yclJ	Signal transduction	*yclJ*	BN194_11790	K0MUE5	-0.9	0.5	-4.5	0.0	-3.7	0.1	-1.2	0.4	-0.4	0.8
Universal stress protein	Signal transduction		BN194_13870	K0NAC5	0.8	1.7	0.8	1.8	0.0	1.0	0.1	1.0	-0.7	0.6
Protein ytsP	Signal transduction	*ytsP*	BN194_14450	K0N4Q9	0.4	1.3	-1.1	0.5	-1.4	0.4	0.2	1.2	-1.8	0.3
Response regulator ArlR	Signal transduction	*arlR*	BN194_18650	K0N5X3	0.3	1.2	-6.0	0.0	-6.3	0.0	-1.0	0.5	-1.9	0.3
Sensory transduction protein BceR	Signal transduction	*bceR_2*	BN194_19250	K0N630	-0.2	0.9	-3.6	0.1	-3.4	0.1	-0.6	0.7	-0.9	0.9
Universal stress protein UspA related nucleotide-binding protein	Signal transduction		BN194_22870	K0NBU7	-0.3	0.8	-1.1	0.5	-0.8	0.6	0.6	1.5	-0.6	0.7
Universal stress protein	Signal transduction		BN194_23500	K0N7J0	2.0	3.9	1.4	2.7	-0.5	0.7	1.4	2.6	-1.1	0.9
Transcriptional regulatory protein YycF	Signal transduction	*yycF_2*	BN194_29510	K0N8E4	0.9	1.9	-2.1	0.2	-3.0	0.1	-3.5	0.1	-1.5	0.3
Ferredoxin--NADP reductase (FNR) (Fd-NADP(+) reductase) (EC 1.18.1.2)	*Membrane bioenergetics*		BN194_08950	K0N337	1.7	3.1	-2.5	0.2	-4.1	0.1	0.2	1.1	-0.3	0.8
ATP synthase subunit b (ATP synthase F(0) sector subunit b) (ATPase subunit I) (F-type ATPase subunit b)	Membrane bioenergetics	*atpF*	BN194_13580	K0N7S9	1.0	2.0	0.6	1.5	-0.4	0.8	1.4	2.6	-0.3	0.8
ATP synthase subunit delta (ATP synthase F(1) sector subunit delta) (F-type ATPase subunit delta)	Membrane bioenergetics	*atpH*	BN194_13590	K0MV16	1.5	2.9	0.5	1.4	-1.1	0.5	0.1	1.0	-0.5	0.7
ATP synthase subunit alpha (EC 3.6.3.14) (ATP synthase F1 sector subunit alpha) (F-ATPase subunit alpha)	Membrane bioenergetics	*atpA*	BN194_13600	K0N4K1	0.7	1.7	0.8	1.7	0.1	1.0	0.4	1.3	-0.6	0.6
ATP synthase gamma chain (ATP synthase F1 sector gamma subunit) (F-ATPase gamma subunit)	Membrane bioenergetics	*atpG*	BN194_13610	K0N4D3	1.3	2.4	0.4	1.3	-0.9	0.5	0.5	1.4	-0.4	0.8
ATP synthase subunit beta (EC 3.6.3.14) (ATP synthase F1 sector subunit beta) (F-ATPase subunit beta)	Membrane bioenergetics	*atpD*	BN194_13620	K0NAB3	1.5	2.8	1.4	2.6	-0.1	0.9	0.9	1.8	-0.5	0.7
Probable manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1)	Membrane bioenergetics	*ppaC*	BN194_16110	K0N4Z4	1.2	2.3	3.2	8.9	1.9	3.8	-0.7	0.6	-1.1	0.9
Putative quinone-oxidoreductase homolog,chloroplastic (EC 1.-.-.-)	*Membrane bioenergetics*		BN194_18780	K0N9E0	0.3	1.3	1.2	2.3	0.9	1.8	0.6	1.5	-1.1	0.9
Cytochrome d ubiquinol oxidase subunit 1 (EC 1.10.3.-)	Membrane bioenergetics	*cydA_2*	BN194_23410	K0N6Y2	2.8	7.0	3.1	8.5	0.3	1.2	3.8	14.4	1.6	3.1
NADH dehydrogenase-like protein yjlD (EC 1.6.99.-)	Membrane bioenergetics	*yjlD*	BN194_24330	K0NAA7	0.7	1.6	0.8	1.7	0.1	1.1	1.2	2.3	-0.1	0.9

Polyphosphate kinase (EC 2.7.4.1) (ATP-polyphosphate phosphotransferase) (Polyphosphoric acid kinase)	Membrane bioenergetics	*ppk*	BN194_27270	K0ND10	-1.2	0.4	-4.0	0.1	-2.8	0.1	-0.9	0.5	1.5	2.8
Exopolyphosphatase	*Membrane bioenergetics*		BN194_27280	K0NAV4	-1.5	0.3	-2.4	0.2	-0.9	0.5	0.7	1.7	2.6	6.0
Signal peptidase I (EC 3.4.21.89)	Protein export	*lepB*	BN194_02610	K0N1V9	0.0	1.0	0.2	1.1	0.2	1.1	1.6	3.1	0.9	1.9
UPF0092 membrane protein yrbF	Protein export	*yrbF*	BN194_08390	K0MTL6	0.0	1.0	-0.3	0.8	-0.3	0.8	0.3	1.2	-0.4	0.8
Protein translocase subunit SecA	Protein export	*secA*	BN194_10170	K0N9J2	0.3	1.3	-1.5	0.4	-1.8	0.3	-0.3	0.8	-1.0	0.5
Signal recognition particle protein (Fifty-four homolog)	Protein export	*ffh*	BN194_17820	K0NB27	-0.1	0.9	-5.8	0.0	-5.7	0.0	-0.7	0.6	-1.2	0.4
Signal recognition particle receptor FtsY (SRP receptor)	Protein export	*ftsY*	BN194_17850	K0N5R8	0.1	1.1	-2.4	0.2	-2.5	0.2	-0.1	0.9	0.0	1.0
Membrane protein insertase YidC 1	Protein export	*yidC1*	BN194_18630	K0N9D1	0.3	1.2	-0.9	0.6	-1.1	0.5	-0.3	0.8	0.6	1.5
Protein translocase subunit SecY	Protein export	*secY*	BN194_26020	K0NCJ6	0.9	1.8	0.4	1.3	-0.5	0.7	0.9	1.8	1.1	2.2
Nucleoid occlusion protein	Cytokinesis	*noc*	BN194_02030	K0N4Z1	0.6	1.5	-0.8	0.6	-1.4	0.4	-3.7	0.1	0.1	1.1
Sporulation initiation inhibitor protein soj	Cytokinesis	*soj*	BN194_02040	K0MS45	-0.2	0.9	-4.7	0.0	-4.6	0.0	2.0	3.9	-2.4	0.2
Stage 0 sporulation protein J	Cytokinesis	*spo0J*	BN194_02050	K0N1F9	-0.4	0.8	-6.3	0.0	-5.9	0.0	-2.5	0.2	-1.2	0.4
Cell division ATP-binding protein FtsE	Cytokinesis	*ftsE*	BN194_10190	K0MTZ2	-0.4	0.8	-0.5	0.7	-0.1	0.9	-1.1	0.5	-0.4	0.8
Cell division protein FtsX	Cytokinesis	*ftsX*	BN194_10200	K0N3G0	-0.6	0.6	-0.8	0.6	-0.1	0.9	0.7	1.7	2.0	4.1
MreB-like protein	Cytokinesis	*mbl*	BN194_13650	K0N4K5	0.1	1.1	-2.1	0.2	-2.2	0.2	1.2	2.3	-1.3	0.4
Septation ring formation regulator EzrA	Cytokinesis	*ezrA*	BN194_14460	K0N4J2	0.3	1.3	-1.5	0.4	-1.8	0.3	0.9	1.8	-1.8	0.3
Rod shape-determining protein MreB	Cytokinesis	*mreB*	BN194_14550	K0N4R7	-0.3	0.8	-1.9	0.3	-1.7	0.3	0.6	1.5	-1.9	0.3
Cell shape-determining protein MreC (Cell shape protein MreC)	Cytokinesis	*mreC*	BN194_14560	K0N4K0	0.0	1.0	-0.8	0.6	-0.8	0.6	1.2	2.3	0.9	1.9
Septum formation inhibitor MinC, C-terminal domain family	Cytokinesis	*minC*	BN194_14580	K0N805	-0.3	0.8	-1.3	0.4	-1.0	0.5	-0.8	0.6	-0.6	0.7
Site-determining protein	Cytokinesis	*minD*	BN194_14590	K0MV70	0.7	1.6	-1.8	0.3	-2.5	0.2	0.1	1.1	-2.1	0.2
Penicillin-binding protein 2B	Cytokinesis	*pbpB*	BN194_14700	K0N4S9	0.3	1.2	-0.3	0.8	-0.6	0.7	3.7	13.4	3.3	10
Cell division protein DivIB	Cytokinesis	*divIB*	BN194_14740	K0MV80	-0.7	0.6	-2.2	0.2	-1.5	0.4	1.1	2.2	0.9	1.8
Cell division protein FtsA	Cytokinesis	*ftsA*	BN194_14750	K0N4T3	0.0	1.0	-3.4	0.1	-3.4	0.1	-0.3	0.8	-1.3	0.4
Cell division protein FtsZ	Cytokinesis	*ftsZ*	BN194_14760	K0N4L6	-0.4	0.8	-2.0	0.2	-1.6	0.3	0.7	1.6	-1.4	0.4
Septum site-determining protein DivIVA	Cytokinesis	*divIVA*	BN194_14800	K0N4T8	1.0	2.0	0.2	1.2	-0.8	0.6	-0.5	0.7	-1.4	0.4
Segregation and condensation protein B	Cytokinesis	*scpB*	BN194_15640	K0MVE6	-0.1	0.9	-2.0	0.2	-1.9	0.3	-1.5	0.4	1.0	2.0

Cell cycle protein GpsB (Guiding PBP1-shuttling protein)	Cytokinesis	*gpsB*	BN194_16690	K0MVN5	0.9	1.9	-0.6	0.7	-1.5	0.4	1.1	2.1	0.6	1.0
Putative N-acetylmuramoyl-L-alanine amidase YrvJ (EC 3.5.1.28)	Cytokinesis	*yrvJ*	BN194_17200	K0N5G4	-1.2	0.5	-1.4	0.4	-0.3	0.8	2.2	4.7	6.8	11
Chromosome partition protein Smc	Cytokinesis	*smc*	BN194_17860	K0N5H9	-0.8	0.6	-4.1	0.1	-3.4	0.1	-0.5	0.7	-3.7	0.1
DNA translocase SftA	Cytokinesis	*sftA*	BN194_18960	K0N5Q1	-0.2	0.8	-2.9	0.1	-2.7	0.2	0.5	1.4	-1.6	0.3
Cell wall surface anchor family protein	*Cell surface proteins/internalins*		BN194_05290	K0MSU3	-1.1	0.5	1.8	3.5	2.9	7.2	0.8	1.8	3.5	11
Dumpy	Cell surface proteins/internalins	*dp*	BN194_05390	K0MSV0	2.2	4.6	2.5	5.6	0.3	1.2	-0.7	0.6	-5.6	0.0
ABC transporter, ATP-binding protein	*Cell surface proteins/internalins*		BN194_15700	K0N514	-1.2	0.4	-1.1	0.5	0.2	1.1	-0.3	0.8	3.2	9.1
Uncharacterized protein yloA	Cell surface proteins/internalins	*yloA*	BN194_16340	K0MVK5	-1.5	0.3	-3.1	0.1	-1.6	0.3	-0.6	0.7	-0.8	0.0
Uncharacterized protein	*Cell surface proteins/internalins*		BN194_20060	K0N5Y7	1.4	2.7	-0.2	0.9	-1.6	0.3	2.1	4.3	-1.3	0.4
Probable dipeptidase A (EC 3.4.-.-)	Amino acid-related metabolism	*pepDA*	BN194_00410	K0N1E0	6.6	95.7	6.0	63.5	-0.6	0.7	4.1	17.4	-2.0	0.2
Putative carboxypeptidase SCO6489 (EC 3.4.16.-)			BN194_01370	K0N787	-0.4	0.8	2.3	5.1	2.7	6.5	-0.1	0.9	-3.2	0.1
4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase) (EC 1.17.1.8)	Amino acid-related metabolism	*dapB*	BN194_01000	K0N166	-0.4	0.7	0.1	1.1	0.5	1.4	2.2	4.6	2.5	5.8
4-hydroxy-tetrahydrodipicolinate synthase (HTPA synthase) (EC 4.3.3.7)	Amino acid-related metabolism	*dapA*	BN194_01010	K0N1I2	4.3	20.3	4.5	22.1	0.1	1.1	5.3	40.0	2.0	3.9
Diaminopimelate decarboxylase (DAP decarboxylase) (DAPDC) (EC 4.1.1.20)	Amino acid-related metabolism	*lysA*	BN194_01030	K0N4I7	0.9	1.9	2.0	4.0	1.1	2.1	1.0	2.0	0.1	1.1
Aspartate-semialdehyde dehydrogenase (ASA dehydrogenase) (ASADH) (EC 1.2.1.11) (Aspartate-beta-semialdehyde dehydrogenase)	Amino acid-related metabolism	*asd*	BN194_01060	K0N1I5	1.0	1.9	2.6	6.0	1.6	3.1	0.5	1.4	-2.7	0.2
Pyrrolidone-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-peptidase) (Pyroglutamyl-peptidase I)	Amino acid-related metabolism	*pcp*	BN194_01980	K0N4Y4	0.5	1.4	2.7	6.3	2.1	4.4	-0.3	0.8	-2.4	0.2
Aspartate racemase (EC 5.1.1.13)	*Amino acid-related metabolism*		BN194_02170	K0N7H2	-1.8	0.3	-3.2	0.1	-1.4	0.4	0.1	1.1	1.4	2.6
Oligoendopeptidase F homolog (EC 3.4.24.-)	Amino acid-related metabolism	*yjbG*	BN194_02530	K0N560	0.6	1.5	-0.5	0.7	-1.0	0.5	-0.2	0.9	-2.0	0.2
Peptidase T (EC 3.-.-.-) (EC 3.4.11.-) (EC 3.4.11.4)	Amino acid-related metabolism	*pepT*	BN194_03110	K0N213	4.1	17.2	5.2	37.6	1.1	2.2	3.3	9.6	-4.0	0.1
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA*	BN194_05120	K0N8B5	0.8	1.7	0.7	1.6	-0.1	0.9	0.4	1.3	-1.7	0.3
Aminopeptidase N (EC 3.4.11.2)	Amino acid-related metabolism	*pepN*	BN194_05410	K0N2F5	1.3	2.5	3.0	7.8	1.6	3.1	1.9	3.6	-2.0	0.3
Cysteine synthase (EC 2.5.1.47)	Amino acid-related metabolism	*cysK*	BN194_05520	K0N8E6	-1.7	0.3	-1.2	0.4	0.6	1.5	-2.1	0.2	0.5	1.4
5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Cobalamin-independent methionine synthase)	Amino acid-related metabolism	*metE*	BN194_06880	K0N658	4.4	20.9	-0.6	0.6	-5.0	0.0	4.6	23.6	0.3	1.3

(Methionine synthase, vitamin-B12 independent isozyme)														
Glutamate dehydrogenase	Amino acid-related metabolism	*gdh*	BN194_06980	K0N666	-0.2	0.8	0.7	1.7	1.0	2.0	0.3	1.3	-3.6	0.
Oligoendopeptidase F	Amino acid-related metabolism	*yjbG_2*	BN194_08130	K0N6H7	-1.0	0.5	-0.8	0.6	0.2	1.2	-0.2	0.9	-2.1	0.
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP*	BN194_08180	K0N6I0	1.5	2.9	0.9	1.9	-0.6	0.6	1.5	2.8	-3.3	0.
Uncharacterized protein yxjH	Amino acid-related metabolism	*yxjH*	BN194_08320	K0N962	2.6	6.2	-1.8	0.3	-4.4	0.0	1.3	2.5	-2.2	0.
S-ribosylhomocysteine lyase (EC 4.4.1.21) (AI-2 synthesis protein) (Autoinducer-2 production protein LuxS)	Amino acid-related metabolism	*luxS*	BN194_08330	K0N6J0	2.4	5.3	5.1	34.0	2.7	6.4	2.6	6.2	-1.1	0.
Xaa-Pro dipeptidase (EC 3.4.13.9)	Amino acid-related metabolism	*pepQ*	BN194_08740	K0MTP0	1.7	3.2	2.4	5.2	0.7	1.6	1.7	3.1	-1.9	0.
Beta-Ala-Xaa dipeptidase (EC 3.4.13.-)	Amino acid-related metabolism	*pepV*	BN194_08800	K0N324	0.4	1.4	2.5	5.5	2.0	4.0	-0.7	0.6	-1.1	0.
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA*	BN194_09090	K0MTR3	1.0	2.0	1.0	1.9	0.0	1.0	2.8	7.0	-2.1	0.
Cystathionine beta-lyase PatB (EC 4.4.1.8)	Amino acid-related metabolism	*patB_2*	BN194_09790	K0MTW3	-0.9	0.5	-1.0	0.5	0.0	1.0	-1.0	0.5	-1.7	0.
Predicted Zn-dependent peptidase	*Amino acid-related metabolism*		BN194_10020	K0N9H8	-0.6	0.6	1.2	2.3	1.9	3.6	1.0	2.0	-2.4	0.
Uncharacterized zinc protease ymfH (EC 3.4.24.-)	Amino acid-related metabolism	*ymfH*	BN194_10030	K0N6V9	-0.5	0.7	1.2	2.4	1.7	3.2	0.4	1.3	-1.7	0.
Oligoendopeptidase, pepF/M3 family	*Amino acid-related metabolism*		BN194_11580	K0N779	0.0	1.0	1.1	2.1	1.0	2.0	0.3	1.2	-2.4	0.
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO*	BN194_12030	K0N7B7	2.3	4.9	2.7	6.6	0.4	1.4	0.8	1.8	-4.1	0.
Aminopeptidase pepS (EC 3.4.11.-)	Amino acid-related metabolism	*pepS*	BN194_12180	K0N7D5	-0.4	0.8	2.6	5.9	2.9	7.7	-2.9	0.1	-3.7	0.
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_13380	K0N7S0	0.0	1.0	2.5	5.7	2.5	5.7	0.5	1.5	-3.8	0.
Serine hydroxymethyltransferase (SHMT) (Serine methylase) (EC 2.1.2.1)	Amino acid-related metabolism	*glyA*	BN194_13540	K0MV12	-1.3	0.4	-5.6	0.0	-4.3	0.1	1.4	2.7	-2.6	0.
Glycine cleavage system H protein	Amino acid-related metabolism	*gcvH*	BN194_13700	K0N4K8	-0.6	0.7	1.7	3.3	2.3	4.9	-1.5	0.4	-0.1	0.
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE*	BN194_13710	K0N4D8	1.6	3.0	2.5	5.5	0.9	1.8	0.2	1.2	-3.2	0.
Probable L-serine dehydratase, beta chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAB*	BN194_13940	K0MV34	-0.4	0.8	-3.9	0.1	-3.6	0.1	-0.4	0.7	-1.8	0.
Probable L-serine dehydratase, alpha chain (EC 4.3.1.17)	Amino acid-related metabolism	*sdaAA*	BN194_13950	K0N4M4	0.1	1.1	-4.0	0.1	-4.1	0.1	-0.3	0.8	-2.6	0.
5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 2 (EC 3.2.2.9) (5'-methylthioadenosine/S-adenosylhomocysteine	Amino acid-related metabolism	*mtnN*	BN194_14890	K0MV90	0.1	1.1	-1.5	0.4	-1.6	0.3	0.4	1.3	-1.9	0.

nucleosidase) (5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase 1)														
Neutral endopeptidase (EC 3.4.24.-)	Amino acid-related metabolism	*pepO_2*	BN194_16630	K0N8Q0	0.2	1.1	2.5	5.6	2.3	4.9	0.1	1.1	-2.7	0.2
Aspartate aminotransferase (EC 2.6.1.1)	Amino acid-related metabolism	*aspC*	BN194_16770	K0NAU6	-0.5	0.7	-1.8	0.3	-1.3	0.4	0.3	1.2	-2.4	0.2
Uncharacterized peptidase yqhT (EC 3.4.-.-)	Amino acid-related metabolism	*yqhT*	BN194_18260	K0N5K4	2.1	4.3	1.1	2.1	-1.0	0.5	4.1	16.9	-1.1	0.5
Glutamine synthetase (EC 6.3.1.2)	Amino acid-related metabolism	*glnA_2*	BN194_18340	K0MW64	-2.3	0.2	-6.5	0.0	-4.2	0.1	0.7	1.6	0.2	1.2
Probable succinyl-diaminopimelate desuccinylase (EC 3.5.1.18)	Amino acid-related metabolism	*dapE_2*	BN194_19740	K0MWF1	0.7	1.7	-0.9	0.5	-1.6	0.3	1.2	2.4	-1.6	0.3
Pyrroline-5-carboxylate reductase (P5C reductase) (P5CR) (EC 1.5.1.2) (PCA reductase)	Amino acid-related metabolism	*proC*	BN194_19900	K0N677	0.1	1.1	2.0	3.9	1.9	3.7	-0.2	0.9	0.0	1.0
Uncharacterized peptidase yuxL (EC 3.4.21.-)	Amino acid-related metabolism	*yuxL*	BN194_19910	K0N5X4	0.1	1.1	-2.0	0.2	-2.2	0.2	-0.1	1.0	-1.7	0.3
Acetolactate synthase (EC 2.2.1.6)	Amino acid-related metabolism	*alsS*	BN194_20150	K0N695	1.6	2.9	3.1	8.4	1.5	2.9	-1.0	0.5	-5.0	0.0
Probable dipeptidase B (EC 3.4.-.-)	Amino acid-related metabolism	*pepDB*	BN194_21110	K0N678	3.2	9.1	5.0	32.8	1.8	3.6	1.8	3.6	-2.6	0.2
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*fpaP_3*	BN194_21160	K0N682	0.8	1.8	-1.6	0.3	-2.5	0.2	0.4	1.3	-2.0	0.2
Putative N-acetyl-LL-diaminopimelate aminotransferase (EC 2.6.1.-)	Amino acid-related metabolism	*patA_2*	BN194_22950	K0N7F8	-2.0	0.3	-4.7	0.0	-2.7	0.1	-1.8	0.3	-2.5	0.2
Asparagine synthetase [glutamine-hydrolyzing] 1 (EC 6.3.5.4)	Amino acid-related metabolism	*asnB*	BN194_22990	K0MX90	-0.4	0.8	-3.3	0.1	-2.9	0.1	0.0	1.0	-0.8	0.0
Probable dipeptidase (EC 3.4.-.-)	*Amino acid-related metabolism*		BN194_23190	K0MXA1	-1.2	0.4	2.2	4.5	3.3	9.9	-1.9	0.3	-3.2	0.1
L-asparaginase (EC 3.5.1.1)	Amino acid-related metabolism	*ansA*	BN194_23900	K0N7L6	0.7	1.6	2.9	7.4	2.2	4.7	-1.0	0.5	-4.1	0.1
Succinate-semialdehyde dehydrogenase [NADP(+)] (EC 1.2.1.79)	Amino acid-related metabolism	*ssdA*	BN194_24140	K0MXE0	-0.2	0.9	-2.9	0.1	-2.7	0.2	0.8	1.8	-1.1	0.5
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC*	BN194_24670	K0NC50	1.9	3.8	3.2	9.2	1.3	2.4	4.2	17.8	-3.0	0.1
Aminopeptidase C (EC 3.4.22.40)	Amino acid-related metabolism	*pepC_2*	BN194_24680	K0NAC2	0.0	1.0	2.1	4.2	2.1	4.3	0.8	1.7	-2.3	0.2
Alanine racemase (EC 5.1.1.1)	Amino acid-related metabolism	*alr*	BN194_26680	K0NAR1	1.1	2.1	1.4	2.7	0.4	1.3	0.6	1.5	-2.1	0.2
Proline iminopeptidase (PIP) (EC 3.4.11.5) (Prolyl aminopeptidase)	Amino acid-related metabolism	*pip_2*	BN194_27140	K0MY30	4.6	23.5	6.1	70.5	1.6	3.0	2.1	4.3	-3.2	0.1
Uncharacterized aminotransferase SSO0104 (EC 2.6.1.-)	*Amino acid-related metabolism*		BN194_27600	K0N8N4	4.9	29.2	6.8	109.8	1.9	3.8	0.1	1.1	-5.3	0.0
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC*	BN194_00080	K0N486	-0.7	0.6	0.8	1.7	1.5	2.8	1.6	3.1	-2.8	0.1

Adenylosuccinate synthetase (AMPSase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase)	Nucleic acid/nucleotide metabolism	*purA*	BN194_01160	K0N1J0	-1.4	0.4	-0.4	0.8	1.1	2.1	0.8	1.7	-1.6	0.3
Anaerobic ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*nrdD*	BN194_01250	K0N190	-0.5	0.7	-3.6	0.1	-3.1	0.1	1.1	2.2	-1.3	0.4
Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205)	Nucleic acid/nucleotide metabolism	*guaB*	BN194_02100	K0N1G3	-0.9	0.6	-4.1	0.1	-3.2	0.1	-2.1	0.2	-1.6	0.3
Deoxyribose-phosphate aldolase (DERA) (EC 4.1.2.4) (2-deoxy-D-ribose 5-phosphate aldolase) (Phosphodeoxyriboaldolase)	Nucleic acid/nucleotide metabolism	*deoC_2,deoC*	BN194_02790	K0MSB5	0.7	1.6	3.3	10.2	2.7	6.4	-1.5	0.3	-1.5	0.4
Phosphopentomutase (EC 5.4.2.7) (Phosphodeoxyribomutase)	Nucleic acid/nucleotide metabolism	*deoB*	BN194_02800	K0N1N0	0.7	1.7	2.9	7.2	2.1	4.4	1.1	2.2	-3.5	0.1
Purine nucleoside phosphorylase DeoD-type (PNP) (EC 2.4.2.1)	Nucleic acid/nucleotide metabolism	*deoD*	BN194_02810	K0N1Z0	0.5	1.4	2.7	6.6	2.2	4.5	0.6	1.5	-0.9	0.0
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	*ndk*	BN194_08160	K0N340	-3.4	0.1	-5.5	0.0	-2.1	0.2	-1.7	0.3	1.3	2.4
Putative nrdI-like protein	*Nucleic acid/nucleotide metabolism*		BN194_08250	K0N300	0.5	1.4	-0.1	0.9	-0.6	0.6	-0.3	0.8	-0.7	0.0
Putative HAD-hydrolase yfnB (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yfnB*	BN194_08780	K0N6M1	-2.1	0.2	-1.9	0.3	0.2	1.1	0.3	1.2	-0.3	0.8
Uncharacterized metallophosphoesterase yunD	Nucleic acid/nucleotide metabolism	*yunD*	BN194_08890	K0MTQ0	1.0	2.0	-0.3	0.8	-1.3	0.4	-0.6	0.7	-1.9	0.3
Uncharacterized hydrolase yutF (EC 3.-.-.-)	Nucleic acid/nucleotide metabolism	*yutF*	BN194_08910	K0N383	-0.2	0.9	-1.5	0.3	-1.4	0.4	0.2	1.1	-1.8	0.3
GTP pyrophosphokinase yjbM (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*yjbM*	BN194_09870	K0N9G5	-1.4	0.4	-4.4	0.0	-3.0	0.1	1.7	3.3	-0.9	0.0
GMP reductase (EC 1.7.1.7) (Guanosine 5'-monophosphate oxidoreductase)	Nucleic acid/nucleotide metabolism	*guaC*	BN194_09960	K0N3H4	-1.4	0.4	-5.9	0.0	-4.5	0.0	-0.2	0.8	-0.2	0.9
Xanthine phosphoribosyltransferase (XPRTase) (EC 2.4.2.22)	Nucleic acid/nucleotide metabolism	*xpt*	BN194_12490	K0MUR6	-1.9	0.3	-3.9	0.1	-2.0	0.2	-2.4	0.2	0.0	1.0
Phosphoribosylglycinamide formyltransferase 2 (EC 2.1.2.-)	Nucleic acid/nucleotide metabolism	*purK*	BN194_12510	K0N441	-1.2	0.4	0.0	1.0	1.2	2.3	-1.4	0.4	-0.7	0.0
Adenylosuccinate lyase (ASL) (EC 4.3.2.2) (Adenylosuccinase)	Nucleic acid/nucleotide metabolism	*purB*	BN194_12520	K0NA41	-4.2	0.1	-8.4	0.0	-4.2	0.1	-2.8	0.1	-0.7	0.0
Guanine deaminase (EC 3.5.4.3)	Nucleic acid/nucleotide metabolism	*guaD*	BN194_13320	K0NA96	1.3	2.4	1.7	3.3	0.4	1.4	1.1	2.2	-2.4	0.2
Thymidine kinase (EC 2.7.1.21)	Nucleic acid/nucleotide metabolism	*tdk*	BN194_13500	K0N4J4	-1.6	0.3	-3.0	0.1	-1.4	0.4	-0.6	0.7	0.2	1.1
Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase)	Nucleic acid/nucleotide metabolism	*upp*	BN194_13550	K0N4J8	-0.9	0.5	-4.8	0.0	-3.9	0.1	-3.0	0.1	-0.7	0.0
Deoxyguanosine kinase (EC 2.7.1.113)	*Nucleic acid/nucleotide metabolism*		BN194_14000	K0N4M7	4.6	24.4	0.1	1.0	-4.6	0.0	3.6	12.0	-1.6	0.3
Multifunctional protein: 5-nucleotidase 2,3-cyclic-nucleotide 2-phosphodiesterase	Nucleic acid/nucleotide metabolism	*ushA*	BN194_15530	K0N8A9	0.5	1.4	2.9	7.4	2.4	5.2	-0.5	0.7	-2.3	0.2
Cytidylate kinase (CK) (EC 2.7.4.25) (Cytidine monophosphate kinase)	Nucleic acid/nucleotide metabolism	*cmk*	BN194_15710	K0N4V1	-0.8	0.6	-2.0	0.3	-1.1	0.5	-0.5	0.7	-2.3	0.2

Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleic acid/nucleotide metabolism	*thyA*	BN194_15800	K0N522	-0.8	0.6	-4.3	0.1	-3.5	0.1	0.3	1.3	-2.5	0.
Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23) (OMP decarboxylase)	Nucleic acid/nucleotide metabolism	*pyrF*	BN194_16430	K0N8M7	-1.7	0.3	-4.0	0.1	-2.2	0.2	-0.2	0.9	3.2	9.
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrD*	BN194_16440	K0MVL3	1.1	2.1	2.9	7.6	1.8	3.6	-0.2	0.9	-1.3	0.
Carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5)	Nucleic acid/nucleotide metabolism	*carB*	BN194_16450	K0N587	0.6	1.5	-1.9	0.3	-2.5	0.2	-0.1	0.9	-3.6	0.
Carbamoyl-phosphate synthase small chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase glutamine chain)	Nucleic acid/nucleotide metabolism	*carA*	BN194_16460	K0N535	0.5	1.4	-2.6	0.2	-3.1	0.1	-0.3	0.8	-3.9	0.
Dihydroorotase (DHOase) (EC 3.5.2.3)	Nucleic acid/nucleotide metabolism	*pyrC*	BN194_16470	K0NAS6	-1.9	0.3	-5.9	0.0	-4.0	0.1	-1.4	0.4	0.5	1.
Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate transcarbamylase)	Nucleic acid/nucleotide metabolism	*pyrB*	BN194_16480	K0N8N2	3.0	7.9	0.5	1.4	-2.5	0.2	1.7	3.2	-1.8	0.
Ribonucleoside-diphosphate reductase (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdE2*	BN194_16600	K0N5A1	0.6	1.5	0.4	1.3	-0.2	0.9	1.2	2.3	-2.6	0.
Ribonucleoside-diphosphate reductase subunit beta (EC 1.17.4.1)	Nucleic acid/nucleotide metabolism	*nrdF*	BN194_16610	K0N552	0.6	1.5	0.4	1.3	-0.2	0.9	0.3	1.2	-1.2	0.
Cytidine deaminase (EC 3.5.4.5)	Nucleic acid/nucleotide metabolism	*cdd*	BN194_17000	K0N5D8	1.2	2.3	3.5	11.7	2.3	5.0	0.1	1.1	-0.6	0.
GTP pyrophosphokinase (EC 2.7.6.5)	Nucleic acid/nucleotide metabolism	*relA*	BN194_17230	K0N8Y0	0.3	1.2	-3.0	0.1	-3.3	0.1	-1.3	0.4	-1.3	0.
Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	Nucleic acid/nucleotide metabolism	*apt*	BN194_17380	K0N902	-0.9	0.5	-2.8	0.1	-1.9	0.3	0.2	1.1	0.0	1.
Uridylate kinase (EC 2.7.4.22)	Nucleic acid/nucleotide metabolism	*pyrH*	BN194_17660	K0N5E6	-0.2	0.8	-3.4	0.1	-3.1	0.1	-0.8	0.6	-1.2	0.
Guanylate kinase (EC 2.7.4.8) (GMP kinase)	Nucleic acid/nucleotide metabolism	*gmk*	BN194_18110	K0N5J6	-1.8	0.3	-4.4	0.0	-2.6	0.2	0.2	1.1	-1.0	0.
Dihydroorotate dehydrogenase (DHOD) (DHODase) (DHOdehase) (EC 1.3.-.-)	Nucleic acid/nucleotide metabolism	*pyrDA, pyrD*	BN194_19150	K0N623	1.5	2.8	3.7	13.5	2.3	4.8	0.6	1.5	-2.3	0.
Anaerobic ribonucleoside-triphosphate reductase-activating protein (EC 1.97.1.-)	Nucleic acid/nucleotide metabolism	*nrdG*	BN194_19270	K0NB93	-0.2	0.9	-1.3	0.4	-1.1	0.5	1.4	2.6	0.6	1.
Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	Nucleic acid/nucleotide metabolism	*purD*	BN194_19290	K0MWC4	-1.3	0.4	-2.2	0.2	-0.9	0.5	-2.9	0.1	-3.0	0.
Bifunctional purine biosynthesis protein PurH	Nucleic acid/nucleotide metabolism	*purH*	BN194_19300	K0N634	-3.4	0.1	-7.6	0.0	-4.1	0.1	-2.0	0.3	-1.2	0.
Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)	Nucleic acid/nucleotide metabolism	*purN*	BN194_19310	K0N5S4	-3.2	0.1	-0.3	0.8	2.9	7.4	-0.1	0.9	-0.4	0.
Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase)	Nucleic acid/nucleotide metabolism	*purM*	BN194_19320	K0NB95	-1.8	0.3	-4.7	0.0	-2.9	0.1	-1.9	0.3	-3.8	0.
Phosphoribosylformylglycinamidine synthase subunit PurL (FGAM synthase) (EC 6.3.5.3)	Nucleic acid/nucleotide metabolism	*purL*	BN194_19330	K0N9H6	-2.2	0.2	-8.3	0.0	-6.2	0.0	-1.0	0.5	-3.2	0.

(Formylglycinamide ribonucleotide amidotransferase subunit II) (Glutamine amidotransferase PurL) (Phosphoribosylformylglycinamidine synthase subunit II)														
Phosphoribosylformylglycinamidine synthase subunit PurQ (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit I) (Glutaminase PurQ) (Phosphoribosylformylglycinamidine synthase subunit I)	Nucleic acid/nucleotide metabolism	*purQ*	BN194_19340	K0MWC7	-1.4	0.4	-6.6	0.0	-5.2	0.0	-1.2	0.4	-2.9	0.
Phosphoribosylformylglycinamidine synthase subunit PurS (FGAM synthase) (EC 6.3.5.3) (Formylglycinamide ribonucleotide amidotransferase subunit III) (Phosphoribosylformylglycinamidine synthase subunit III)	Nucleic acid/nucleotide metabolism	*yexA,purS*	BN194_19350	K0N638	-2.4	0.2	-5.2	0.0	-2.8	0.1	-2.0	0.3	-0.8	0.
Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6) (SAICAR synthetase)	Nucleic acid/nucleotide metabolism	*purC*	BN194_19360	K0N5S8	-1.2	0.4	-9.4	0.0	-8.2	0.0	-0.1	1.0	-2.9	0.
N5-carboxyaminoimidazole ribonucleotide synthase (N5-CAIR synthase) (EC 6.3.4.18) (5-(carboxyamino)imidazole ribonucleotide synthetase)	Nucleic acid/nucleotide metabolism	*purK_2, purK*	BN194_19370	K0NB96	-4.1	0.1	-8.2	0.0	-4.1	0.1	-2.5	0.2	-0.5	0.
N5-carboxyaminoimidazole ribonucleotide mutase (N5-CAIR mutase) (EC 5.4.99.18) (5-(carboxyamino)imidazole ribonucleotide mutase)	Nucleic acid/nucleotide metabolism	*purE*	BN194_19380	K0N9H9	-0.4	0.7	-0.1	0.9	0.3	1.3	-2.0	0.2	-1.2	0.
GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	Nucleic acid/nucleotide metabolism	*guaA*	BN194_21070	K0NBJ2	-1.4	0.4	-5.3	0.0	-3.9	0.1	-1.7	0.3	-1.7	0.
Guanylate kinase (EC 2.7.4.8)	Nucleic acid/nucleotide metabolism	*gmk_2*	BN194_21480	K0N9Y7	-1.0	0.5	-1.6	0.3	-0.6	0.7	1.6	3.0	-1.6	0.
Pyrimidine-nucleoside phosphorylase (EC 2.4.2.2)	Nucleic acid/nucleotide metabolism	*pdp*	BN194_23430	K0NA73	-0.1	0.9	-3.9	0.1	-3.7	0.1	-0.5	0.7	-1.2	0.
Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase)	Nucleic acid/nucleotide metabolism	*add*	BN194_23440	K0MXB1	-0.3	0.8	2.1	4.3	2.4	5.2	0.2	1.1	-3.1	0.
Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	Nucleic acid/nucleotide metabolism	*tmk*	BN194_23950	K0N7L9	-1.6	0.3	-1.8	0.3	-0.3	0.8	-1.0	0.5	-0.1	0.
Adenosylcobalamin-dependent ribonucleoside-triphosphate reductase (EC 1.17.4.2)	Nucleic acid/nucleotide metabolism	*rtpR*	BN194_24230	K0NAA3	0.1	1.1	-4.4	0.0	-4.5	0.0	0.4	1.3	-2.3	0.
Nucleoside deoxyribosyltransferase (EC 2.4.2.6)	Nucleic acid/nucleotide metabolism	*ntd*	BN194_24240	K0MXE6	0.3	1.2	-3.3	0.1	-3.6	0.1	1.2	2.3	-1.9	0.
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	*dut*	BN194_24640	K0MXG3	-1.2	0.4	-3.7	0.1	-2.5	0.2	0.3	1.2	5.5	44
Uridine phosphorylase (EC 2.4.2.3)	Nucleic acid/nucleotide metabolism	*udp*	BN194_24830	K0NAD0	1.1	2.1	-3.6	0.1	-4.7	0.0	0.5	1.5	-3.2	0.
Adenylate kinase (EC 2.7.4.3)	Nucleic acid/nucleotide metabolism	*adk*	BN194_26010	K0N7F0	-0.9	0.5	-2.3	0.2	-1.3	0.4	-1.9	0.3	-1.1	0.
Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)	Nucleic acid/nucleotide metabolism	*hpt*	BN194_26470	K0NCR2	-0.2	0.9	1.5	2.9	1.7	3.2	-0.1	1.0	-3.1	0.

CTP synthase (EC 6.3.4.2) (CTP synthetase) (UTP--ammonia ligase)	Nucleic acid/nucleotide metabolism	*pyrG*	BN194_26790	K0MXZ1	-0.9	0.5	-4.6	0.0	-3.7	0.1	0.3	1.2	-1.8	0.3
Ribose-phosphate pyrophosphokinase (RPPK) (EC 2.7.6.1) (5-phospho-D-ribosyl alpha-1-diphosphate) (Phosphoribosyl diphosphate synthase) (Phosphoribosyl pyrophosphate synthase)	Nucleic acid/nucleotide metabolism	*prs1,prs*	BN194_26930	K0NAT2	-1.4	0.4	-4.7	0.0	-3.3	0.1	0.3	1.2	-1.0	0.5
Uncharacterized protein	*Nucleic acid/nucleotide metabolism*		BN194_27260	K0N7R1	-1.4	0.4	-3.5	0.1	-2.1	0.2	-3.1	0.1	-1.2	0.4
Ribose-phosphate pyrophosphokinase 1 (EC 2.7.6.1)	Nucleic acid/nucleotide metabolism	*prs1_2*	BN194_30370	K0NDQ5	-1.1	0.5	-4.9	0.0	-3.8	0.1	-0.5	0.7	-0.2	0.8
Oleate hydratase (EC 4.2.1.53)	Lipid-related metabolism	*sph*	BN194_04930	K0N5Q0	0.8	1.7	-0.5	0.7	-1.3	0.4	0.9	1.8	-2.4	0.2
Bifunctional protein BirA (EC 6.3.4.15)	Lipid-related metabolism	*birA*	BN194_08790	K0MTP3	-0.8	0.6	0.8	1.7	1.6	3.0	-0.1	1.0	1.2	2.2
Uncharacterized protein yutG	Lipid-related metabolism	*yutG*	BN194_08940	K0MTQ3	-1.6	0.3	-5.3	0.0	-3.7	0.1	1.5	2.9	0.8	1.7
Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94) (NAD(P)H-dependent glycerol-3-phosphate dehydrogenase)	Lipid-related metabolism	*gpsA*	BN194_10350	K0N3I2	-2.8	0.1	-6.4	0.0	-3.5	0.1	0.2	1.1	0.1	1.1
Uncharacterized protein	*Lipid-related metabolism*		BN194_11980	K0N7B3	0.2	1.1	-4.9	0.0	-5.1	0.0	-0.5	0.7	0.5	1.4
Mevalonate kinase (EC 2.7.1.36)	Lipid-related metabolism	*mvk*	BN194_12270	K0NA23	-0.9	0.5	-5.1	0.0	-4.2	0.1	-0.5	0.7	-0.4	0.8
Diphosphomevalonate decarboxylase (EC 4.1.1.33)	Lipid-related metabolism	*mvd1*	BN194_16830	K0N8S2	-1.8	0.3	-3.6	0.1	-1.8	0.3	-0.2	0.9	2.5	5.8
Isopentenyl-diphosphate delta-isomerase (IPP isomerase) (EC 5.3.3.2) (Isopentenyl diphosphate:dimethylallyl diphosphate isomerase) (Isopentenyl pyrophosphate isomerase) (Type 2 isopentenyl diphosphate isomerase)	Lipid-related metabolism	*fni*	BN194_16840	K0MVP7	-1.0	0.5	-1.6	0.3	-0.7	0.6	-0.3	0.8	0.5	1.4
Isoprenyl transferase (EC 2.5.1.-)	Lipid-related metabolism	*uppS*	BN194_17640	K0MVX1	-0.2	0.8	-1.8	0.3	-1.6	0.3	-0.3	0.8	3.4	10
1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.-)	Lipid-related metabolism	*plsC*	BN194_17710	K0N5F1	0.0	1.0	-0.2	0.8	-0.3	0.8	2.1	4.1	0.7	1.6
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP*	BN194_17930	K0N988	1.6	3.1	4.6	24.4	3.0	7.9	-1.5	0.3	1.3	2.4
Phosphate acyltransferase (EC 2.3.1.n2) (Acyl-ACP phosphotransacylase) (Acyl-[acyl-carrier-protein]--phosphate acyltransferase) (Phosphate-acyl-ACP acyltransferase)	Lipid-related metabolism	*plsX*	BN194_17940	K0MW37	-0.5	0.7	-2.2	0.2	-1.8	0.3	-0.7	0.6	0.0	1.0
Farnesyl diphosphate synthase (EC 2.5.1.10)	Lipid-related metabolism	*ispA*	BN194_18180	K0N9A2	-0.1	0.9	-1.4	0.4	-1.2	0.4	0.3	1.3	0.6	1.6
Hydroxymethylglutaryl-CoA synthase	Lipid-related metabolism	*hmgCS1*	BN194_19680	K0N9K3	-1.4	0.4	-2.3	0.2	-0.9	0.5	-0.1	0.9	-2.4	0.2
3-hydroxy-3-methylglutaryl coenzyme A reductase (HMG-CoA reductase) (EC 1.1.1.88)	Lipid-related metabolism	*mvaA*	BN194_19690	K0MWE8	-1.9	0.3	-3.6	0.1	-1.7	0.3	-1.6	0.3	-0.2	0.8
Branched-chain-amino-acid aminotransferase (EC 2.6.1.42)	Lipid-related metabolism	*ilvE*	BN194_21620	K0NBM4	0.9	1.9	1.6	3.0	0.6	1.5	3.8	13.8	-1.8	0.3
Probable fatty acid methyltransferase (EC 2.1.1.-)	*Lipid-related metabolism*		BN194_22460	K0N6M0	1.5	2.8	-3.3	0.1	-4.8	0.0	1.5	2.8	0.6	1.5

Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	*accA*	BN194_22470	K0NBS6	4.6	23.7	0.3	1.3	-4.2	0.1	1.3	2.5	-2.0	0.3
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta (ACCase subunit beta) (Acetyl-CoA carboxylase carboxyltransferase subunit beta) (EC 6.4.1.2)	Lipid-related metabolism	*accD*	BN194_22480	K0NA32	3.9	15.2	0.1	1.1	-3.8	0.1	1.0	2.0	-1.8	0.3
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	*fabZ*	BN194_22520	K0NBS8	-1.4	0.4	-4.1	0.1	-2.6	0.2	0.7	1.7	3.6	12
Biotin carboxyl carrier protein of acetyl-CoA carboxylase	Lipid-related metabolism	*accB*	BN194_22530	K0NA35	1.0	2.0	0.8	1.8	-0.2	0.9	0.8	1.7	-2.9	0.1
3-oxoacyl-[acyl-carrier-protein] synthase 2 (EC 2.3.1.179)	Lipid-related metabolism	*fabF*	BN194_22540	K0MX40	0.9	1.9	1.1	2.1	0.2	1.1	2.0	4.0	-0.2	0.9
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	*bkr4*	BN194_22550	K0N799	-1.0	0.5	-2.7	0.2	-1.7	0.3	0.6	1.5	4.0	15
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	*fabG*	BN194_22560	K0N6N3	-1.1	0.5	-4.0	0.1	-2.9	0.1	0.0	1.0	2.7	6.7
Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)	Lipid-related metabolism	*fabD*	BN194_22570	K0NBT1	-0.4	0.8	-3.1	0.1	-2.7	0.2	-0.2	0.9	-0.9	0.5
Probable nitronate monooxygenase (EC 1.13.12.16)	Lipid-related metabolism	*fabK*	BN194_22580	K0NA38	1.5	2.9	-1.7	0.3	-3.2	0.1	0.8	1.8	-1.7	0.3
Acyl carrier protein (ACP)	Lipid-related metabolism	*acpP_2, acpP*	BN194_22590	K0MX45	1.0	2.0	2.5	5.6	1.5	2.7	1.0	2.0	-0.1	0.9
3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC 2.3.1.180) (3-oxoacyl-[acyl-carrier-protein] synthase III) (Beta-ketoacyl-ACP synthase III)	Lipid-related metabolism	*fabH*	BN194_22600	K0N7B0	0.8	1.7	-3.0	0.1	-3.8	0.1	-0.2	0.9	-1.6	0.3
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	*fabZ_2*	BN194_22620	K0NBT3	-1.4	0.4	-5.2	0.0	-3.8	0.1	0.1	1.0	1.0	2.0
Acyl-ACP thioesterase	*Lipid-related metabolism*		BN194_23910	K0N709	-0.5	0.7	-1.6	0.3	-1.1	0.5	0.1	1.1	-4.2	0.3
Predicted acetyltransferase			BN194_11820	K0N9Y9	-0.1	0.9	-0.9	0.5	-0.8	0.6	1.0	2.0	-1.6	0.3
Biotin carboxylase (EC 6.3.4.14) (EC 6.4.1.2)		*accC*	BN194_22510	K0N6M5	0.1	1.1	-1.0	0.5	-1.1	0.5	2.0	4.0	-0.3	0.8
Acyltransferase 3			BN194_15460	K0N4S6	0.3	1.3	-1.3	0.4	-1.7	0.3	0.8	1.7	2.2	4.0
Pyridoxine 5'-phosphate oxidase V related favin-nucleotide-binding protein	*Cofactor-related metabolism*		BN194_01900	K0N1E7	2.6	6.0	3.4	10.7	0.8	1.8	0.9	1.9	-3.1	0.1
Uncharacterized protein MJ0282	*Cofactor-related metabolism*		BN194_03700	K0N1T2	0.4	1.3	2.6	6.2	2.2	4.7	-2.0	0.2	-0.7	0.0
Hydroxymethylpyrimidine/phosphomethylpyrimidine kinase (EC 2.7.1.49) (EC 2.7.4.7)	Cofactor-related metabolism	*thiD_2*	BN194_07650	K0N2U9	-0.5	0.7	-1.4	0.4	-0.9	0.5	1.0	2.0	-2.6	0.2
S-adenosylmethionine synthase (AdoMet synthase) (EC 2.5.1.6) (MAT) (Methionine adenosyltransferase)	Cofactor-related metabolism	*metK*	BN194_09150	K0N352	1.8	3.4	0.8	1.7	-1.0	0.5	1.3	2.5	-2.3	0.2
ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136) (ADP-dependent NAD(P)HX dehydratase)	Cofactor-related metabolism	*nnrD*	BN194_09250	K0N360	1.9	3.6	-0.3	0.8	-2.2	0.2	2.0	4.0	3.4	10
Probable ABC transporter ATP-binding protein spyM18_0273	*Cofactor-related metabolism*		BN194_13770	K0NAC0	0.0	1.0	-3.8	0.1	-3.9	0.1	0.3	1.2	-0.9	0.5

FeS cluster assembly protein sufD	Cofactor-related metabolism	*sufD*	BN194_13780	K0N7U0	0.1	1.0	-3.7	0.1	-3.8	0.1	0.0	1.0	-2.4	0.
Cysteine desulfurase (EC 2.8.1.7)	Cofactor-related metabolism	*csd*	BN194_13790	K0MV25	1.8	3.6	2.9	7.6	1.1	2.1	-0.6	0.7	-2.8	0.
NifU-like protein	Cofactor-related metabolism	*nifU*	BN194_13800	K0N4L4	-0.2	0.9	-1.0	0.5	-0.8	0.6	-1.0	0.5	-0.4	0.
FeS cluster assembly protein sufB	Cofactor-related metabolism	*sufB*	BN194_13810	K0N4E5	-0.1	0.9	-5.1	0.0	-5.0	0.0	1.0	2.0	-2.3	0.
Glutamate--cysteine ligase/gamma-glutamylcysteine synthetase	Cofactor-related metabolism	*gshAB*	BN194_13910	K0N4F0	1.0	2.1	-4.6	0.0	-5.7	0.0	2.9	7.7	-2.5	0.
NifS/IcsS protein homolog	*Cofactor-related metabolism*		BN194_14470	K0NAF3	0.9	1.8	-0.3	0.8	-1.1	0.5	1.0	2.0	-1.9	0.
Probable tRNA sulfurtransferase (EC 2.8.1.4) (Sulfur carrier protein ThiS sulfurtransferase) (Thiamine biosynthesis protein ThiI) (tRNA 4-thiouridine synthase)	Cofactor-related metabolism	*thiI*	BN194_14480	K0N7Z7	0.1	1.1	-3.2	0.1	-3.3	0.1	0.6	1.5	0.3	1.
Putative cysteine desulfurase IscS 1 (EC 2.8.1.7)	Cofactor-related metabolism	*iscS1*	BN194_14900	K0N4U8	-0.7	0.6	1.0	2.0	1.7	3.3	0.3	1.3	-2.1	0.
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate adenylyltransferase)	Cofactor-related metabolism	*coaD*	BN194_15200	K0N4X3	-5.0	0.0	-5.4	0.0	-0.4	0.8	0.4	1.4	1.6	3.
Protein RibT (EC 2.3.1.-)	Cofactor-related metabolism	*ribT*	BN194_15620	K0NAL0	0.0	1.0	-1.8	0.3	-1.9	0.3	-0.2	0.9	0.0	1.
Dihydrofolate reductase (EC 1.5.1.3)	Cofactor-related metabolism	*folA*	BN194_15810	K0N4W0	-0.3	0.8	1.5	2.8	1.7	3.3	-1.9	0.3	-3.3	0.
Formate--tetrahydrofolate ligase (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	Cofactor-related metabolism	*fhs*	BN194_16520	K0NAT0	0.4	1.3	2.1	4.2	1.7	3.2	0.5	1.4	-3.2	0.
Lipoate--protein ligase (EC 2.7.7.63)	Cofactor-related metabolism	*lplJ*	BN194_16640	K0MVN0	-0.6	0.6	-2.8	0.1	-2.2	0.2	0.4	1.3	-2.3	0.
Bifunctional protein FolD	Cofactor-related metabolism	*folD*	BN194_18210	K0N5K0	-2.4	0.2	-4.2	0.1	-1.7	0.3	0.4	1.3	0.2	1.
Uncharacterized protein	*Cofactor-related metabolism*		BN194_18720	K0NB69	-1.6	0.3	-3.1	0.1	-1.5	0.4	-0.8	0.6	-1.6	0.
Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase)	Cofactor-related metabolism	*coaE*	BN194_18910	K0N5P8	-0.9	0.5	-1.2	0.4	-0.3	0.8	-0.8	0.6	-3.5	0.
NH(3)-dependent NAD(+) synthetase (EC 6.3.1.5)	Cofactor-related metabolism	*nadE*	BN194_19840	K0MWF6	0.1	1.1	2.3	4.9	2.2	4.6	0.5	1.4	-2.4	0.
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB*	BN194_19860	K0N5X0	-0.6	0.7	-4.0	0.1	-3.5	0.1	0.9	1.9	-3.3	0.
Pantothenate kinase (EC 2.7.1.33) (Pantothenic acid kinase)	Cofactor-related metabolism	*coaA*	BN194_21080	K0N9V9	-0.8	0.6	-2.9	0.1	-2.2	0.2	-0.5	0.7	-2.0	0.
Thiamine biosynthesis lipoprotein ApbE	Cofactor-related metabolism	*apbE_3*	BN194_21550	K0N6S8	-3.1	0.1	-6.3	0.0	-3.3	0.1	0.4	1.4	-2.8	0.
Glutathione reductase, chloroplastic (EC 1.8.1.7)	Cofactor-related metabolism	*GOR*	BN194_23200	K0N7H3	-1.7	0.3	-4.7	0.0	-3.0	0.1	1.2	2.3	-0.2	0.

Holo-[acyl-carrier-protein] synthase (Holo-ACP synthase) (EC 2.7.8.7) (4'-phosphopantetheinyl transferase AcpS)	Cofactor-related metabolism	*acpS*	BN194_26690	K0MXY2	-1.6	0.3	-4.4	0.0	-2.7	0.2	0.6	1.5	-0.3	0.8
Glutathione amide reductase (EC 1.8.1.16)	Cofactor-related metabolism	*garB*	BN194_27400	K0N8K3	0.8	1.8	0.7	1.6	-0.2	0.9	0.4	1.4	-1.9	0.3
Nicotinate phosphoribosyltransferase (EC 6.3.4.21)	Cofactor-related metabolism	*pncB_2*	BN194_29110	K0N8A4	1.2	2.3	2.8	6.8	1.6	3.0	2.3	5.0	-1.8	0.3
Chromosomal replication initiator protein DnaA	DNA replication-related	*dnaA*	BN194_00010	K0N1B5	-0.2	0.9	-4.6	0.0	-4.4	0.0	-0.5	0.7	-4.0	0.1
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	*dnaN*	BN194_00020	K0N6S3	0.3	1.2	0.6	1.5	0.3	1.3	1.4	2.6	1.3	2.4
DNA gyrase subunit B (EC 5.99.1.3)	DNA replication-related	*gyrB*	BN194_00060	K0N1B8	-0.8	0.6	-5.5	0.0	-4.7	0.0	1.0	2.0	-1.4	0.4
DNA gyrase subunit A (EC 5.99.1.3)	DNA replication-related	*gyrA*	BN194_00070	K0N6S7	-1.1	0.5	-7.1	0.0	-6.1	0.0	-1.3	0.4	-0.5	0.7
Single-stranded DNA-binding protein (SSB)	DNA replication-related	*ssb*	BN194_00110	K0N1C2	0.1	1.1	0.8	1.8	0.7	1.7	-0.7	0.6	0.0	1.0
Replicative DNA helicase (EC 3.6.4.12)	DNA replication-related	*dnaC*	BN194_01140	K0MRW2	-0.4	0.7	-2.9	0.1	-2.4	0.2	-1.2	0.4	-1.8	0.3
DNA ligase (EC 6.5.1.2) (Polydeoxyribonucleotide synthase [NAD(+)])	DNA replication-related	*ligA*	BN194_11930	K0N7A9	-0.8	0.6	-3.6	0.1	-2.8	0.1	-1.0	0.5	-1.4	0.4
GTPase Obg (EC 3.6.5.-) (GTP-binding protein Obg)	DNA replication-related	*obg*	BN194_15440	K0MVD3	-0.5	0.7	-5.6	0.0	-5.1	0.0	-1.3	0.4	-2.4	0.2
DNA-binding protein HU	DNA replication-related	*hup*	BN194_15740	K0MVF4	0.7	1.6	-3.2	0.1	-3.9	0.1	0.4	1.3	1.9	3.8
DNA topoisomerase 1 (EC 5.99.1.2) (DNA topoisomerase I)	DNA replication-related	*topA*	BN194_15970	K0NAP0	-3.0	0.1	-5.9	0.0	-2.9	0.1	-1.7	0.3	3.4	10
DNA topoisomerase 4 subunit B (EC 5.99.1.3) (Topoisomerase IV subunit B)	DNA replication-related	*parE*	BN194_16050	K0N545	-0.9	0.5	-3.7	0.1	-2.8	0.1	-0.6	0.7	0.2	1.2
DNA replication protein dnaD	DNA replication-related	*dnaD*	BN194_16750	K0N5B1	-0.3	0.8	-3.0	0.1	-2.7	0.2	-1.9	0.3	-2.0	0.2
DNA polymerase III PolC-type (PolIII) (EC 2.7.7.7)	DNA replication-related	*polC*	BN194_17600	K0N5L6	0.1	1.1	-3.0	0.1	-3.2	0.1	1.2	2.2	-2.5	0.2
Primosomal protein DnaI	DNA replication-related	*dnaI*	BN194_18880	K0N9E5	-0.7	0.6	-3.1	0.1	-2.5	0.2	-0.6	0.7	-2.5	0.2
DNA polymerase III subunit delta (EC 2.7.7.7)	DNA replication-related	*holB*	BN194_23930	K0NA93	-0.5	0.7	-2.9	0.1	-2.4	0.2	0.9	1.9	-0.5	0.7
DNA polymerase III subunit gamma/tau (EC 2.7.7.7)	DNA replication-related	*dnaX*	BN194_23990	K0MXD3	-0.4	0.8	-2.9	0.1	-2.5	0.2	0.6	1.5	-1.6	0.3
Nuclease sbcCD subunit D	DNA repair/recombination	*sbcD*	BN194_07530	K0N6B1	-0.9	0.5	-1.3	0.4	-0.4	0.7	-0.5	0.7	-1.3	0.4
SMC domain protein	*DNA repair/recombination*		BN194_07540	K0MTC3	-2.2	0.2	-4.7	0.0	-2.5	0.2	1.0	2.1	-1.3	0.4
LexA repressor (EC 3.4.21.-) (EC 3.4.21.88)	DNA repair/recombination	*lexA*	BN194_07970	K0N944	2.9	7.3	-1.7	0.3	-4.6	0.0	-1.6	0.3	-3.7	0.1
Putative pre-16S rRNA nuclease (EC 3.1.-.-)	*DNA repair/recombination*		BN194_08520	K0N972	-2.7	0.2	-5.1	0.0	-2.4	0.2	-1.9	0.3	-0.9	0.5
Endonuclease MutS2 (EC 3.1.-.-)	DNA repair/recombination	*mutS2*	BN194_08560	K0N359	-0.6	0.6	-0.3	0.8	0.4	1.3	-1.3	0.4	0.9	1.9
UvrABC system protein B (Protein UvrB) (Excinuclease ABC subunit B)	DNA repair/recombination	*uvrB*	BN194_10440	K0MU09	-0.4	0.8	-4.0	0.1	-3.6	0.1	-0.9	0.5	-2.6	0.2
UvrABC system protein A (UvrA protein) (Excinuclease ABC subunit A)	DNA repair/recombination	*uvrA*	BN194_10450	K0N3J2	-0.4	0.7	-5.8	0.0	-5.3	0.0	-0.3	0.8	-0.9	0.5

Uracil-DNA glycosylase (UDG) (EC 3.2.2.27)	DNA repair/recombination	*ung*	BN194_11330	K0N758	0.6	1.5	-3.7	0.1	-4.3	0.0	-1.1	0.5	-2.4	0.
Exodeoxyribonuclease (EC 3.1.11.2)	DNA repair/recombination	*exoA*	BN194_11390	K0MUA0	0.3	1.2	-1.8	0.3	-2.1	0.2	0.2	1.1	0.2	1.
Uncharacterized protein ytxK	DNA repair/recombination	*ytxK*	BN194_11680	K0N791	1.4	2.6	0.8	1.8	-0.5	0.7	0.9	1.9	-1.0	0.
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*pcrA*	BN194_11920	K0N9Z6	-1.5	0.4	-4.6	0.0	-3.1	0.1	-0.4	0.8	0.0	1.
UvrABC system protein A	DNA repair/recombination	*uvrA_2*	BN194_14920	K0NAH3	0.8	1.8	-4.5	0.0	-5.3	0.0	0.0	1.0	-4.7	0.
ATP-dependent helicase/nuclease subunit A (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease AddA)	DNA repair/recombination	*addA*	BN194_16800	K0N5B6	-0.9	0.5	-4.2	0.1	-3.3	0.1	-0.4	0.8	-3.1	0.
ATP-dependent helicase/deoxyribonuclease subunit B (EC 3.1.-.-) (EC 3.6.4.12) (ATP-dependent helicase/nuclease RexB)	DNA repair/recombination	*rexB*	BN194_16810	K0N573	-0.7	0.6	-3.1	0.1	-2.4	0.2	-0.8	0.6	-5.0	0.
Probable endonuclease 4 (EC 3.1.21.2) (Endodeoxyribonuclease IV) (Endonuclease IV)	DNA repair/recombination	*nfo*	BN194_17070	K0NAW5	1.1	2.2	-1.7	0.3	-2.8	0.1	-1.0	0.5	-3.3	0.
Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	DNA repair/recombination	*recJ*	BN194_17390	K0MVT7	-0.7	0.6	-1.9	0.3	-1.3	0.4	-2.2	0.2	1.4	2.
Exodeoxyribonuclease 7 small subunit (EC 3.1.11.6) (Exodeoxyribonuclease VII small subunit)	DNA repair/recombination	*xseB*	BN194_18190	K0MW55	1.6	3.0	0.5	1.4	-1.1	0.5	2.7	6.5	0.2	1.
DNA polymerase I (EC 2.7.7.7)	DNA repair/recombination	*polA*	BN194_18930	K0N9E7	-0.1	0.9	-6.6	0.0	-6.5	0.0	0.4	1.4	-5.0	0.
DNA helicase (EC 3.6.4.12)	DNA repair/recombination	*helD*	BN194_21130	K0N9W3	-1.4	0.4	-7.3	0.0	-5.9	0.0	-1.1	0.5	-1.3	0.
DNA mismatch repair protein MutL	DNA repair/recombination	*mutL*	BN194_23710	K0N6Z8	-0.7	0.6	-4.2	0.1	-3.5	0.1	0.8	1.8	-2.6	0.
DNA mismatch repair protein MutS	DNA repair/recombination	*mutS*	BN194_23720	K0NBY9	-0.9	0.5	-4.8	0.0	-3.9	0.1	0.2	1.1	-3.5	0.
Recombination protein RecR	DNA repair/recombination	*recR*	BN194_23970	K0NC03	-2.1	0.2	-4.1	0.1	-2.0	0.3	-1.5	0.3	0.4	1.
Transcription-repair-coupling factor (TRCF) (EC 3.6.4.-)	DNA repair/recombination	*mfd*	BN194_26540	K0MXW9	-1.3	0.4	-1.7	0.3	-0.4	0.7	1.5	2.8	-0.6	0.
UvrABC system protein A	DNA repair/recombination	*uvrA_3*	BN194_27500	K0N8M1	0.1	1.1	-3.8	0.1	-3.9	0.1	0.5	1.4	-3.3	0.
Ribonuclease H (EC 3.1.26.4)	DNA repair/recombination	*rnhA*	BN194_27580	K0NAX8	0.1	1.1	-0.3	0.8	-0.4	0.8	1.5	2.8	5.5	45
Protein RecA (Recombinase A)	DNA repair/recombination	*recA_2,recA*	BN194_27650	K0N8P0	-2.2	0.2	-5.2	0.0	-3.0	0.1	-1.2	0.4	-2.4	0.
Ribosomal RNA small subunit methyltransferase G (EC 2.1.1.-) (16S rRNA 7-methylguanosine methyltransferase)	tRNA/Ribosome assembly/processing	*rsmG*	BN194_02020	K0N7F1	0.4	1.3	-4.2	0.1	-4.6	0.0	-0.6	0.7	-2.7	0.
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17) (Queuosine biosynthesis protein QueA)	tRNA/Ribosome assembly/processing	*queA*	BN194_08370	K0N965	1.5	2.8	-2.4	0.2	-3.9	0.1	1.7	3.3	0.1	1.
DEAD-box ATP-dependent RNA helicase CshB (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshB*	BN194_08460	K0N356	-1.4	0.4	-5.5	0.0	-4.1	0.1	-3.5	0.1	0.8	1.
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*ytzG*	BN194_09230	K0N6P7	0.1	1.1	-1.6	0.3	-1.7	0.3	-0.3	0.8	3.3	10

Putative tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207) (tRNA (cytidine/uridine-2'-O-)-methyltransferase)	*tRNA/Ribosome assembly/processing*		BN194_09990	K0MTX9	0.4	1.3	-0.1	1.0	-0.5	0.7	0.8	1.7	-0.5	0.7
Uncharacterized protein SE_0534	*tRNA/Ribosome assembly/processing*		BN194_10150	K0N3F2	-0.7	0.6	-5.5	0.0	-4.8	0.0	-1.7	0.3	-1.1	0.5
Ribonuclease R (RNase R) (EC 3.1.13.1)	tRNA/Ribosome assembly/processing	*rnr*	BN194_11100	K0N3S4	-0.3	0.8	-6.6	0.0	-6.3	0.0	-0.5	0.7	0.0	1.0
Uncharacterized RNA methyltransferase lp_1151 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_11990	K0MUI2	0.3	1.2	-5.4	0.0	-5.7	0.0	0.8	1.8	-2.5	0.2
Putative ATP-dependent RNA helicase yfmL (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*yfmL*	BN194_12120	K0NA13	-0.8	0.6	-3.8	0.1	-3.0	0.1	-4.1	0.1	-1.5	0.3
Threonylcarbamoyl-AMP synthase (TC-AMP synthase) (EC 2.7.7.87) (L-threonylcarbamoyladenylate synthase)	tRNA/Ribosome assembly/processing	*ywlC*	BN194_13530	K0N7S6	0.0	1.0	-2.2	0.2	-2.2	0.2	1.4	2.6	-2.1	0.2
Ribosomal RNA small subunit methyltransferase H (EC 2.1.1.199) (16S rRNA m(4)C1402 methyltransferase) (rRNA (cytosine-N(4)-)-methyltransferase RsmH)	tRNA/Ribosome assembly/processing	*rsmH*	BN194_14680	K0N814	-0.6	0.6	-3.2	0.1	-2.5	0.2	-0.1	0.9	0.8	1.7
tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.-)	tRNA/Ribosome assembly/processing	*mnmA*	BN194_14930	K0N844	-0.2	0.9	-0.1	0.9	0.1	1.1	0.5	1.4	-4.6	0.0
Probable GTP-binding protein EngB	tRNA/Ribosome assembly/processing	*engB*	BN194_15350	K0N4Y5	0.9	1.8	-2.1	0.2	-2.9	0.1	-0.1	0.9	0.6	1.5
Ribonuclease Z (RNase Z) (EC 3.1.26.11) (tRNA 3 endonuclease) (tRNase Z)	tRNA/Ribosome assembly/processing	*rnz*	BN194_15470	K0NAK0	1.5	2.9	-1.4	0.4	-2.9	0.1	-0.8	0.6	-2.6	0.2
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*rluB*	BN194_15650	K0N509	0.2	1.1	-0.6	0.7	-0.8	0.6	-0.5	0.7	5.1	35
GTPase Der (GTP-binding protein EngA)	tRNA/Ribosome assembly/processing	*der*	BN194_15730	K0N8E1	-0.8	0.6	-4.1	0.1	-3.3	0.1	-0.6	0.7	-2.6	0.2
CCA-adding enzyme (EC 2.7.7.72) (CCA tRNA nucleotidyltransferase) (tRNA CCA-pyrophosphorylase) (tRNA adenylyl-/cytidylyl-transferase) (tRNA nucleotidyltransferase) (tRNA-NT)	tRNA/Ribosome assembly/processing	*cca*	BN194_15770	K0NAM4	0.5	1.4	-2.5	0.2	-3.0	0.1	-0.7	0.6	-2.4	0.2
Ribosome biogenesis GTPase A	tRNA/Ribosome assembly/processing	*rbgA*	BN194_15940	K0MVH2	0.3	1.2	-2.5	0.2	-2.7	0.1	0.6	1.5	-2.2	0.2
Putative RNA methyltransferase YpsC (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ypsC*	BN194_16670	K0NAU0	0.9	1.9	-3.2	0.1	-4.1	0.1	0.9	1.9	1.1	2.1
Ribosomal RNA small subunit methyltransferase F (EC 2.1.1.178)	tRNA/Ribosome assembly/processing	*rsmF*	BN194_16850	K0N5C0	-0.4	0.8	-1.8	0.3	-1.4	0.4	-1.5	0.4	0.9	1.9
tRNA (Adenine(22)-N(1))-methyltransferase (EC 2.1.1.217)	tRNA/Ribosome assembly/processing	*trmK*	BN194_16910	K0N584	-1.2	0.4	-3.8	0.1	-2.6	0.2	-0.6	0.7	-0.4	0.7
GTPase Era	tRNA/Ribosome assembly/processing	*era*	BN194_16990	K0MVQ8	-0.3	0.8	-3.7	0.1	-3.4	0.1	-0.7	0.6	-0.2	0.9
Endoribonuclease YbeY (EC 3.1.-.-)	tRNA/Ribosome assembly/processing	*ybeY*	BN194_17010	K0N594	-0.3	0.8	-2.0	0.3	-1.6	0.3	-1.4	0.4	-0.3	0.8

Ribosomal RNA small subunit methyltransferase E (EC 2.1.1.193)	tRNA/Ribosome assembly/processing	*rsmE*	BN194_17250	K0N5G8	-0.8	0.6	-2.5	0.2	-1.6	0.3	0.8	1.7	-1.4	0.4
Ribosomal protein L11 methyltransferase (L11 Mtase) (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*prmA*	BN194_17260	K0N5B0	-1.4	0.4	-2.1	0.2	-0.8	0.6	0.3	1.3	-1.0	0.5
Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase (EC 4.2.-.-)	*tRNA/Ribosome assembly/processing*		BN194_17370	K0NAY4	1.2	2.3	-1.5	0.4	-2.7	0.2	-1.0	0.5	1.0	2.0
tRNA pseudouridine synthase B (EC 5.4.99.25) (tRNA pseudouridine(55) synthase) (tRNA pseudouridylate synthase) (tRNA-uridine isomerase)	tRNA/Ribosome assembly/processing	*truB*	BN194_17520	K0NAZ5	-1.1	0.5	-3.3	0.1	-2.2	0.2	-2.0	0.2	-1.1	0.5
Ribosome-binding factor A	tRNA/Ribosome assembly/processing	*rbfA*	BN194_17540	K0MVV7	0.0	1.0	-0.2	0.9	-0.1	0.9	0.3	1.2	0.7	1.0
Ribosome maturation factor RimP	tRNA/Ribosome assembly/processing	*rimP*	BN194_17590	K0MVW3	1.0	2.0	-1.5	0.3	-2.5	0.2	-1.2	0.4	1.7	3.2
Ribosome maturation factor RimM	tRNA/Ribosome assembly/processing	*rimM*	BN194_17790	K0MVZ6	0.7	1.6	-4.8	0.0	-5.5	0.0	-2.6	0.2	-1.5	0.4
Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III)	tRNA/Ribosome assembly/processing	*rnc*	BN194_17870	K0NB31	-1.9	0.3	-5.3	0.0	-3.3	0.1	0.0	1.0	0.3	1.2
Putative ribosome biogenesis GTPase RsgA (EC 3.6.1.-)	tRNA/Ribosome assembly/processing	*rsgA*	BN194_18010	K0N5J0	-1.3	0.4	-2.9	0.1	-1.6	0.3	-1.2	0.4	-1.3	0.4
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*ysgA*	BN194_18610	K0N5M8	-0.3	0.8	-1.3	0.4	-1.1	0.5	0.9	1.9	5.3	39
Ribosomal silencing factor RsfS	tRNA/Ribosome assembly/processing	*yqeL,rsfS*	BN194_18710	K0N5N6	-0.4	0.7	-4.7	0.0	-4.3	0.1	-2.5	0.2	-1.1	0.5
Uncharacterized protein yqeH	tRNA/Ribosome assembly/processing	*yqeH*	BN194_18740	K0MW90	-1.3	0.4	-5.5	0.0	-4.2	0.1	-0.9	0.5	0.1	1.0
tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA (guanine(46)-N(7))-methyltransferase) (tRNA(m7G46)-methyltransferase)	tRNA/Ribosome assembly/processing	*trmB*	BN194_19000	K0N606	-3.0	0.1	-4.0	0.1	-1.0	0.5	0.1	1.0	3.2	8.9
Uncharacterized RNA methyltransferase lp_3226 (EC 2.1.1.-)	*tRNA/Ribosome assembly/processing*		BN194_19580	K0N9J4	0.1	1.1	-2.8	0.1	-2.9	0.1	-0.9	0.6	-2.3	0.2
Uncharacterized RNA pseudouridine synthase YhcT (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	*yhcT_2*	BN194_20220	K0NBE7	-0.8	0.6	-1.5	0.4	-0.6	0.6	0.1	1.1	-0.1	0.9
GTPase HflX (GTP-binding protein HflX)	tRNA/Ribosome assembly/processing	*hflX*	BN194_21260	K0N689	2.5	5.7	-2.6	0.2	-5.1	0.0	1.8	3.4	-3.7	0.1
tRNA-specific adenosine deaminase (EC 3.5.4.33)	tRNA/Ribosome assembly/processing	*tadA*	BN194_24000	K0N7M1	0.2	1.1	0.7	1.6	0.5	1.4	-1.6	0.3	-0.3	0.8
Uncharacterized protein ybxB	tRNA/Ribosome assembly/processing	*ybxB*	BN194_24020	K0NC08	-0.4	0.7	-4.3	0.1	-3.9	0.1	0.0	1.0	-3.2	0.1
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	*yacO*	BN194_24420	K0NC34	-0.3	0.8	-5.1	0.0	-4.8	0.0	0.1	1.1	2.3	5.0
tRNA pseudouridine synthase A (EC 5.4.99.12) (tRNA pseudouridine(38-40) synthase) (tRNA pseudouridylate synthase I) (tRNA-uridine isomerase I)	tRNA/Ribosome assembly/processing	*truA*	BN194_25910	K0N7E2	-1.5	0.4	0.0	1.0	1.5	2.8	0.9	1.8	-0.6	0.7

tRNA-dihydrouridine synthase (EC 1.3.1.-)	tRNA/Ribosome assembly/processing	*dus1*	BN194_26390	K0MXV9	0.3	1.3	-3.8	0.1	-4.1	0.1	-0.7	0.6	-1.7	0.3
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	*yabR*	BN194_26500	K0N8A7	1.1	2.1	-3.2	0.1	-4.3	0.1	-0.3	0.8	3.7	12
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	*yabO*	BN194_26520	K0NCR8	-1.2	0.4	-3.4	0.1	-2.2	0.2	-1.7	0.3	4.6	24
DEAD-box ATP-dependent RNA helicase CshA (EC 3.6.4.13)	tRNA/Ribosome assembly/processing	*cshA*	BN194_26700	K0N8C7	-1.6	0.3	-7.0	0.0	-5.4	0.0	0.8	1.7	0.1	1.1
Ribosomal RNA small subunit methyltransferase A (EC 2.1.1.182) (16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase) (16S rRNA dimethyladenosine transferase) (16S rRNA dimethylase) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase)	tRNA/Ribosome assembly/processing	*rsmA,ksgA*	BN194_27020	K0NCX3	-1.1	0.5	-4.0	0.1	-2.8	0.1	-1.1	0.5	-2.5	0.2
tRNA uridine 5-carboxymethylaminomethyl modification enzyme MnmG (Glucose-inhibited division protein A)	tRNA/Ribosome assembly/processing	*mnmG,gidA*	BN194_30590	K0MYX4	2.4	5.1	-0.3	0.8	-2.6	0.2	3.0	7.9	-0.3	0.8
tRNA modification GTPase MnmE (EC 3.6.-.-)	tRNA/Ribosome assembly/processing	*mnmE,trmE*	BN194_30600	K0N9F0	1.1	2.2	-1.6	0.3	-2.7	0.2	0.7	1.6	-1.9	0.3
Ribonuclease P protein component (RNase P protein) (RNaseP protein) (EC 3.1.26.5) (Protein C5)	tRNA/Ribosome assembly/processing	*rnpA*	BN194_30620	K0NDS2	2.3	4.8	-2.1	0.2	-4.4	0.0	-0.1	1.0	2.8	6.8
Thioredoxin	Posttranslational modification	*trxA_2*	BN194_08570	K0N975	-0.3	0.8	0.5	1.4	0.8	1.8	-1.3	0.4	-1.7	0.3
Thioredoxin reductase (EC 1.8.1.9)	Posttranslational modification	*trxB*	BN194_10360	K0N3L1	-0.2	0.9	-0.8	0.6	-0.5	0.7	-0.2	0.9	-0.9	0.5
SsrA-binding protein (Small protein B)	Posttranslational modification	*smpB*	BN194_11110	K0N3S3	0.7	1.6	-1.2	0.4	-1.9	0.3	-2.1	0.2	1.9	3.8
Peptide methionine sulfoxide reductase MsrA (Protein-methionine-S-oxide reductase) (EC 1.8.4.11) (Peptide-methionine (S)-S-oxide reductase)	Posttranslational modification	*msrA_2,msrA*	BN194_15860	K0N4W6	1.2	2.3	0.7	1.7	-0.5	0.7	1.5	2.8	-2.2	0.2
Peptide methionine sulfoxide reductase MsrB (EC 1.8.4.12) (Peptide-methionine (R)-S-oxide reductase)	Posttranslational modification	*msrB*	BN194_17090	K0MVR6	2.5	5.7	0.4	1.3	-2.1	0.2	0.7	1.6	-3.9	0.1
Serine/threonine-protein kinase PrkC (EC 2.7.11.1)	Posttranslational modification	*prkC*	BN194_18020	K0NB40	-0.3	0.8	-0.8	0.6	-0.5	0.7	-0.2	0.9	0.4	1.3
Uncharacterized protein	Posttranslational modification	*pp2C*	BN194_18030	K0N993	-0.3	0.8	-1.9	0.3	-1.6	0.3	-0.7	0.6	-0.5	0.7
Thioredoxin-like protein ytpP	Posttranslational modification	*ytpP*	BN194_18980	K0N9F1	-1.1	0.5	0.4	1.3	1.5	2.8	-1.7	0.3	-1.9	0.3
Putative tyrosine-protein phosphatase H16_A0669 (EC 3.1.3.48)	Posttranslational modification	*ptp3*	BN194_23520	K0NBX6	0.1	1.1	-0.6	0.6	-0.7	0.6	1.6	3.0	-1.8	0.3
Transcriptional regulator	*Posttranslational modification*		BN194_29310	K0N8C2	0.4	1.3	0.9	1.9	0.5	1.4	0.1	1.1	-3.9	0.1
18 kDa heat shock protein	Protein folding/turnover	*hsp18*	BN194_07570	K0N8Z3	0.6	1.5	3.5	11.4	2.9	7.7	1.0	2.0	-1.3	0.4
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	*Protein folding/turnover*		BN194_08960	K0N387	1.2	2.3	-2.9	0.1	-4.1	0.1	-0.2	0.9	-1.8	0.3

ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	*clpP_2, clpP*	BN194_10510	K0N3M4	-1.5	0.3	-3.9	0.1	-2.4	0.2	2.1	4.2	2.6	6.0
Trigger factor (TF) (EC 5.2.1.8) (PPIase)	Protein folding/turnover	*tig*	BN194_15330	K0N884	-0.1	0.9	-1.6	0.3	-1.5	0.3	-1.2	0.4	-1.1	0.5
ATP-dependent Clp protease ATP-binding subunit ClpX	Protein folding/turnover	*clpX*	BN194_15340	K0MVC6	-0.3	0.8	-5.7	0.0	-5.5	0.0	-0.2	0.8	-0.9	0.5
Chaperone protein ClpB	Protein folding/turnover	*clpB*	BN194_15500	K0N4Z8	-0.4	0.8	-6.1	0.0	-5.8	0.0	-1.1	0.5	-0.1	0.9
Carboxy-terminal processing protease CtpA (EC 3.4.21.102)	Protein folding/turnover	*ctpA*	BN194_15880	K0N8G1	1.1	2.1	-0.2	0.9	-1.3	0.4	-0.3	0.8	1.5	2.9
ATP-dependent protease subunit HslV (EC 3.4.25.2)	Protein folding/turnover	*hslV*	BN194_16000	K0N542	-1.8	0.3	-3.8	0.1	-1.9	0.3	-4.1	0.1	-1.7	0.3
ATP-dependent protease ATPase subunit HslU	Protein folding/turnover	*hslU*	BN194_16010	K0N4Y1	-1.6	0.3	-5.9	0.0	-4.3	0.1	0.2	1.1	-2.1	0.2
Chaperone protein DnaJ	Protein folding/turnover	*dnaJ*	BN194_17450	K0N5J4	2.1	4.3	-2.1	0.2	-4.3	0.1	0.3	1.3	-0.5	0.7
Chaperone protein DnaK (HSP70) (Heat shock 70 kDa protein) (Heat shock protein 70)	Protein folding/turnover	*dnaK*	BN194_17460	K0N5C7	0.9	1.9	3.1	8.6	2.2	4.4	-0.8	0.6	-2.9	0.1
Protein GrpE (HSP-70 cofactor)	Protein folding/turnover	*grpE*	BN194_17470	K0NAZ2	-0.2	0.9	-3.8	0.1	-3.5	0.1	1.2	2.3	0.7	1.6
Foldase protein PrsA (EC 5.2.1.8)	Protein folding/turnover	*prsA*	BN194_19060	K0N5Q8	0.7	1.6	-0.6	0.7	-1.3	0.4	1.8	3.4	0.6	1.5
ATP-dependent Clp protease ATP-binding subunit ClpE	Protein folding/turnover	*clpE*	BN194_19450	K0N644	0.0	1.0	-4.9	0.0	-4.9	0.0	-1.2	0.4	-1.1	0.5
Uncharacterized protein	*Protein folding/turnover*		BN194_19460	K0N5T8	-0.1	0.9	-6.1	0.0	-6.0	0.0	-1.1	0.5	-1.1	0.5
Probable ATP-dependent Clp protease ATP-binding subunit	Protein folding/turnover	*clpC*	BN194_21680	K0N9Z7	1.6	3.1	-1.4	0.4	-3.0	0.1	0.7	1.6	0.1	1.1
60 kDa chaperonin (GroEL protein) (Protein Cpn60)	Protein folding/turnover	*groL,groEL*	BN194_23750	K0N7K7	0.6	1.6	-3.4	0.1	-4.0	0.1	1.0	2.0	-1.3	0.4
10 kDa chaperonin (GroES protein) (Protein Cpn10)	Protein folding/turnover	*groS,grES*	BN194_23760	K0N700	1.8	3.4	2.7	6.7	1.0	2.0	0.6	1.5	-1.5	0.4
Chaperone protein ClpB	Protein folding/turnover	*clpB_2*	BN194_26350	K0N887	-0.8	0.6	-7.2	0.0	-6.4	0.0	-2.2	0.2	-1.2	0.4
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	*hslO*	BN194_26400	K0N893	-0.9	0.5	-3.8	0.1	-2.9	0.1	-1.4	0.4	1.3	2.9
ATP-dependent zinc metalloprotease FtsH (EC 3.4.24.-)	Protein folding/turnover	*ftsH*	BN194_26460	K0N7I8	-0.7	0.6	-1.2	0.4	-0.5	0.7	0.1	1.1	-0.6	0.7
Peptidyl-tRNA hydrolase (PTH) (EC 3.1.1.29)	Protein folding/turnover	*pth*	BN194_26550	K0N8B3	0.5	1.4	-3.3	0.1	-3.8	0.1	-0.4	0.8	-0.9	0.5
Acid shock protein	*Protein folding/turnover*		BN194_29440	K0MYM2	4.6	24.4	3.8	14.3	-0.8	0.6	0.8	1.7	-2.8	0.1
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	*htrA*	BN194_29460	K0N8D9	-2.1	0.2	-1.4	0.4	0.7	1.6	-2.9	0.1	2.5	5.9
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox*	BN194_01780	K0N4U4	-2.1	0.2	-4.0	0.1	-2.0	0.3	0.8	1.8	-0.2	0.8
Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E,P100*	BN194_02180	K0N513	-0.1	0.9	0.9	1.9	1.0	2.0	-0.5	0.7	-1.7	0.3
NADH oxidase (EC 1.6.99.3)	Cell defense/detoxification	*nox_2*	BN194_02850	K0N1N9	-1.1	0.5	1.4	2.7	2.5	5.8	-2.4	0.2	-2.5	0.2
NADH peroxidase (EC 1.11.1.1)	Cell defense/detoxification	*npr*	BN194_04740	K0MSP8	0.1	1.1	1.4	2.7	1.3	2.5	0.5	1.4	-2.0	0.3
Penicillin acylase (EC 3.5.1.11)	*Cell defense/detoxification*		BN194_04910	K0N2B8	2.8	6.8	4.8	27.7	2.0	4.1	-0.1	0.9	-2.3	0.2

Probable reductase (EC 1.1.-.-)	Cell defense/detoxification	*11E_2,P100*	BN194_05160	K0N2D7	2.6	6.1	3.9	14.5	1.2	2.4	-0.4	0.8	-4.3	0.
Uncharacterized protein ACIAD3023	*Cell defense/detoxification*		BN194_07010	K0N2T5	1.3	2.5	2.8	6.7	1.4	2.7	1.7	3.2	0.6	1.
Probable deferrochelatase/peroxidase YfeX (EC 1.11.1.-)	Cell defense/detoxification	*yfeX*	BN194_07170	K0N8U9	-1.6	0.3	0.1	1.1	1.7	3.2	-1.3	0.4	-2.4	0.
Probable thiol peroxidase (EC 1.11.1.-)	Cell defense/detoxification	*tpx*	BN194_08090	K0MTJ5	0.3	1.3	1.4	2.7	1.1	2.1	0.1	1.1	-1.2	0.
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	*dkgB*	BN194_08260	K0N347	-0.1	0.9	-1.2	0.4	-1.1	0.5	2.4	5.1	1.6	3.
Glutathione peroxidase	Cell defense/detoxification	*gpo*	BN194_09780	K0N6T6	0.3	1.2	-3.9	0.1	-4.2	0.1	-2.1	0.2	-1.7	0.
CutC-like protein M6_Spy0363	*Cell defense/detoxification*		BN194_09910	K0N3H0	-0.5	0.7	1.3	2.5	1.8	3.6	-0.6	0.7	-0.2	0.
Uncharacterized protein Lin2081	*Cell defense/detoxification*		BN194_14850	K0N4U3	0.5	1.4	-1.9	0.3	-2.4	0.2	-0.6	0.7	-1.1	0.
Uncharacterized protein ynbB	Cell defense/detoxification	*ynbB*	BN194_18380	K0N9B7	1.7	3.4	3.7	13.3	2.0	3.9	2.2	4.5	-2.5	0.
Putative acetyltransferase YJL218W (EC 2.3.1.-)	*Cell defense/detoxification*		BN194_25280	K0NAG2	0.3	1.3	2.3	4.8	1.9	3.8	0.8	1.8	-1.1	0.
Multicopper oxidase mco (EC 1.-.-.-)	Cell defense/detoxification	*mco*	BN194_25410	K0N7A4	2.5	5.7	5.0	31.4	2.5	5.5	1.0	2.0	-4.6	0.
Alkyl hydroperoxide reductase subunit C (EC 1.11.1.15)	Cell defense/detoxification	*ahpC*	BN194_26250	K0N876	-0.2	0.9	0.7	1.6	0.9	1.9	0.8	1.7	-1.7	0.
Putative acetyltransferase YJL218W (EC 2.3.1.-)	Cell defense/detoxification	*maa*	BN194_30010	K0N8I9	-0.4	0.8	-1.0	0.5	-0.5	0.7	-1.6	0.3	-2.0	0.
Uncharacterized protein	Prophage genome		BN194_09330	K0N6Q4	-0.3	0.8	-2.8	0.1	-2.4	0.2	0.6	1.5	2.4	5.
Phage capsid protein	Prophage genome		BN194_30330	K0NBD3	3.2	9.2	0.2	1.2	-3.0	0.1	-0.4	0.8	-3.5	0.
Cell growth regulatory protein	*IS elements/foreign DNA defense*		BN194_00940	K0MRU4	0.6	1.5	-0.7	0.6	-1.3	0.4	0.0	1.0	0.1	1.
Type I restriction enzyme EcoR124II M protein (EC 2.1.1.72)	IS elements/foreign DNA defense	*hsdM*	BN194_22340	K0MX17	1.3	2.4	-3.7	0.1	-4.9	0.0	-0.9	0.6	-3.7	0.
Uncharacterized protein yaaA	General prediction only	*yaaA*	BN194_00040	K0MRL5	0.0	1.0	-0.1	0.9	-0.1	1.0	-0.7	0.6	4.8	27
Uncharacterized protein ybfG	General prediction only	*ybfG*	BN194_00330	K0N4B3	-1.3	0.4	0.3	1.2	1.6	3.0	-0.4	0.7	-0.2	0.
Uncharacterized protein	*General prediction only*		BN194_01300	K0N194	0.9	1.9	-2.0	0.3	-2.9	0.1	1.5	2.9	2.0	3.
GNAT family acetyltransferase	*General prediction only*		BN194_01510	K0N1L8	-0.9	0.5	-2.5	0.2	-1.6	0.3	-1.6	0.3	-0.9	0.
Probable flavodoxin-1	General prediction only	*ykuN*	BN194_01860	K0N1P2	0.7	1.6	3.7	13.0	3.0	8.1	0.3	1.2	0.0	1.
Putative 2-hydroxyacid dehydrogenase SH0752 (EC 1.1.1.-)	*General prediction only*		BN194_01890	K0MS33	0.0	1.0	3.0	8.0	3.0	8.0	1.8	3.4	-0.9	0.
Metalloreductase STEAP4 (EC 1.16.1.-)	General prediction only	*Steap4*	BN194_01990	K0MS41	1.3	2.5	0.8	1.7	-0.6	0.7	1.6	3.1	-1.9	0.
Uncharacterized oxidoreductase ykwC (EC 1.1.-.-)	General prediction only	*ykwC*	BN194_02520	K0N7M3	0.2	1.2	0.2	1.1	0.0	1.0	1.4	2.7	-0.4	0.
Transcriptional regulator TetR family with acetyltransferase GNAT family domain	*General prediction only*		BN194_03130	K0N5D9	-2.8	0.1	-0.3	0.8	2.5	5.7	0.6	1.6	-1.0	0.
Uncharacterized protein MJ1651	*General prediction only*		BN194_04410	K0N281	-3.5	0.1	-1.2	0.4	2.3	4.8	-3.2	0.1	-1.7	0.

Uncharacterized protein YxeH	General prediction only	*yxeH*	BN194_04750	K0N1Y7	-1.8	0.3	-4.3	0.1	-2.5	0.2	1.5	2.7	-2.0	0.2
Uncharacterized protein HI_0912	General prediction only	*thiF3*	BN194_05090	K0MSS8	-2.3	0.2	-4.2	0.1	-1.9	0.3	-0.1	1.0	0.1	1.1
UPF0337 protein lp_1708	*General prediction only*		BN194_05810	K0N2J8	-4.1	0.1	-0.2	0.9	4.0	15.5	-3.3	0.1	2.4	5.3
Uncharacterized protein yieF	General prediction only	*yieF_2*	BN194_06540	K0MT25	-0.9	0.5	-4.8	0.0	-3.9	0.1	0.9	1.8	-2.7	0.2
UPF0659 protein YMR090W	General prediction only	*ylbE*	BN194_07030	K0N671	0.0	1.0	2.5	5.8	2.5	5.8	0.3	1.3	-0.2	0.8
Uncharacterized protein yeaE	General prediction only	*yeaE*	BN194_07040	K0MT72	0.9	1.8	1.3	2.4	0.4	1.3	1.3	2.4	-3.9	0.1
Monooxygenase	*General prediction only*		BN194_07600	K0N2U5	0.2	1.1	0.4	1.3	0.3	1.2	0.7	1.6	-4.4	0.0
Putative quinone oxidoreductase YhfP (EC 1.6.5.-)	General prediction only	*yhfP*	BN194_07740	K0MTE1	-2.4	0.2	-2.4	0.2	0.0	1.0	-2.1	0.2	-0.8	0.0
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI*	BN194_07860	K0N327	1.3	2.4	3.7	13.4	2.5	5.6	0.0	1.0	-1.8	0.3
Zinc-type alcohol dehydrogenase-like protein SE_1777	*General prediction only*		BN194_07910	K0N329	1.9	3.8	3.1	8.4	1.2	2.2	0.2	1.2	-3.8	0.1
Gluconate 5-dehydrogenase (EC 1.1.1.69)	General prediction only	*idnO*	BN194_08150	K0N2Z5	-0.2	0.8	-1.4	0.4	-1.2	0.4	3.5	11.0	4.9	30
Acetyltransferase	*General prediction only*		BN194_08200	K0N2Z8	-1.2	0.4	1.2	2.3	2.4	5.1	-0.5	0.7	1.1	2.2
5'-nucleotidase (EC 3.1.3.5)	*General prediction only*		BN194_08220	K0N957	0.2	1.1	-1.7	0.3	-1.9	0.3	1.1	2.2	-1.7	0.3
Hydrolase of the alpha/beta superfamily	*General prediction only*		BN194_08240	K0MTK6	0.4	1.3	0.6	1.5	0.2	1.1	1.6	3.1	0.1	1.1
Phosphoesterase (EC 3.1.4.-)	General prediction only	*ysnB*	BN194_08650	K0N317	0.3	1.2	-2.4	0.2	-2.7	0.2	-0.7	0.6	-1.7	0.3
Uncharacterized protein MJ1445	*General prediction only*		BN194_08880	K0N6M7	0.2	1.1	-0.9	0.5	-1.1	0.5	0.0	1.0	-0.5	0.7
Uncharacterized protein yjbK	General prediction only	*yjbK*	BN194_09860	K0N3G6	1.1	2.2	-3.1	0.1	-4.2	0.1	1.6	3.0	-2.1	0.2
Putative competence-damage inducible protein	General prediction only	*cinA*	BN194_10070	K0N9I3	0.6	1.5	-1.1	0.5	-1.7	0.3	1.2	2.3	-1.4	0.4
Predicted hydrolase of HD superfamily	*General prediction only*		BN194_10430	K0N6Z0	0.7	1.6	-3.6	0.1	-4.3	0.1	-0.1	0.9	-1.5	0.3
Nucleotide-binding protein BN194_10470	*General prediction only*		BN194_10470	K0N9L7	-0.3	0.8	-5.4	0.0	-5.1	0.0	-2.3	0.2	-1.0	0.5
Putative gluconeogenesis factor	General prediction only	*yjiF*	BN194_10480	K0N6Z4	0.0	1.0	-2.0	0.3	-2.0	0.2	0.2	1.1	0.0	1.0
Uncharacterized phosphatase YwpJ (EC 3.1.3.-)	General prediction only	*ywpJ*	BN194_11320	K0N9U2	-0.6	0.7	-2.4	0.2	-1.8	0.3	-0.7	0.6	-1.5	0.4
Uncharacterized lipoprotein yerH	General prediction only	*yerH*	BN194_11940	K0MUH2	0.6	1.5	0.3	1.2	-0.3	0.8	1.0	1.9	0.9	1.9
Cof protein	*General prediction only*		BN194_12010	K0N401	-1.6	0.3	-2.9	0.1	-1.3	0.4	-0.4	0.8	-1.2	0.4
Putative monooxygenase ycnE (EC 1.-.-.-)	General prediction only	*ycnE*	BN194_13230	K0N7R3	-0.4	0.7	-3.1	0.1	-2.6	0.2	0.1	1.1	-1.3	0.4
Virulence factor mviM	General prediction only	*mviM*	BN194_13310	K0N4B2	1.5	2.9	-0.4	0.8	-1.9	0.3	2.4	5.2	-0.3	0.8
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB*	BN194_13410	K0N4C0	-1.6	0.3	-3.2	0.1	-1.6	0.3	-1.2	0.4	0.4	1.4
Uncharacterized protein	*General prediction only*		BN194_13850	K0N4L8	-0.6	0.7	-3.2	0.1	-2.6	0.2	0.5	1.4	-1.5	0.4

Uncharacterized protein	General prediction only	*gpm1*	BN194_13960	K0N4F5	1.0	2.0	-0.2	0.8	-1.2	0.4	0.6	1.6	-3.1	0.
Histidinol-phosphatase	*General prediction only*		BN194_14010	K0N4F8	0.5	1.4	2.2	4.5	1.7	3.2	1.2	2.4	-3.0	0.
Uncharacterized protein ydcI	General prediction only	*ydcI*	BN194_14310	K0N4I1	0.6	1.5	-1.7	0.3	-2.3	0.2	1.8	3.6	-0.4	0.
Uncharacterized protein in fgs 3'region	*General prediction only*		BN194_14530	K0N802	-2.0	0.3	-3.7	0.1	-1.7	0.3	0.6	1.5	-1.2	0.
Putative RNA-binding protein ylmH	General prediction only	*ylmH*	BN194_14790	K0MV84	-1.4	0.4	-2.7	0.2	-1.3	0.4	-1.1	0.5	2.1	4.
5-bromo-4-chloroindolyl phosphate hydrolysis protein	*General prediction only*		BN194_14860	K0N4M3	-0.5	0.7	-2.6	0.2	-2.0	0.2	0.4	1.3	-1.2	0.
Uncharacterized protein	*General prediction only*		BN194_14990	K0MV99	-2.0	0.3	-4.0	0.1	-2.1	0.2	-1.0	0.5	-0.3	0.
Predicted pyrophosphatase	*General prediction only*		BN194_15360	K0N4R6	1.6	3.0	0.9	1.9	-0.7	0.6	1.5	2.8	-1.3	0.
Uncharacterized oxidoreductase yqjQ (EC 1.-.-.-)	General prediction only	*yqjQ*	BN194_15480	K0N8A1	-0.2	0.8	-3.4	0.1	-3.1	0.1	-0.6	0.7	-0.7	0.
Uncharacterized protein yitL	General prediction only	*yitL*	BN194_15600	K0N505	-0.1	0.9	0.2	1.2	0.3	1.2	0.6	1.5	7.4	16
Uncharacterized protein ypmR	General prediction only	*ypmR*	BN194_15840	K0MVG3	-0.1	0.9	-0.7	0.6	-0.5	0.7	0.3	1.2	-0.3	0.
Putative NAD(P)H nitroreductase ydgI (EC 1.-.-.-)	General prediction only	*ydgI_2*	BN194_16210	K0N508	0.2	1.1	-0.6	0.7	-0.8	0.6	1.8	3.4	-2.8	0.
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	*HBN1*	BN194_16550	K0N597	-0.8	0.6	2.4	5.3	3.3	9.6	-1.7	0.3	1.3	2.
D-2-hydroxyacid dehydrogenase (EC 1.1.1.-)	General prediction only	*ddh*	BN194_16660	K0N557	-1.1	0.5	0.1	1.1	1.2	2.4	1.4	2.6	3.8	14
PhoH-like protein	General prediction only	*phoH*	BN194_17020	K0NAW2	0.0	1.0	-4.7	0.0	-4.6	0.0	0.0	1.0	-2.2	0.
Uncharacterized protein	*General prediction only*		BN194_17420	K0NAY8	-0.9	0.5	-1.8	0.3	-0.9	0.5	-1.2	0.4	-1.2	0.
Uncharacterized protein ylxR	General prediction only	*ylxR*	BN194_17570	K0NAZ6	0.4	1.3	-4.2	0.1	-4.6	0.0	-1.2	0.4	-0.2	0.
Zinc metalloprotease (EC 3.4.24.-)	General prediction only	*eep*	BN194_17620	K0NAZ9	0.0	1.0	0.2	1.1	0.1	1.1	0.3	1.2	0.4	1.
Uncharacterized protein yqhL	General prediction only	*yqhL*	BN194_18410	K0N5L5	0.4	1.3	-0.5	0.7	-0.9	0.5	1.1	2.1	0.3	1.
Uncharacterized protein YneR	General prediction only	*yneR*	BN194_18480	K0N9C1	-1.4	0.4	0.0	1.0	1.3	2.5	-1.5	0.4	0.4	1.
Putative ring-cleaving dioxygenase mhqA (EC 1.13.11.-)	General prediction only	*mhqA_3*	BN194_18760	K0N5N7	0.4	1.4	-0.2	0.9	-0.6	0.7	-0.6	0.6	-4.1	0.
Putative hydrolase MhqD (EC 3.1.-.-)	General prediction only	*mhqD*	BN194_18770	K0NB71	-0.4	0.7	-2.6	0.2	-2.1	0.2	-0.5	0.7	-1.8	0.
Putative tRNA-binding protein ytpR	General prediction only	*ytpR*	BN194_18970	K0NB80	-0.4	0.7	1.2	2.4	1.7	3.2	0.2	1.1	-1.9	0.
Uncharacterized protein yhfI	General prediction only	*yhfI*	BN194_19200	K0N627	2.0	4.0	3.5	11.1	1.5	2.8	5.0	32.0	-1.2	0.
UPF0039 protein SAR1027	*General prediction only*		BN194_19510	K0N5U0	-3.5	0.1	-3.5	0.1	0.0	1.0	0.9	1.9	0.6	1.
GCN5-related N-acetyltransferase	*General prediction only*		BN194_19760	K0N5W1	0.6	1.5	-0.7	0.6	-1.3	0.4	0.4	1.3	-1.7	0.
Uncharacterized protein ywnB	General prediction only	*ywnB_2*	BN194_20050	K0N687	0.2	1.2	-1.2	0.4	-1.5	0.4	1.4	2.6	0.1	1.
Esterase/lipase	General prediction only	*yneB*	BN194_20230	K0N9P7	6.4	84.3	7.7	202.9	1.3	2.4	4.0	16.3	-3.2	0.

Uncharacterized protein	*General prediction only*		BN194_21200	K0N6M8	-1.5	0.4	-7.1	0.0	-5.6	0.0	0.5	1.4	0.6	1.0
Uncharacterized N-acetyltransferase ycf52-like (EC 2.3.1.-)	General prediction only	*speE1*	BN194_21490	K0MWT4	-2.0	0.2	-3.8	0.1	-1.8	0.3	0.0	1.0	-0.9	0.5
Uncharacterized protein	*General prediction only*		BN194_21910	K0N6F1	0.6	1.5	-0.3	0.8	-0.9	0.5	0.4	1.3	-0.3	0.8
Queuosine transporter QueT	General prediction only	*queT*	BN194_21930	K0NA07	-0.3	0.8	0.3	1.2	0.6	1.5	0.0	1.0	2.2	4.0
Probable phosphoglycerate mutase GpmB (EC 5.4.2.1)	General prediction only	*gpmB_2*	BN194_21970	K0NBP6	-2.4	0.2	-5.0	0.0	-2.6	0.2	-3.4	0.1	-1.8	0.3
FemAB family protein	*General prediction only*		BN194_22880	K0NA57	1.0	2.0	-2.5	0.2	-3.4	0.1	0.0	1.0	-0.5	0.7
UbiE/COQ5 family methyltransferase	*General prediction only*		BN194_23620	K0NBY4	0.7	1.6	-0.9	0.5	-1.5	0.3	0.5	1.4	-1.5	0.4
Maf-like protein maf	General prediction only	*maf*	BN194_23700	K0N7K3	-0.4	0.8	2.4	5.3	2.8	6.9	1.1	2.2	0.2	1.1
Uncharacterized ABC transporter ATP-binding protein YdiF	General prediction only	*ydiF*	BN194_23830	K0NA88	-2.2	0.2	-4.0	0.1	-1.8	0.3	0.8	1.7	-1.6	0.3
tRNA N6-adenosine threonylcarbamoyltransferase (EC 2.3.1.234) (N6-L-threonylcarbamoyladenine synthase) (t(6)A37 threonylcarbamoyladenosine biosynthesis protein TsaD) (tRNA threonylcarbamoyladenosine biosynthesis protein TsaD)	General prediction only	*tsaD,gcp*	BN194_23850	K0N7L3	-1.0	0.5	-3.3	0.1	-2.3	0.2	0.3	1.2	-1.7	0.3
Uncharacterized protein YdiC	General prediction only	*ydiC_3*	BN194_23870	K0NBZ8	-1.4	0.4	-3.6	0.1	-2.2	0.2	-1.2	0.4	-2.6	0.2
Nucleoid-associated protein BN194_23980	*General prediction only*		BN194_23980	K0NA95	0.6	1.5	0.5	1.4	-0.1	1.0	1.1	2.2	0.4	1.3
6-aminohexanoate-cyclic-dimer hydrolase	*General prediction only*		BN194_24180	K0NAA2	0.0	1.0	0.3	1.2	0.4	1.3	0.0	1.0	-4.5	0.0
FMN-binding domain protein	*General prediction only*		BN194_24320	K0NC29	0.0	1.0	0.5	1.4	0.4	1.4	0.1	1.1	0.5	1.4
Glycolate oxidase subunit glcD	General prediction only	*glcD*	BN194_24440	K0MXF3	2.9	7.5	4.9	28.9	2.0	3.9	1.6	3.0	-2.2	0.2
Dehydrogenase	*General prediction only*		BN194_24480	K0NAB4	0.3	1.2	1.1	2.2	0.8	1.7	0.1	1.1	-0.9	0.5
Uncharacterized protein yjdJ	General prediction only	*yjdJ*	BN194_24650	K0N7R2	-0.9	0.5	-0.2	0.9	0.7	1.7	-3.3	0.1	-2.1	0.2
UPF0337 protein yhjA	General prediction only	*yhjA*	BN194_24800	K0N7S1	-2.1	0.2	6.2	75.1	8.4	326.6	0.3	1.3	3.7	12
Oxidoreductase YdhF (EC 1.-.-.-)	General prediction only	*ydhF*	BN194_25320	K0NCA1	-1.7	0.3	-3.5	0.1	-1.8	0.3	1.0	2.1	1.4	2.7
Probable NADH-dependent flavin oxidoreductase yqiG (EC 1.-.-.-)	General prediction only	*yqiG*	BN194_25330	K0NAG4	0.8	1.7	0.0	1.0	-0.8	0.6	1.7	3.2	-2.3	0.2
NAD-dependent epimerase/dehydratase:3-beta hydroxysteroid dehydrogenase/isomerase:NmrA-like	*General prediction only*		BN194_25520	K0NCC8	2.2	4.7	4.6	24.1	2.4	5.1	2.1	4.3	-3.0	0.1
Putative ADP-ribose pyrophosphatase yjhB (EC 3.6.1.-)	General prediction only	*yjhB*	BN194_25530	K0NAH4	-1.9	0.3	-3.4	0.1	-1.5	0.4	-0.9	0.5	-1.2	0.4
Uncharacterized protein	*General prediction only*		BN194_26820	K0NCV9	0.8	1.8	-3.6	0.1	-4.4	0.0	-0.7	0.6	-3.4	0.1
Uncharacterized protein ywfO	General prediction only	*ywfO*	BN194_26840	K0MXZ5	0.8	1.7	0.8	1.8	0.0	1.0	0.1	1.1	-4.1	0.1

Phosphohydrolase (MutT/nudix family protein)	*General prediction only*		BN194_27160	K0N7P9	0.5	1.4	0.2	1.2	-0.3	0.8	1.4	2.6	0.4	1.3
NAD-dependent protein deacetylase (EC 3.5.1.-)	General prediction only	*cobB*	BN194_27190	K0MY36	0.6	1.5	-1.9	0.3	-2.5	0.2	-0.6	0.7	-2.7	0.2
Uncharacterized protein yxkA	General prediction only	*yxkA*	BN194_27230	K0NAV1	1.2	2.2	2.7	6.5	1.5	2.9	0.1	1.1	-2.2	0.2
Uncharacterized oxidoreductase YcsN (EC 1.-.-.-)	General prediction only	*ycsN*	BN194_27290	K0MY45	-1.2	0.4	-3.4	0.1	-2.2	0.2	-0.9	0.5	2.6	6.2
Uncharacterized protein ypgQ	General prediction only	*ypgQ*	BN194_27480	K0NAX0	-0.5	0.7	-5.6	0.0	-5.2	0.0	-1.6	0.3	-4.3	0.1
Uncharacterized protein yghZ	General prediction only	*yghZ*	BN194_27510	K0N7U8	-0.6	0.7	0.8	1.7	1.4	2.6	-0.5	0.7	-1.2	0.4
Uncharacterized protein	*General prediction only*		BN194_28370	K0NDC5	1.3	2.5	4.5	22.3	3.2	9.0	0.0	1.0	-2.1	0.2
Phosphatase YidA (EC 3.1.3.-)	General prediction only	*yidA*	BN194_28520	K0NDD5	-2.0	0.2	-4.1	0.1	-2.1	0.2	-1.2	0.4	-0.3	0.8
Uncharacterized isochorismatase family protein pncA (EC 3.-.-.-)	General prediction only	*pncA*	BN194_29120	K0NDH8	-0.4	0.7	3.7	13.3	4.2	18.1	-0.9	0.5	-1.5	0.3
GNAT family acetyltransferase	*General prediction only*		BN194_29620	K0NDL0	-0.7	0.6	1.0	2.0	1.7	3.2	0.8	1.8	-0.5	0.7
Uncharacterized protein ycaC	General prediction only	*ycaC*	BN194_29650	K0N948	0.9	1.9	3.5	11.6	2.6	6.1	1.2	2.3	-2.6	0.2
Kinase, putative	*General prediction only*		BN194_29890	K0MYR0	1.1	2.2	0.2	1.1	-1.0	0.5	0.5	1.4	-3.7	0.1
Uncharacterized protein	*General prediction only*		BN194_30000	K0N979	1.4	2.6	1.2	2.2	-0.2	0.9	-0.6	0.7	-3.9	0.1
Phosphatase YbjI (EC 3.1.3.-)	General prediction only	*ybjI*	BN194_30020	K0NDN5	-1.9	0.3	-3.8	0.1	-1.9	0.3	-0.1	0.9	-1.1	0.5
Putative oxidoreductase GLYR1 (EC 1.-.-.-)	General prediction only	*glyr1*	BN194_30100	K0N992	-1.1	0.5	-0.1	0.9	0.9	1.9	0.0	1.0	-2.5	0.2
Esterase/lipase	*General prediction only*		BN194_30390	K0MYV7	1.2	2.3	-1.9	0.3	-3.1	0.1	2.3	4.8	-3.0	0.1
Predicted hydrolase of the HAD superfamily	General prediction only	*mtlD*	BN194_30450	K0N9D4	0.8	1.7	1.9	3.7	1.1	2.1	0.7	1.7	-2.4	0.2
Putative amidohydrolase yhaA (EC 3.5.1.-)	General prediction only	*yhaA*	BN194_30550	K0N9E4	-1.0	0.5	-0.3	0.8	0.7	1.7	-0.2	0.9	-2.3	0.2
Possible TrsG protein	Unknown/uncharacterized		BN194_00240	K0MRM8	0.4	1.3	1.7	3.2	1.3	2.4	3.3	10.2	5.0	32
Uncharacterized protein	Unknown/uncharacterized		BN194_00400	K0N116	0.1	1.1	-3.3	0.1	-3.4	0.1	-0.2	0.9	0.5	1.4
Uncharacterized protein	Unknown/uncharacterized		BN194_01080	K0N4J7	1.1	2.1	-1.6	0.3	-2.6	0.2	4.0	15.5	8.6	39
Uncharacterized protein	Unknown/uncharacterized		BN194_01150	K0N181	-0.3	0.8	-2.7	0.2	-2.4	0.2	-0.1	0.9	-0.8	0.6
Uncharacterized protein	Unknown/uncharacterized		BN194_01600	K0N1B9	-2.1	0.2	-0.7	0.6	1.4	2.6	-1.9	0.3	-0.5	0.7
Putative integral membrane protein	Unknown/uncharacterized		BN194_01660	K0N1M7	0.6	1.5	-0.4	0.8	-1.0	0.5	2.5	5.6	-0.9	0.5
Uncharacterized protein	Unknown/uncharacterized		BN194_01760	K0N1N3	-6.6	0.0	-7.0	0.0	-0.4	0.7	-3.2	0.1	1.7	3.3
Uncharacterized protein	Unknown/uncharacterized		BN194_01790	K0MS25	-1.6	0.3	-1.7	0.3	-0.1	0.9	0.4	1.3	2.9	7.2
Uncharacterized protein	Unknown/uncharacterized		BN194_01830	K0N4V4	-0.1	0.9	0.1	1.1	0.3	1.2	-2.5	0.2	-2.2	0.2
Uncharacterized protein	Unknown/uncharacterized		BN194_01870	K0N7D4	1.3	2.5	2.9	7.5	1.6	3.0	-0.9	0.5	-2.4	0.2

Uncharacterized protein	Unknown/uncharacterized		BN194_02470	K0N7L7	-0.4	0.8	-0.3	0.8	0.0	1.0	-1.0	0.5	-1.3	0.4
Uncharacterized protein	Unknown/uncharacterized		BN194_02480	K0N555	-1.2	0.4	-5.4	0.0	-4.1	0.1	-2.8	0.1	-0.4	0.8
Integral membrane protein	Unknown/uncharacterized		BN194_02590	K0MS97	-0.7	0.6	-1.0	0.5	-0.4	0.8	0.1	1.1	0.7	1.7
Uncharacterized protein	Unknown/uncharacterized		BN194_02900	K0N1P1	0.3	1.2	-3.1	0.1	-3.4	0.1	0.5	1.4	3.3	10
Uncharacterized protein	Unknown/uncharacterized	yvcC	BN194_05260	K0N2E5	0.0	1.0	1.3	2.5	1.3	2.5	1.8	3.4	4.1	17
Uncharacterized protein	Unknown/uncharacterized		BN194_05550	K0N257	-0.8	0.6	-2.1	0.2	-1.3	0.4	0.1	1.1	5.5	44
Uncharacterized protein	Unknown/uncharacterized		BN194_05660	K0N2I2	1.8	3.5	2.3	5.1	0.5	1.4	3.6	12.3	0.0	1.0
Uncharacterized protein	Unknown/uncharacterized		BN194_07060	K0N2T7	0.3	1.3	-6.5	0.0	-6.9	0.0	-0.4	0.8	0.9	1.8
UPF0145 protein BN194_07140	Unknown/uncharacterized		BN194_07140	K0MT82	0.3	1.2	1.5	2.8	1.2	2.3	0.6	1.5	-0.3	0.8
Uncharacterized protein	Unknown/uncharacterized		BN194_07460	K0N2W9	0.9	1.8	2.3	5.0	1.5	2.7	0.5	1.5	-1.1	0.5
Uncharacterized protein	Unknown/uncharacterized		BN194_07550	K0N2T9	1.4	2.7	6.5	89.7	5.1	33.8	9.0	495.3	6.7	10
Uncharacterized protein	Unknown/uncharacterized		BN194_07660	K0N2Y6	0.2	1.2	-2.7	0.2	-2.9	0.1	0.3	1.2	-0.7	0.6
Uncharacterized protein	Unknown/uncharacterized		BN194_07670	K0N910	0.2	1.1	-2.4	0.2	-2.6	0.2	0.8	1.8	-1.8	0.3
Integral membrane protein	Unknown/uncharacterized		BN194_07890	K0MTI0	1.8	3.6	-1.7	0.3	-3.5	0.1	0.8	1.7	-0.7	0.6
Uncharacterized protein	Unknown/uncharacterized		BN194_08020	K0N947	-1.3	0.4	-2.0	0.2	-0.8	0.6	0.8	1.7	2.0	4.0
Uncharacterized protein yeaO	Unknown/uncharacterized	yeaO	BN194_08040	K0MTJ2	2.7	6.6	-1.2	0.4	-3.9	0.1	0.8	1.8	2.0	4.1
Uncharacterized protein	Unknown/uncharacterized		BN194_08190	K0MTK3	0.1	1.1	-3.4	0.1	-3.5	0.1	0.9	1.9	-0.3	0.8
Uncharacterized protein	Unknown/uncharacterized		BN194_08270	K0N959	-0.8	0.6	-0.3	0.8	0.5	1.5	0.7	1.7	0.7	1.0
UPF0297 protein BN194_08510	Unknown/uncharacterized		BN194_08510	K0N358	-1.0	0.5	-3.7	0.1	-2.7	0.1	0.7	1.7	2.4	5.2
UPF0473 protein BN194_08530	Unknown/uncharacterized		BN194_08530	K0N6K6	0.1	1.0	-2.0	0.3	-2.0	0.2	-0.7	0.6	-0.2	0.9
Uncharacterized protein yslB	Unknown/uncharacterized	yslB	BN194_08630	K0N6L4	-0.7	0.6	-2.5	0.2	-1.8	0.3	-0.3	0.8	0.3	1.2
CBS domain-containing protein ykuL	Unknown/uncharacterized	ykuL	BN194_08670	K0N981	-0.5	0.7	-3.8	0.1	-3.3	0.1	0.3	1.2	1.0	2.0
Uncharacterized protein	Unknown/uncharacterized		BN194_08720	K0N984	0.5	1.4	-0.1	0.9	-0.6	0.6	0.5	1.5	-1.1	0.5
Protein dedA	Unknown/uncharacterized	dedA	BN194_08930	K0N6M9	-1.6	0.3	-3.3	0.1	-1.7	0.3	-0.8	0.6	1.1	2.2
Uncharacterized protein ykuJ	Unknown/uncharacterized	ykuJ	BN194_09100	K0N348	0.6	1.5	1.9	3.7	1.3	2.5	-1.2	0.4	-1.6	0.3
UPF0237 protein BN194_09820	Unknown/uncharacterized		BN194_09820	K0N9F9	-0.8	0.6	-0.2	0.8	0.5	1.5	-0.8	0.6	-0.7	0.6
UPF0210 protein BN194_09830	Unknown/uncharacterized		BN194_09830	K0N6U0	-0.1	0.9	2.1	4.2	2.2	4.6	0.6	1.5	0.1	1.1
Uncharacterized protein	Unknown/uncharacterized		BN194_10000	K0N3D6	0.0	1.0	-1.4	0.4	-1.4	0.4	-0.3	0.8	0.5	1.4
PspC domain-containing protein	Unknown/uncharacterized	ythC	BN194_10300	K0N3H5	-1.2	0.4	-6.1	0.0	-4.9	0.0	-1.2	0.4	-0.7	0.6

Uncharacterized protein ybbP	Unknown/uncharacterized	ybbP	BN194_11530	K0N776	3.0	8.0	0.9	1.9	-2.1	0.2	1.3	2.4	-0.4	0.7
YbbR-like domain-containing protein ybbR	Unknown/uncharacterized	ybbR	BN194_11540	K0MUB6	-0.8	0.6	-1.9	0.3	-1.2	0.4	0.5	1.4	0.1	1.0
Uncharacterized protein	Unknown/uncharacterized		BN194_11770	K0N9Y6	0.2	1.2	-1.7	0.3	-2.0	0.3	0.1	1.1	1.3	2.5
Uncharacterized protein	Unknown/uncharacterized		BN194_11890	K0MUG0	0.2	1.1	-0.4	0.8	-0.6	0.7	2.7	6.4	1.4	2.7
DegV domain-containing protein CPE0026	Unknown/uncharacterized		BN194_12060	K0N405	0.6	1.5	-1.5	0.4	-2.0	0.2	0.4	1.3	-1.3	0.4
Protein QmcA	Unknown/uncharacterized	qmcA	BN194_12070	K0NA10	0.7	1.6	0.3	1.2	-0.4	0.8	1.3	2.4	-2.0	0.3
Uncharacterized protein	Unknown/uncharacterized		BN194_12100	K0N456	-0.1	0.9	-0.5	0.7	-0.4	0.8	1.5	2.9	1.2	2.4
Uncharacterized protein	Unknown/uncharacterized		BN194_12110	K0N410	-1.5	0.4	-3.6	0.1	-2.2	0.2	-1.9	0.3	0.1	1.1
Uncharacterized protein	Unknown/uncharacterized		BN194_12200	K0N464	-1.6	0.3	-2.2	0.2	-0.7	0.6	2.7	6.6	4.7	26
Hypothetical lipoprotein	Unknown/uncharacterized		BN194_12440	K0MUR1	-0.7	0.6	-0.7	0.6	0.0	1.0	3.3	9.6	2.0	3.9
Uncharacterized protein	Unknown/uncharacterized		BN194_13400	K0N4I9	-0.1	0.9	-2.0	0.3	-1.9	0.3	-0.3	0.8	-1.2	0.4
Uncharacterized protein	Unknown/uncharacterized		BN194_13680	K0N7T4	0.2	1.1	0.3	1.3	0.2	1.1	-0.7	0.6	2.2	4.7
Uncharacterized protein	Unknown/uncharacterized		BN194_13840	K0MV29	-0.4	0.8	-3.9	0.1	-3.5	0.1	0.8	1.8	0.2	1.1
Uncharacterized protein yueI	Unknown/uncharacterized	yueI	BN194_13920	K0NAC7	-1.5	0.4	1.3	2.5	2.8	7.2	-1.8	0.3	-0.9	0.5
Uncharacterized protein	Unknown/uncharacterized		BN194_14910	K0N4M6	-0.8	0.6	-0.6	0.7	0.2	1.1	-1.8	0.3	-0.1	0.5
TPR repeats containing protein	Unknown/uncharacterized		BN194_14960	K0N4M8	-0.2	0.8	-1.8	0.3	-1.6	0.3	1.7	3.2	-0.4	0.8
UPF0356 protein BN194_15030	Unknown/uncharacterized		BN194_15030	K0N856	0.4	1.3	0.7	1.6	0.3	1.2	-1.1	0.5	-0.5	0.7
BS_ysoA related protein with TPR repeats	Unknown/uncharacterized		BN194_15300	K0N4Y3	-0.3	0.8	-2.2	0.2	-1.8	0.3	0.3	1.2	-2.9	0.1
Uncharacterized protein	Unknown/uncharacterized		BN194_15370	K0NAJ2	0.8	1.8	3.5	11.6	2.7	6.6	-1.4	0.4	3.3	10
Uncharacterized protein	Unknown/uncharacterized		BN194_15520	K0NAK2	2.3	4.9	-1.1	0.5	-3.4	0.1	2.3	5.0	0.5	1.4
Uncharacterized protein	Unknown/uncharacterized		BN194_15540	K0MVD8	1.3	2.4	0.3	1.2	-1.0	0.5	1.8	3.6	0.3	1.2
TPR repeat-containing protein ypiA	Unknown/uncharacterized	ypiA	BN194_15750	K0N517	1.4	2.6	0.7	1.6	-0.7	0.6	-2.7	0.2	-2.1	0.2
Uncharacterized protein	Unknown/uncharacterized		BN194_15780	K0N8E8	0.4	1.3	-0.6	0.7	-1.0	0.5	0.8	1.8	-0.9	0.5
DegV domain-containing protein SP_1112	Unknown/uncharacterized		BN194_15830	K0N8F3	-1.5	0.3	-3.9	0.1	-2.3	0.2	-1.8	0.3	0.0	1.0
Uncharacterized protein	Unknown/uncharacterized		BN194_15850	K0N527	-0.4	0.7	-0.6	0.7	-0.2	0.9	1.0	2.0	0.7	1.0
UPF0346 protein BN194_15870	Unknown/uncharacterized		BN194_15870	K0NAN2	-2.7	0.2	2.0	4.1	4.7	26.8	-0.9	0.5	2.3	5.0
DegV domain-containing protein lin2658	Unknown/uncharacterized		BN194_16330	K0N8L5	-0.7	0.6	-2.6	0.2	-1.9	0.3	-1.0	0.5	-0.7	0.0
Uncharacterized protein	Unknown/uncharacterized		BN194_16570	K0NAT3	4.5	22.8	2.7	6.6	-1.8	0.3	2.6	6.0	-2.7	0.2
Uncharacterized protein	Unknown/uncharacterized		BN194_16650	K0N5A4	0.3	1.2	-1.0	0.5	-1.3	0.4	-3.3	0.1	2.1	4.4

GTP cyclohydrolase 1 type 2 homolog	Unknown/uncharacterized		BN194_16900	K0N5C6	1.5	2.8	3.6	12.3	2.1	4.4	-0.9	0.6	-2.4	0.2
Uncharacterized protein yqeY	Unknown/uncharacterized	yqeY	BN194_17040	K0MVR2	2.2	4.5	3.1	8.6	0.9	1.9	4.7	25.2	0.2	1.1
Uncharacterized protein	Unknown/uncharacterized		BN194_17290	K0MVS9	0.3	1.3	0.6	1.5	0.3	1.2	0.7	1.6	0.4	1.3
Uncharacterized protein	Unknown/uncharacterized		BN194_17360	K0N5B9	2.3	4.8	-0.4	0.8	-2.7	0.2	-1.1	0.5	-3.0	0.1
Uncharacterized protein	Unknown/uncharacterized		BN194_17400	K0N5I7	4.7	26.1	2.0	4.0	-2.7	0.2	4.9	29.1	-2.3	0.2
UPF0154 protein BN194_17740	Unknown/uncharacterized		BN194_17740	K0MVY5	0.6	1.5	-0.2	0.9	-0.8	0.6	0.9	1.8	1.1	2.2
UPF0291 protein BN194_17750	Unknown/uncharacterized		BN194_17750	K0N5P0	2.7	6.4	4.3	19.0	1.6	3.0	-0.5	0.7	0.4	1.3
Uncharacterized protein SAR1202	Unknown/uncharacterized		BN194_17960	K0N5I6	-0.4	0.8	-4.4	0.0	-4.0	0.1	-0.3	0.8	-0.4	0.8
Uncharacterized protein YqhY	Unknown/uncharacterized	yqhY	BN194_18230	K0N9A7	0.0	1.0	-5.4	0.0	-5.4	0.0	-1.4	0.4	-0.1	0.9
Uncharacterized protein	Unknown/uncharacterized		BN194_18400	K0N5V7	-0.2	0.9	-0.7	0.6	-0.5	0.7	0.5	1.5	-3.5	0.1
UPF0755 protein yrrL	Unknown/uncharacterized	yrrL	BN194_18550	K0N5W7	0.8	1.7	0.1	1.1	-0.7	0.6	1.5	2.9	0.5	1.4
Uncharacterized protein	Unknown/uncharacterized	FNV1452	BN194_18830	K0N9E3	-0.3	0.8	-2.0	0.2	-1.7	0.3	-2.4	0.2	-1.0	0.5
Uncharacterized protein	Unknown/uncharacterized		BN194_19050	K0N613	-0.5	0.7	-2.1	0.2	-1.6	0.3	0.7	1.6	-1.3	0.4
UPF0342 protein yheA	Unknown/uncharacterized	yheA	BN194_19080	K0N9F7	0.0	1.0	3.2	9.2	3.2	9.4	1.9	3.8	0.9	1.8
Uncharacterized protein	Unknown/uncharacterized		BN194_19210	K0N5R7	2.6	6.1	2.7	6.4	0.1	1.0	2.1	4.3	0.9	1.9
Uncharacterized protein	Unknown/uncharacterized		BN194_19470	K0NBA0	0.9	1.9	-2.6	0.2	-3.5	0.1	0.1	1.1	0.7	1.7
Uncharacterized protein	Unknown/uncharacterized		BN194_19530	K0N9J0	0.5	1.4	-3.1	0.1	-3.6	0.1	0.3	1.2	-2.7	0.1
Uncharacterized protein	Unknown/uncharacterized		BN194_19810	K0N5W5	0.7	1.6	-4.0	0.1	-4.7	0.0	-0.4	0.7	-1.3	0.4
Uncharacterized protein	Unknown/uncharacterized		BN194_20070	K0NBE0	2.8	6.9	2.4	5.2	-0.4	0.8	5.3	39.0	0.5	1.4
Uncharacterized protein	Unknown/uncharacterized		BN194_20160	K0N5Z4	-0.5	0.7	-7.0	0.0	-6.5	0.0	0.3	1.2	-2.4	0.2
Uncharacterized protein	Unknown/uncharacterized		BN194_20190	K0MWI0	2.0	4.0	2.1	4.3	0.1	1.1	1.5	2.9	-0.3	0.8
Uncharacterized protein	Unknown/uncharacterized		BN194_20240	K0MWI3	-0.1	0.9	2.2	4.5	2.3	4.9	2.1	4.3	3.9	14
Uncharacterized protein	Unknown/uncharacterized		BN194_20720	K0NBH5	1.2	2.3	-0.1	0.9	-1.3	0.4	1.1	2.2	-1.9	0.3
Uncharacterized protein	Unknown/uncharacterized		BN194_21170	K0NBJ9	-0.7	0.6	-2.8	0.1	-2.1	0.2	-2.0	0.2	-1.2	0.4
Uncharacterized protein	Unknown/uncharacterized		BN194_21380	K0N9Y1	1.1	2.2	-0.9	0.5	-2.0	0.2	0.1	1.1	3.7	13
Uncharacterized protein	Unknown/uncharacterized		BN194_21450	K0N6R7	0.5	1.4	-0.8	0.6	-1.3	0.4	-0.6	0.6	-4.2	0.1
Uncharacterized protein	Unknown/uncharacterized		BN194_22290	K0MX11	0.6	1.5	-2.5	0.2	-3.1	0.1	0.0	1.0	-3.2	0.1
Membrane protein	Unknown/uncharacterized		BN194_22700	K0N7C6	0.0	1.0	-0.1	0.9	-0.1	0.9	1.3	2.5	1.8	3.4
Uncharacterized protein yuaG	Unknown/uncharacterized	yuaG	BN194_22920	K0NBV0	-3.2	0.1	-3.4	0.1	-0.3	0.8	0.3	1.3	-0.1	0.9

Uncharacterized protein M6_Spy0233	Unknown/uncharacterized		BN194_22970	K0NBV1	0.0	1.0	1.5	2.8	1.5	2.8	0.9	1.8	1.0	2.
Uncharacterized protein	Unknown/uncharacterized		BN194_23460	K0N6Y5	0.6	1.5	-1.5	0.4	-2.1	0.2	-0.1	1.0	-1.1	0.
Uncharacterized protein	Unknown/uncharacterized		BN194_23540	K0MXB4	-0.2	0.9	-0.5	0.7	-0.3	0.8	0.0	1.0	0.5	1.
Uncharacterized protein	Unknown/uncharacterized		BN194_23630	K0NA78	-1.2	0.4	-1.5	0.4	-0.3	0.8	-0.3	0.8	6.2	73
Uncharacterized protein	Unknown/uncharacterized		BN194_23650	K0N7J8	0.0	1.0	0.8	1.7	0.8	1.7	0.9	1.8	-3.8	0.
Uncharacterized protein	Unknown/uncharacterized		BN194_23740	K0MXC2	-1.0	0.5	-1.4	0.4	-0.4	0.8	-0.6	0.7	1.9	3.
Folate transporter FolT	Unknown/uncharacterized	folT	BN194_23890	K0MXC9	-1.3	0.4	-2.2	0.2	-0.9	0.5	-1.9	0.3	-4.5	0.
Uncharacterized protein yaaQ	Unknown/uncharacterized	yaaQ	BN194_23940	K0MXD1	0.8	1.7	2.3	5.0	1.6	2.9	1.6	2.9	-3.2	0.
Uncharacterized protein	Unknown/uncharacterized		BN194_24010	K0N715	-0.2	0.9	-2.0	0.2	-1.8	0.3	-0.3	0.8	-1.7	0.
Uncharacterized protein	Unknown/uncharacterized		BN194_24220	K0NC21	1.5	2.8	-0.3	0.8	-1.8	0.3	5.3	39.2	3.2	9.
Uncharacterized protein	Unknown/uncharacterized		BN194_24780	K0NAC8	-0.7	0.6	-2.9	0.1	-2.2	0.2	-0.5	0.7	1.1	2.
Uncharacterized protein	Unknown/uncharacterized		BN194_24860	K0N764	-0.8	0.6	-6.0	0.0	-5.2	0.0	-1.3	0.4	3.2	8.
Uncharacterized protein YPL245W	Unknown/uncharacterized		BN194_25000	K0N7U3	1.8	3.5	-3.6	0.1	-5.4	0.0	1.8	3.5	-3.2	0.
Uncharacterized protein	Unknown/uncharacterized		BN194_25540	K0MXN3	1.7	3.2	-1.4	0.4	-3.1	0.1	0.4	1.3	0.6	1.
Uncharacterized protein			BN194_19420	K0NB98	0.5	1.4	1.8	3.4	1.3	2.4	-1.5	0.4	-4.3	0.
Uncharacterized protein			BN194_21520	K0NBL8	1.5	2.9	-0.8	0.6	-2.4	0.2	-1.8	0.3	-4.3	0.
Uncharacterized protein			BN194_22500	K0N788	0.3	1.2	-4.8	0.0	-5.1	0.0	1.8	3.6	-3.0	0.
Uncharacterized protein			BN194_02080	K0N4Z7	-0.6	0.7	-0.3	0.8	0.2	1.2	-0.3	0.8	0.4	1.
Uncharacterized protein			BN194_07360	K0N2W3	-3.3	0.1	-4.1	0.1	-0.7	0.6	-0.1	0.9	0.2	1.
Uncharacterized protein			BN194_16060	K0N4Y8	-0.4	0.8	-2.2	0.2	-1.8	0.3	-2.5	0.2	-0.2	0.
Uncharacterized protein yeaC		*yeaC*	*BN194_29960*	*K0N8I6*	-1.8	0.3	-3.3	0.1	-1.5	0.4	-1.1	0.5	1.0	2.
Uncharacterized protein	*Unknown/uncharacterized*		*BN194_25820*	*K0NCG9*	0.6	1.5	-1.8	0.3	-2.4	0.2	0.9	1.9	-1.6	0.
Uncharacterized protein	*Unknown/uncharacterized*		*BN194_25890*	*K0MXR4*	4.1	17.1	6.1	70.5	2.0	4.1	5.1	33.3	-3.1	0.
CBS domain-containing protein	*Unknown/uncharacterized*		*BN194_26610*	*K0N7J7*	2.1	4.2	-1.4	0.4	-3.5	0.1	1.0	1.9	1.0	2.
Protein veg	Unknown/uncharacterized	*veg*	*BN194_27010*	*K0N7N4*	1.4	2.6	-0.7	0.6	-2.1	0.2	-0.1	0.9	1.1	2.
Uncharacterized protein	*Unknown/uncharacterized*		*BN194_27210*	*K0N7Q6*	1.5	2.8	-4.9	0.0	-6.4	0.0	0.8	1.7	0.0	1.
Uncharacterized protein ypuA	Unknown/uncharacterized	*ypuA*	*BN194_27250*	*K0N8I3*	-0.8	0.6	-0.3	0.8	0.5	1.5	1.8	3.5	3.0	8.
Protein LemA	Unknown/uncharacterized	*lemA*	*BN194_27350*	*K0N8J7*	-1.1	0.5	-1.2	0.4	-0.2	0.9	0.6	1.5	0.1	1.
Uncharacterized protein	*Unknown/uncharacterized*		*BN194_27530*	*K0NAX5*	0.6	1.5	0.3	1.2	-0.3	0.8	1.2	2.3	0.0	1.

Uncharacterized protein	*Unknown/uncharacterized*		*BN194_28350*	*K0N8V3*	2.2	4.7	3.9	15.4	1.7	3.3	0.6	1.5	0.1	1.1
Uncharacterized protein	*Unknown/uncharacterized*		*BN194_29450*	*K0N932*	2.4	5.4	2.8	7.1	0.4	1.3	1.1	2.1	-2.3	0.2
Uncharacterized protein	*Unknown/uncharacterized*		*BN194_29560*	*K0N8E9*	0.3	1.3	2.1	4.3	1.8	3.4	0.3	1.2	0.0	1.0
SPFH/Band 7/PHB domain protein	*Unknown/uncharacterized*		*BN194_29820*	*K0NDM1*	-0.1	0.9	-0.2	0.9	-0.1	0.9	1.6	3.0	1.2	2.2
Uncharacterized protein	*Unknown/uncharacterized*		*BN194_29850*	*K0N968*	0.6	1.5	-2.8	0.1	-3.4	0.1	0.1	1.0	-0.6	0.7
Uncharacterized protein IRC4	Unknown/uncharacterized	*IRC4*	*BN194_30110*	*K0N8K0*	-1.1	0.5	-3.9	0.1	-2.8	0.1	-0.3	0.8	-2.0	0.2
Uncharacterized protein	*Unknown/uncharacterized*		*BN194_30140*	*K0MYT6*	1.2	2.2	-0.9	0.5	-2.1	0.2	0.4	1.3	-3.3	0.2
Adapter protein MecA	Competence (DNA uptake)	*mecA*	*BN194_19170*	*K0NB89*	0.9	1.9	-2.1	0.2	-3.0	0.1	-3.0	0.1	-1.2	0.4
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE*	*BN194_02970*	*K0N7U7*	0.3	1.2	0.3	1.2	0.0	1.0	-2.3	0.2	-1.1	0.5
PTS family mannose/fructose/sorbose porter component IIC	*Phosphotransferase systems*		*BN194_02980*	*K0N5D0*	0.2	1.1	-0.1	0.9	-0.2	0.8	-0.4	0.8	-1.7	0.3
Mannose permease IID component	Phosphotransferase systems	*manZ*	*BN194_02990*	*K0MSE1*	-0.2	0.9	-0.3	0.8	-0.1	0.9	-0.5	0.7	-0.5	0.7
Putative PTS system mannose-specific EIIAB component	*Phosphotransferase systems*		*BN194_03000*	*K0N1P6*	1.7	3.2	1.9	3.8	0.2	1.2	0.8	1.7	-0.6	0.7
Putative PTS system mannose-specific EIIAB component	*Phosphotransferase systems*		*BN194_03940*	*K0MSJ3*	-1.6	0.3	-2.0	0.3	-0.4	0.8	1.2	2.4	0.3	1.2
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_2*	*BN194_04490*	*K0MSM9*	-3.3	0.1	-2.4	0.2	0.9	1.8	-3.9	0.1	-4.6	0.0
Phosphoenolpyruvate-protein phosphotransferase (EC 2.7.3.9) (Phosphotransferase system, enzyme I)		*ptsI*	*BN194_19410*	*K0N5T2*	0.4	1.3	1.7	3.4	1.3	2.5	0.7	1.6	-1.4	0.4
Mannose permease IID component	Phosphotransferase systems	*manZ_4*	*BN194_04510*	*K0N287*	-1.5	0.4	-0.4	0.8	1.1	2.1	0.2	1.2	-0.2	0.9
Fructose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*levE_3*	*BN194_04780*	*K0N5N9*	-1.4	0.4	-1.0	0.5	0.4	1.3	-1.2	0.4	-1.1	0.5
Uncharacterized protein	*Phosphotransferase systems*		*BN194_04820*	*K0N885*	-0.1	1.0	3.2	9.1	3.2	9.4	0.6	1.5	-0.8	0.6
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*bglP*	*BN194_06940*	*K0MT60*	0.3	1.2	-1.3	0.4	-1.6	0.3	0.3	1.3	3.1	8.7
Sorbitol PTS, EIIA	*Phosphotransferase systems*		*BN194_09940*	*K0MTX4*	0.3	1.3	1.4	2.7	1.1	2.1	0.3	1.3	-0.2	0.9
HPr kinase/phosphorylase (HPrK/P) (EC 2.7.11.-) (EC 2.7.4.-) (HPr(Ser) kinase/phosphorylase)	Phosphotransferase systems	*hprK*	*BN194_10330*	*K0N6Y3*	-2.1	0.2	-5.9	0.0	-3.7	0.1	-2.2	0.2	0.4	1.3
PTS system fructose-specific EIIABC component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*fruA_3*	*BN194_15410*	*K0N4S1*	1.3	2.4	0.0	1.0	-1.3	0.4	0.0	1.0	-0.2	0.9
Phosphocarrier protein HPr (EC 2.7.11.-)	Phosphotransferase systems	*ptsH*	*BN194_19430*	*K0N9I2*	0.3	1.2	1.5	2.8	1.2	2.3	0.0	1.0	-0.2	0.9
Oligo-beta-mannoside-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*gmuB*	*BN194_23840*	*K0MXC7*	-0.1	0.9	-0.2	0.9	-0.1	1.0	0.1	1.0	-2.0	0.2

Phosphoenolpyruvate-dependent sugar phosphotransferase system EIIA, galactitol/fructose specific	*Phosphotransferase systems*		*BN194_27050*	*K0N8F9*	-0.1	0.9	-1.9	0.3	-1.8	0.3	0.0	1.0	-1.0	0.5
Sorbose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	*sorB_2*	*BN194_29180*	*K0NB63*	-1.7	0.3	-0.5	0.7	1.2	2.3	-0.9	0.5	2.4	5.4
Mannose permease IID component	Phosphotransferase systems	*manZ_9*	*BN194_29700*	*K0N954*	1.6	3.1	1.6	3.0	-0.1	0.9	2.0	4.0	0.1	1.1
Sorbose permease IIC component	Phosphotransferase systems	*sorA_4*	*BN194_29710*	*K0N8G4*	1.7	3.3	1.8	3.4	0.0	1.0	1.9	3.8	-0.5	0.7
PTS system mannose-specific EIIAB component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	*manX_5*	*BN194_29720*	*K0NDL4*	1.5	2.9	0.9	1.8	-0.7	0.6	-1.4	0.4	-0.6	0.6
Mannitol-specific phosphotransferase enzyme IIA component (EC 2.7.1.-)	Phosphotransferase systems	*mtlF*	*BN194_30410*	*K0N8N0*	-0.9	0.5	-0.7	0.6	0.2	1.1	-0.9	0.5	-1.7	0.3
Glycine betaine/carnitine/choline-binding protein OpuCC	ABC-type transporter systems	*opuCC*	*BN194_00670*	*K0N6Z3*	0.6	1.5	0.1	1.0	-0.5	0.7	1.5	2.8	0.4	1.4
Glycine betaine/carnitine/choline transport ATP-binding protein OpuCA	ABC-type transporter systems	*opuCA*	*BN194_00680*	*K0N4E4*	0.2	1.2	-0.7	0.6	-1.0	0.5	-1.0	0.5	-0.6	0.6
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE*	*BN194_01720*	*K0N7C1*	2.5	5.7	1.4	2.7	-1.1	0.5	3.8	13.6	0.0	1.6
ABC transporter, permease protein	*ABC-type transporter systems*		*BN194_02890*	*K0MSD4*	1.7	3.4	0.8	1.7	-1.0	0.5	1.8	3.4	-0.8	0.6
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_2*	*BN194_03120*	*K0N7V6*	3.8	14.0	0.5	1.4	-3.3	0.1	5.1	34.3	-1.7	0.3
D-ribose-binding protein	ABC-type transporter systems	*rbsB*	*BN194_03290*	*K0MSF6*	-5.1	0.0	-5.5	0.0	-0.4	0.8	-2.3	0.2	0.9	1.9
Probable amino-acid ABC transporter-binding protein HI_1080	*ABC-type transporter systems*		*BN194_06710*	*K0N2R6*	3.9	15.1	0.8	1.8	-3.1	0.1	4.5	22.9	0.3	1.2
Nod factor export ATP-binding protein I (EC 3.6.3.-)	ABC-type transporter systems	*nodI*	*BN194_06850*	*K0N2J7*	-1.3	0.4	-0.9	0.5	0.4	1.3	-2.6	0.2	-0.9	0.5
Uncharacterized ABC transporter ATP-binding protein YfiB	ABC-type transporter systems	*yfiB*	*BN194_06890*	*K0MT56*	-0.4	0.8	-0.5	0.7	-0.1	0.9	-0.5	0.7	0.3	1.2
Uncharacterized ABC transporter ATP-binding protein TM_0288	*ABC-type transporter systems*		*BN194_06900*	*K0N2K4*	-0.3	0.8	-0.2	0.9	0.1	1.1	-2.0	0.2	0.5	1.4
Uncharacterized ABC transporter ATP-binding protein YkpA	ABC-type transporter systems	*ykpA*	*BN194_07220*	*K0N8V6*	-1.1	0.5	-5.9	0.0	-4.8	0.0	0.1	1.1	-2.2	0.2
ABC transporter substrate-binding protein	*ABC-type transporter systems*		*BN194_07700*	*K0N2V5*	-9.9	0.0	-8.6	0.0	1.3	2.5	-5.6	0.0	5.1	35
ABC transporter substrate-binding protein	*ABC-type transporter systems*		*BN194_07710*	*K0N2Z3*	-4.2	0.1	-0.6	0.6	3.6	11.9	-4.4	0.0	1.5	2.8
Uncharacterized protein RP368	*ABC-type transporter systems*		*BN194_07720*	*K0N914*	0.5	1.4	-0.1	0.9	-0.6	0.7	-4.7	0.0	-1.0	0.5
ABC-type uncharacterized transport system, ATPase component	*ABC-type transporter systems*		*BN194_07730*	*K0N6C9*	-6.4	0.0	-3.7	0.1	2.8	6.9	-6.3	0.0	-0.5	0.7
Phosphate-binding protein pstS 1	ABC-type transporter systems	*pstS1*	*BN194_10240*	*K0MTZ5*	-0.1	0.9	-0.9	0.5	-0.8	0.6	-0.4	0.7	0.4	1.3

Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB1,pstB*	*BN194_10270*	*K0N9K1*	0.1	1.1	-0.4	0.7	-0.5	0.7	0.1	1.1	0.0	1.0
Phosphate import ATP-binding protein PstB (EC 3.6.3.27) (ABC phosphate transporter) (Phosphate-transporting ATPase)	ABC-type transporter systems	*pstB2,pstB*	*BN194_10280*	*K0N6X8*	-0.4	0.8	-1.9	0.3	-1.5	0.3	0.6	1.5	-1.6	0.3
Multiple sugar-binding transport ATP-binding protein MsmK	ABC-type transporter systems	*msmK*	*BN194_11180*	*K0N747*	-1.0	0.5	-1.6	0.3	-0.6	0.6	0.2	1.2	-0.6	0.7
Maltose ABC transporter, periplasmic maltose-binding protein	*ABC-type transporter systems*		*BN194_11200*	*K0N3U4*	-3.2	0.1	-3.5	0.1	-0.2	0.9	0.9	1.8	0.1	1.1
Glycerol-3-phosphate ABC transporter substrate-binding protein	*ABC-type transporter systems*		*BN194_11260*	*K0N3T6*	-0.1	0.9	-0.9	0.5	-0.8	0.6	0.9	1.9	0.4	1.3
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA*	*BN194_11290*	*K0MU90*	-0.1	0.9	-0.8	0.6	-0.7	0.6	-0.5	0.7	0.5	1.4
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ*	*BN194_11360*	*K0N3U2*	-0.5	0.7	-0.5	0.7	0.0	1.0	-0.2	0.8	-0.5	0.7
ABC-type Na+ efflux pump permease component-like protein	*ABC-type transporter systems*		*BN194_11370*	*K0N9U5*	-0.8	0.6	-1.4	0.4	-0.6	0.7	-0.3	0.8	-0.1	0.9
Spermidine/putrescine import ATP-binding protein PotA (EC 3.6.3.31)	ABC-type transporter systems	*potA_2, potA*	*BN194_11430*	*K0N765*	-0.5	0.7	-1.6	0.3	-1.0	0.5	-0.1	0.9	-1.2	0.4
Spermidine/putrescine-binding periplasmic protein	ABC-type transporter systems	*potD*	*BN194_11460*	*K0N3U9*	0.0	1.0	-1.2	0.5	-1.2	0.4	0.1	1.1	-0.1	0.9
Lipoprotein	ABC-type transporter systems	*metQ_2*	*BN194_13740*	*K0MV23*	2.6	6.0	0.9	1.9	-1.6	0.3	3.3	10.1	1.6	3.0
Methionine import ATP-binding protein MetN (EC 3.6.3.-)	ABC-type transporter systems	*metN*	*BN194_13750*	*K0N4L1*	2.5	5.8	1.0	1.9	-1.6	0.3	2.7	6.5	0.5	1.5
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_3*	*BN194_14020*	*K0NAD1*	1.2	2.3	0.1	1.1	-1.1	0.5	3.0	8.2	1.2	2.3
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ*	*BN194_14610*	*K0N4K4*	-1.7	0.3	-1.2	0.4	0.5	1.4	-0.1	1.0	4.5	22
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_2*	*BN194_15390*	*K0MVD0*	0.6	1.5	-1.8	0.3	-2.4	0.2	-2.0	0.2	-0.4	0.7
Uncharacterized ABC transporter ATP-binding protein YfmR (EC 3.6.3.-)	ABC-type transporter systems	*yfmR*	*BN194_15790*	*K0MVF8*	-0.9	0.5	-5.6	0.0	-4.6	0.0	-0.6	0.7	-4.8	0.0
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA*	*BN194_17880*	*K0N983*	1.7	3.3	0.6	1.5	-1.1	0.5	1.4	2.6	-0.7	0.6
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC*	*BN194_17890*	*K0MW34*	0.5	1.4	-0.5	0.7	-1.0	0.5	0.8	1.7	-0.3	0.8
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	oppB	BN194_17900	K0N5S3	1.7	3.4	0.8	1.8	-0.9	0.5	1.2	2.3	3.8	13
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	oppF	BN194_17910	K0N5I3	0.5	1.4	-0.2	0.9	-0.7	0.6	0.8	1.8	-0.8	0.6
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	oppD	BN194_17920	K0NB35	0.3	1.3	-0.5	0.7	-0.9	0.5	-0.2	0.9	-0.5	0.7

ABC transporter substrate-binding protein	ABC-type transporter systems		BN194_19800	K0N670	-0.2	0.9	-0.3	0.8	-0.1	0.9	-0.5	0.7	0.8	1.8
ABC-type antimicrobial peptide transport system,ATPase component	ABC-type transporter systems		BN194_19940	K0MWG2	-0.4	0.8	-0.2	0.8	0.1	1.1	0.6	1.5	-2.3	0.1
Uncharacterized ABC transporter ATP-binding protein YhaQ	ABC-type transporter systems	*yhaQ_2*	BN194_20470	K0NBG3	1.5	2.8	0.5	1.5	-0.9	0.5	0.5	1.4	-2.5	0.2
Oligopeptide transport ATP-binding protein OppF	ABC-type transporter systems	*oppF_2*	BN194_20590	K0MWL1	-5.0	0.0	-6.2	0.0	-1.2	0.4	-2.8	0.1	0.4	1.1
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_2*	BN194_20600	K0N6C6	-3.7	0.1	-4.3	0.1	-0.6	0.7	-3.3	0.1	-0.7	0.6
Oligopeptide transport system permease protein oppC	ABC-type transporter systems	*oppC_2*	BN194_20620	K0NBH0	0.0	1.0	-0.9	0.5	-0.9	0.5	-1.2	0.4	-0.2	0.9
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	*oppB_2*	BN194_20630	K0N9S5	-1.2	0.4	-2.4	0.2	-1.2	0.4	-2.3	0.2	1.3	2.4
Oligopeptide-binding protein oppA	ABC-type transporter systems	*oppA_2*	BN194_20640	K0MWL6	-5.0	0.0	-0.3	0.8	4.6	24.8	-1.7	0.3	2.8	7.1
Uncharacterized protein	*ABC-type transporter systems*		BN194_21220	K0NBK2	0.0	1.0	0.5	1.4	0.5	1.4	-0.4	0.8	-0.9	0.5
Bacitracin export ATP-binding protein BceA	ABC-type transporter systems	*bceA_2*	BN194_21230	K0N9X1	0.2	1.1	0.4	1.3	0.2	1.2	-1.1	0.5	0.5	1.4
Probable glutamine ABC transporter permease protein glnP	ABC-type transporter systems	*glnP*	BN194_21410	K0N6A4	1.0	2.0	-0.8	0.6	-1.7	0.3	-0.3	0.8	-1.6	0.3
ABC transporter glutamine-binding protein glnH	ABC-type transporter systems	*glnH*	BN194_21430	K0N9Y4	-0.4	0.7	-0.6	0.7	-0.1	0.9	0.3	1.2	0.6	1.5
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_3*	BN194_21440	K0MWS9	0.3	1.2	-0.2	0.9	-0.5	0.7	-0.7	0.6	-0.1	0.9
Oligopeptide transport ATP-binding protein OppD	ABC-type transporter systems	*oppD_3*	BN194_21990	K0MWY0	1.7	3.2	0.2	1.1	-1.5	0.4	0.9	1.9	-2.6	0.2
Dipeptide-binding protein dppE	ABC-type transporter systems	*dppE_4*	BN194_22020	K0NBQ1	1.7	3.3	0.4	1.3	-1.4	0.4	2.7	6.6	-0.4	0.8
Uncharacterized ABC transporter ATP-binding protein YdbJ	ABC-type transporter systems	*ydbJ*	BN194_24600	K0N7Q8	0.3	1.2	0.1	1.1	-0.2	0.9	0.8	1.7	-3.7	0.1
Manganese ABC transporter substrate-binding lipoprotein	ABC-type transporter systems	*fimA*	BN194_25450	K0N7Y2	-5.0	0.0	-5.1	0.0	-0.2	0.9	-3.8	0.1	1.7	3.4
Manganese transport system ATP-binding protein MntB	ABC-type transporter systems	*mntB*	BN194_25460	K0N7A8	-4.8	0.0	-3.0	0.1	1.8	3.4	-1.0	0.5	0.9	1.8
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25510	K0N7B2	0.4	1.3	-0.1	1.0	-0.4	0.7	3.3	10.1	2.6	6.2
ABC transporter substrate binding protein	*ABC-type transporter systems*		BN194_25570	K0NCD4	-1.6	0.3	-3.0	0.1	-1.4	0.4	-2.2	0.2	-0.4	0.1
ABC-type phosphate/phosphonate transport system,periplasmic component	*ABC-type transporter systems*		BN194_25680	K0NAI1	-2.5	0.2	-1.6	0.3	0.9	1.8	-2.4	0.2	0.2	1.1
Phosphonates import ATP-binding protein PhnC (EC 3.6.3.28)	ABC-type transporter systems	*phnC_2,phnC*	BN194_25690	K0MXP5	-2.6	0.2	-1.8	0.3	0.8	1.7	-0.9	0.5	-0.6	0.1

Energy-coupling factor transporter ATP-binding protein EcfA (ECF transporter A component EcfA) (EC 3.6.3.-)	ABC-type transporter systems	*ecfA2, ecfA*	BN194_25920	K0NCI4	0.0	1.0	-2.0	0.2	-2.0	0.2	0.7	1.7	-1.8	0.
Inner membrane amino-acid ABC transporter permease protein yecS	ABC-type transporter systems	*yecS_3*	BN194_29780	K0NB99	-0.1	0.9	-0.3	0.8	-0.2	0.9	4.8	28.7	3.9	15
ABC transporter, permease protein	*ABC-type transporter systems*		BN194_29810	K0N8H4	-0.2	0.9	-0.8	0.6	-0.6	0.6	1.0	2.0	0.3	1.
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	*glnQ_4*	BN194_29900	K0N971	-0.7	0.6	-1.0	0.5	-0.3	0.8	-0.7	0.6	1.1	2.
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_2*	BN194_29910	K0N8I1	-1.0	0.5	-0.8	0.6	0.2	1.2	0.1	1.1	1.4	2.
Glutamine-binding periplasmic protein	ABC-type transporter systems	*glnH_3*	BN194_29920	K0NDN0	-0.3	0.8	0.0	1.0	0.3	1.2	-0.4	0.8	0.4	1.
Transport protein	*Other transporter proteins*		BN194_00630	K0N4D9	0.4	1.3	-0.5	0.7	-0.9	0.5	0.3	1.2	-0.3	0.
Xanthine/uracil/vitamin C permease	*Other transporter proteins*		BN194_01470	K0N796	0.4	1.3	0.4	1.3	0.0	1.0	-1.0	0.5	-1.5	0.
MFS permease-like protein	*Other transporter proteins*		BN194_06910	K0N2S6	-2.6	0.2	-4.3	0.1	-1.7	0.3	-3.9	0.1	-1.2	0.
Uncharacterized amino acid permease YfnA	Other transporter proteins	*yfnA*	BN194_06960	K0N2T0	-0.8	0.6	-0.7	0.6	0.1	1.1	-0.2	0.9	1.6	3.
Probable cation-transporting ATPase exp7 (EC 3.6.3.-)	Other transporter proteins	*exp7*	BN194_08170	K0N955	-0.4	0.8	-1.0	0.5	-0.6	0.7	0.1	1.1	-0.4	0.
Uncharacterized MscS family protein YkuT	Other transporter proteins	*ykuT*	BN194_08700	K0N322	0.0	1.0	0.0	1.0	-0.1	1.0	-0.6	0.6	1.2	2.
Probable calcium-transporting ATPase (EC 3.6.3.8)	Other transporter proteins	*pacL*	BN194_11490	K0MUB1	1.3	2.5	1.3	2.4	-0.1	0.9	1.4	2.7	-3.2	0.
Xanthine permease	Other transporter proteins	*pbuX*	BN194_12500	K0N490	-0.7	0.6	-0.5	0.7	0.2	1.1	-1.1	0.5	1.0	2.
Probable copper-transporting P-type ATPase B (EC 3.6.3.-)	Other transporter proteins	*copB*	BN194_19280	K0N9H1	-0.8	0.6	-2.6	0.2	-1.7	0.3	1.0	2.0	0.9	1.
Calcium-transporting ATPase lmo0841 (EC 3.6.3.8)	*Other transporter proteins*		BN194_19820	K0NBC5	-0.3	0.8	-0.6	0.7	-0.3	0.8	-0.7	0.6	-1.0	0.
Cadmium efflux system accessory protein	Other transporter proteins	*cadC*	BN194_21540	K0MWU0	0.0	1.0	-5.3	0.0	-5.3	0.0	-2.0	0.3	-0.2	0.
Large-conductance mechanosensitive channel	Other transporter proteins	*mscL*	BN194_26890	K0MY02	1.3	2.5	0.1	1.1	-1.3	0.4	2.0	4.0	-0.2	0.
Zinc-transporting ATPase (EC 3.6.3.5)	Other transporter proteins	*zosA_2*	BN194_29430	K0NB79	-0.7	0.6	0.9	1.9	1.6	3.0	-0.2	0.9	-0.6	0.
Uncharacterized protein	Signal transduction		BN194_18490	K0MW74	-0.5	0.7	-5.1	0.0	-4.6	0.0	-0.8	0.6	-1.7	0.
Probable flavodoxin-1	Membrane bioenergetics	*ykuN_2*	BN194_12220	K0NA19	0.1	1.1	1.6	3.0	1.5	2.8	0.4	1.4	-2.1	0.
D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_01410	K0N1L0	0.5	1.4	2.5	5.7	2.0	4.1	0.4	1.4	-0.7	0.
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA*	BN194_01620	K0N7B1	-1.9	0.3	-4.5	0.0	-2.7	0.2	1.0	2.0	-2.5	0.
Mannose-6-phosphate isomerase (EC 5.3.1.8)	Carbohydrate-related metabolism	*pmi*	BN194_02920	K0N7U2	-0.3	0.8	1.6	3.1	1.9	3.7	-1.4	0.4	-1.8	0.
Putative tagatose-6-phosphate ketose/aldose isomerase (EC 5.3.1.-)	Carbohydrate-related metabolism	*agaS*	BN194_02940	K0MSD9	1.8	3.5	3.4	10.9	1.6	3.1	1.4	2.6	-2.2	0.

N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*manD*	BN194_02950	K0N1P4	1.4	2.7	-3.1	0.1	-4.5	0.0	0.8	1.8	-2.3	0.
Beta-galactosidase 17 (EC 3.2.1.23)	Carbohydrate-related metabolism	*BGAL17*	BN194_02960	K0N204	1.7	3.2	4.3	19.9	2.6	6.2	-1.7	0.3	-5.4	0.
L-sorbose 1-phosphate reductase (EC 1.1.1.-)	Carbohydrate-related metabolism	*sorE*	BN194_04300	K0N1W2	1.3	2.5	2.9	7.7	1.6	3.0	0.7	1.7	-2.1	0.
Oligo-1,6-glucosidase (EC 3.2.1.10)	Carbohydrate-related metabolism	*malL*	BN194_04830	K0N5P4	0.2	1.1	3.1	8.7	2.9	7.7	0.0	1.0	-1.0	0.
Putative thiamine pyrophosphate-containing protein ydaP	Carbohydrate-related metabolism	*ydaP*	BN194_05070	K0N8B1	7.5	184.8	2.8	6.8	-4.8	0.0	5.8	57.2	-1.2	0.
D-lactate dehydrogenase (EC 1.1.1.28)	Carbohydrate-related metabolism	*dld*	BN194_06590	K0MT28	0.7	1.6	-0.1	0.9	-0.8	0.6	1.1	2.1	-1.7	0.
Trehalose-6-phosphate hydrolase (EC 3.2.1.93)	Carbohydrate-related metabolism	*treA*	BN194_06930	K0N662	0.1	1.0	2.3	5.0	2.2	4.7	-0.2	0.9	-3.3	0.
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh1,ldh*	BN194_06970	K0N8S5	-0.9	0.5	-3.8	0.1	-2.9	0.1	0.2	1.1	-2.7	0.
6-phospho-beta-galactosidase (EC 3.2.1.85) (Beta-D-phosphogalactoside galactohydrolase) (P-beta-Gal)	Carbohydrate-related metabolism	*lacG*	BN194_07320	K0N8W7	0.1	1.1	4.0	16.5	3.9	15.5	-0.6	0.7	-0.7	0.
Galactokinase (EC 2.7.1.6) (Galactose kinase)	Carbohydrate-related metabolism	*galK*	BN194_07340	K0MTA3	-0.9	0.5	1.8	3.6	2.7	6.7	0.4	1.3	-1.9	0.
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*lacC*	BN194_07470	K0N8Y4	-0.9	0.5	-0.4	0.8	0.5	1.5	-2.6	0.2	-3.0	0.
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2,lacD*	BN194_07480	K0N6A8	-1.8	0.3	1.5	2.8	3.3	9.5	-2.2	0.2	-1.6	0.
Galactose-6-phosphate isomerase subunit lacB (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacB*	BN194_07490	K0MTB7	0.6	1.5	-2.5	0.2	-3.1	0.1	0.2	1.1	-1.9	0.
Galactose-6-phosphate isomerase subunit lacA (EC 5.3.1.26)	Carbohydrate-related metabolism	*lacA*	BN194_07500	K0N2T4	1.1	2.1	-1.3	0.4	-2.4	0.2	0.9	1.9	-2.6	0.
Aldehyde-alcohol dehydrogenase	Carbohydrate-related metabolism	*ADH2*	BN194_08400	K0N307	-5.8	0.0	-5.9	0.0	-0.1	0.9	-3.4	0.1	0.1	1.
Uncharacterized protein YwcC	Carbohydrate-related metabolism	*ywcC*	BN194_09930	K0N6V0	-0.5	0.7	1.9	3.9	2.4	5.5	-1.2	0.4	-2.3	0.
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	*pta*	BN194_11340	K0MU95	-0.9	0.5	0.6	1.5	1.5	2.9	-0.3	0.8	1.2	2.
Archaeal fructose-1,6-bisphosphatase related enzyme of inositol monophosphatase family	*Carbohydrate-related metabolism*		BN194_15140	K0MVB0	-0.4	0.7	-3.1	0.1	-2.6	0.2	0.2	1.1	0.9	1.
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	*fruK*	BN194_15420	K0NAJ6	0.3	1.2	0.3	1.2	0.0	1.0	1.0	1.9	1.8	3.
Formate acetyltransferase (EC 2.3.1.54)	Carbohydrate-related metabolism	*pflB*	BN194_16080	K0N8I5	-7.9	0.0	-8.8	0.0	-0.9	0.5	-1.1	0.5	0.2	1.
Pyruvate formate-lyase-activating enzyme (EC 1.97.1.4)	Carbohydrate-related metabolism	*act*	BN194_16090	K0MVI3	-1.9	0.3	-2.2	0.2	-0.4	0.8	0.4	1.3	0.0	1.
Acylphosphatase	Carbohydrate-related metabolism	*acyP*	BN194_18620	K0NB65	-0.1	0.9	-0.9	0.5	-0.8	0.6	-0.4	0.7	-1.7	0.

Pyruvate oxidase (EC 1.2.3.3)	Carbohydrate-related metabolism	*pox5*	BN194_19670	K0NBB6	-2.0	0.3	2.3	4.8	4.2	18.6	0.2	1.2	-2.9	0.
N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25) (GlcNAc 6-P deacetylase)	Carbohydrate-related metabolism	*nagA*	BN194_19890	K0MWF9	-2.2	0.2	-2.0	0.3	0.2	1.1	0.5	1.4	0.9	1.
Alpha-acetolactate decarboxylase (EC 4.1.1.5)	Carbohydrate-related metabolism	*aldB*	BN194_20140	K0MWH5	-0.8	0.6	0.8	1.7	1.6	3.0	-1.9	0.3	-2.0	0.
Glucose-1-phosphate adenylyltransferase, GlgD subunit	Carbohydrate-related metabolism	*glgD*	BN194_21590	K0MWU4	-2.4	0.2	-4.4	0.0	-1.9	0.3	0.6	1.6	-1.0	0.
Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) (ADP-glucose pyrophosphorylase) (ADP-glucose synthase)	Carbohydrate-related metabolism	*glgC*	BN194_21600	K0N6T3	-0.4	0.7	-1.4	0.4	-1.0	0.5	-0.5	0.7	-1.3	0.
Alpha-galactosidase 2 (EC 3.2.1.22)	Carbohydrate-related metabolism	*agaS_2*	BN194_22160	K0N6I2	-0.3	0.8	-8.6	0.0	-8.3	0.0	2.6	6.1	-1.4	0.
Fructoselysine kinase (EC 2.7.1.-)	Carbohydrate-related metabolism	*frlD*	BN194_22240	K0MX05	0.9	1.8	-0.2	0.9	-1.1	0.5	0.4	1.4	-2.3	0.
Sucrose-6-phosphate hydrolase (EC 3.2.1.26)	Carbohydrate-related metabolism	*scrB*	BN194_22440	K0MX27	-0.8	0.6	-1.8	0.3	-0.9	0.5	1.1	2.1	-1.8	0.
NADH-dependent butanol dehydrogenase A (EC 1.1.1.-)	Carbohydrate-related metabolism	*bdhA*	BN194_22640	K0MX50	1.1	2.1	1.4	2.6	0.3	1.2	1.4	2.7	-3.7	0.
Acetate kinase (EC 2.7.2.1) (Acetokinase)	Carbohydrate-related metabolism	*ackA_2,ackA*	BN194_23060	K0N6W4	-3.2	0.1	-4.3	0.1	-1.0	0.5	0.0	1.0	0.3	1.
L-lactate dehydrogenase (L-LDH) (EC 1.1.1.27)	Carbohydrate-related metabolism	*ldh*	BN194_26560	K0N7J5	0.6	1.5	0.8	1.8	0.3	1.2	1.0	1.9	-1.9	0.
Tagatose 1,6-diphosphate aldolase (EC 4.1.2.40) (D-tagatose-1,6-bisphosphate aldolase) (Tagatose-bisphosphate aldolase)	Carbohydrate-related metabolism	*lacD2_2,lacD*	BN194_27060	K0N7P0	0.6	1.5	2.1	4.3	1.6	2.9	0.3	1.3	-1.6	0.
Protein lacX, plasmid	Carbohydrate-related metabolism	*lacX*	BN194_27070	K0NCY0	2.5	5.8	4.8	27.8	2.3	4.8	1.9	3.8	-1.5	0.
L-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-)	*Carbohydrate-related metabolism*		BN194_27170	K0NCZ6	1.0	2.0	1.4	2.6	0.4	1.3	2.5	5.7	-2.5	0.
Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase) (Glycerokinase)	Carbohydrate-related metabolism	*glpK_2,glpK*	BN194_27720	K0ND65	-0.4	0.8	1.9	3.6	2.2	4.7	1.3	2.4	-0.7	0.
Galactose-1-phosphate uridylyltransferase (Gal-1-P uridylyltransferase) (EC 2.7.7.12) (UDP-glucose--hexose-1-phosphate uridylyltransferase)		*galT*	BN194_07370	K0N8X1	-2.8	0.1	-3.9	0.1	-1.0	0.5	0.0	1.0	-0.6	0.
Alpha-glucosidase (EC 3.2.1.20)	Carbohydrate-related metabolism	*agl*	BN194_27950	K0N8T1	0.5	1.5	0.8	1.7	0.2	1.2	1.3	2.5	-2.6	0.
3-keto-L-gulonate-6-phosphate decarboxylase sgbH (EC 4.1.1.85)	Carbohydrate-related metabolism	*sgbH*	BN194_28550	K0N8W6	-0.3	0.8	3.1	8.3	3.4	10.5	-0.4	0.7	0.0	1.
Protein IolS (EC 1.1.1.-)	Carbohydrate-related metabolism	*iolS*	BN194_29680	K0NB94	-0.2	0.9	-2.3	0.2	-2.1	0.2	0.1	1.1	-2.2	0.
Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)	Carbohydrate-related metabolism	*mtlD_3mtlD*	BN194_30400	K0N9C8	0.6	1.6	4.2	18.1	3.5	11.5	2.5	5.6	-2.7	0.
Glucosamine-6-phosphate deaminase (EC 3.5.99.6)	Carbohydrate-related metabolism	*nagB*	BN194_30440	K0MYW0	0.9	1.9	4.3	20.1	3.4	10.8	-0.1	0.9	-3.6	0.

Uncharacterized oxidoreductase YbdH (EC 1.1.-.-)	Carbohydrate-related metabolism	*ybdH*	BN194_30540	K0MYX0	-0.9	0.5	-0.7	0.6	0.2	1.1	-0.5	0.7	-2.8	0.
Probable phosphoketolase (EC 4.1.2.-)	Central glycolytic/intermediary pathways	*xpkA*	BN194_01710	K0N1M9	0.8	1.8	2.1	4.4	1.3	2.5	0.1	1.0	-2.7	0.
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*yqeC*	BN194_02330	K0N532	0.0	1.0	1.0	1.9	0.9	1.9	2.9	7.3	3.2	9.
Gluconokinase (EC 2.7.1.12)	Central glycolytic/intermediary pathways	*gntK*	BN194_02340	K0MS76	-2.3	0.2	-1.9	0.3	0.4	1.3	-1.7	0.3	-1.2	0.
Ribokinase (EC 2.7.1.15)	Central glycolytic/intermediary pathways	*rbsK*	BN194_03300	K0N1R2	-1.4	0.4	0.2	1.1	1.6	3.1	-0.5	0.7	-0.9	0.
PTS-dependent dihydroxyacetone kinase,phosphotransferase subunit dhaM (EC 2.7.1.-)	Central glycolytic/intermediary pathways	*dhaM*	BN194_04960	K0N2C2	1.5	2.9	-0.2	0.9	-1.7	0.3	1.7	3.3	-1.2	0.
Uncharacterized protein	*Central glycolytic/intermediary pathways*		BN194_04970	K0N8A3	0.8	1.7	2.8	7.0	2.0	4.1	2.2	4.5	-2.7	0.
PTS-dependent dihydroxyacetone kinase,dihydroxyacetone-binding subunit dhaK (EC 2.7.-.-)	Central glycolytic/intermediary pathways	*dhaK_2*	BN194_04980	K0N5Q3	1.1	2.2	2.5	5.5	1.3	2.5	2.2	4.7	-1.5	0.
Fructose-bisphosphate aldolase (EC 4.1.2.13)	Central glycolytic/intermediary pathways	*fba_2*	BN194_05060	K0N2C9	-1.5	0.4	-4.1	0.1	-2.6	0.2	-0.5	0.7	0.6	1.
Aldose 1-epimerase (EC 5.1.3.3)	*Central glycolytic/intermediary pathways*		BN194_07390	K0MTA8	-0.9	0.5	1.3	2.5	2.3	4.8	0.0	1.0	-2.8	0.
Glucose-6-phosphate 1-dehydrogenase (G6PD) (EC 1.1.1.49)	Central glycolytic/intermediary pathways	*zwf*	BN194_08420	K0N966	-0.2	0.9	-2.5	0.2	-2.3	0.2	-1.1	0.5	-1.9	0.
Phosphoglucomutase (EC 5.4.2.2)	Central glycolytic/intermediary pathways	*pgcA*	BN194_10370	K0N9K8	0.4	1.3	2.4	5.4	2.1	4.1	1.6	3.0	-2.8	0.
Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	Central glycolytic/intermediary pathways	*gap*	BN194_11010	K0N3R3	0.2	1.2	1.8	3.5	1.6	2.9	0.7	1.6	-0.6	0.
Phosphoglycerate kinase (EC 2.7.2.3)	Central glycolytic/intermediary pathways	*pgk*	BN194_11020	K0N9R1	0.3	1.2	1.4	2.6	1.1	2.1	-0.3	0.8	-1.9	0.
Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	Central glycolytic/intermediary pathways	*tpiA*	BN194_11030	K0N736	2.1	4.4	4.4	21.8	2.3	5.0	1.2	2.3	-0.7	0.
Enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (2-phosphoglycerate dehydratase)	Central glycolytic/intermediary pathways	*eno*	BN194_11040	K0MU67	0.5	1.4	2.5	5.5	1.9	3.8	0.7	1.7	0.1	1.

Putative beta-phosphoglucomutase (EC 5.4.2.6)	Central glycolytic/intermediary pathways	*yvdM*	BN194_11170	K0N9S7	-1.8	0.3	-2.7	0.2	-0.8	0.6	0.5	1.4	-0.3	0.8
Glucose-6-phosphate isomerase (GPI) (EC 5.3.1.9) (Phosphoglucose isomerase) (Phosphohexose isomerase)	Central glycolytic/intermediary pathways	*pgi*	BN194_12580	K0N7I6	0.5	1.4	2.9	7.3	2.4	5.1	1.6	3.1	-2.1	0.2
Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhA*	BN194_15080	K0N860	0.2	1.2	-6.4	0.0	-6.7	0.0	0.8	1.7	-1.5	0.4
Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1)	Central glycolytic/intermediary pathways	*pdhB*	BN194_15090	K0MVA7	0.5	1.4	-4.5	0.0	-5.0	0.0	0.6	1.5	-1.9	0.3
Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	Central glycolytic/intermediary pathways	*pdhC*	BN194_15100	K0N4W5	0.0	1.0	-1.2	0.4	-1.1	0.5	0.4	1.3	-0.9	0.5
Dihydrolipoyl dehydrogenase (EC 1.8.1.4)	Central glycolytic/intermediary pathways	*pdhD*	BN194_15110	K0N4P1	0.1	1.1	-4.1	0.1	-4.2	0.1	0.9	1.8	0.2	1.1
ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphohexokinase)	Central glycolytic/intermediary pathways	*pfkA*	BN194_15570	K0NAK6	-2.2	0.2	-4.0	0.1	-1.7	0.3	0.5	1.4	-0.1	0.9
Pyruvate kinase (EC 2.7.1.40)	Central glycolytic/intermediary pathways	*pyk*	BN194_15580	K0N8B6	-0.3	0.8	-2.4	0.2	-2.1	0.2	0.0	1.0	-1.3	0.4
Aldose 1-epimerase	*Central glycolytic/intermediary pathways*		BN194_16020	K0NAP4	-0.8	0.6	-0.1	0.9	0.7	1.6	-0.1	1.0	0.8	1.7
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	*rpe*	BN194_18000	K0N5T1	-5.2	0.0	-5.4	0.0	-0.2	0.9	-0.2	0.9	4.5	22
Glucokinase (EC 2.7.1.2)	Central glycolytic/intermediary pathways	*glcK*	BN194_18420	K0NB57	-0.6	0.7	0.2	1.2	0.8	1.7	-1.6	0.3	-0.4	0.7
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	*gnd*	BN194_18660	K0N5N2	0.5	1.4	-0.3	0.8	-0.8	0.6	1.8	3.5	-2.4	0.2
Fructose-1,6-bisphosphatase class 3 (FBPase class 3) (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase class 3)	Central glycolytic/intermediary pathways	*fbp*	BN194_21660	K0N6C3	-0.9	0.5	-1.7	0.3	-0.8	0.6	-0.3	0.8	-0.9	0.5
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA2,gpmA*	BN194_22740	K0MX58	0.4	1.4	-2.8	0.1	-3.2	0.1	1.6	3.0	-0.4	0.8
Glucose 1-dehydrogenase 2 (EC 1.1.1.47)	Central glycolytic/intermediary pathways	*gdhII*	BN194_23130	K0NA64	2.8	6.8	2.0	3.9	-0.8	0.6	3.8	13.7	-0.1	0.9

2,3-bisphosphoglycerate-dependent phosphoglycerate mutase (BPG-dependent PGAM) (PGAM) (Phosphoglyceromutase) (dPGM) (EC 5.4.2.11)	Central glycolytic/intermediary pathways	*gpmA1,gpmA*	BN194_24750	K0N7R7	-3.9	0.1	-4.9	0.0	-0.9	0.5	0.9	1.9	0.2	1.1
Hydroxyacid oxidase (EC 1.1.3.15)	Central glycolytic/intermediary pathways	*haox*	BN194_24790	K0MXH5	4.5	22.5	5.6	48.6	1.1	2.2	3.8	13.7	-2.7	0.2
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase 2 (EC 5.4.2.1)	Central glycolytic/intermediary pathways	*gpmA2_2*	BN194_27560	K0N7W0	0.1	1.1	-0.4	0.8	-0.5	0.7	1.3	2.4	-2.3	0.2
Transaldolase (EC 2.2.1.2)	Central glycolytic/intermediary pathways	*fsa*	BN194_28440	K0MYF0	3.4	10.2	2.5	5.8	-0.8	0.6	4.8	28.8	1.2	2.3
Ribose-5-phosphate isomerase A (EC 5.3.1.6) (Phosphoriboisomerase A)	Central glycolytic/intermediary pathways	*rpiA_2, ripA*	BN194_28600	K0N8W9	-0.7	0.6	-6.0	0.0	-5.2	0.0	0.1	1.1	-0.7	0.0
Probable phosphoketolase (EC 4.1.2.-)	*Central glycolytic/intermediary pathways*		BN194_28700	K0N8X7	0.2	1.1	2.2	4.5	2.0	4.1	0.1	1.1	-3.8	0.1
Malolactic enzyme (EC 1.-.-.-)	Tricarboxylic acid pathway	*mleA*	BN194_08070	K0N949	2.0	4.0	6.4	82.5	4.4	20.8	3.4	10.4	-0.9	0.0
Pyruvate carboxylase (EC 6.4.1.1)	Tricarboxylic acid pathway	*pyc*	BN194_15170	K0NAI2	-4.1	0.1	-7.3	0.0	-3.1	0.1	-0.7	0.6	0.2	1.1
Phosphoenolpyruvate carboxykinase (ATP)	*Tricarboxylic acid pathway*		BN194_20000	K0N684	-2.8	0.1	-3.5	0.1	-0.7	0.6	-0.2	0.9	-3.1	0.1
Pyruvate carboxylase subunit B (EC 6.4.1.1)	Tricarboxylic acid pathway	*pycB*	BN194_20290	K0MWI8	-5.8	0.0	-4.5	0.0	1.4	2.6	-2.2	0.2	-2.6	0.2
Probable apo-citrate lyase phosphoribosyl-dephospho-CoA transferase (EC 2.7.7.61)	Tricarboxylic acid pathway	*citX*	BN194_20300	K0N6A3	-0.6	0.6	-1.9	0.3	-1.3	0.4	1.3	2.5	-0.9	0.5
Citrate lyase alpha chain (EC 2.8.3.10) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citF*	BN194_20310	K0N607	-4.4	0.0	-1.8	0.3	2.6	6.0	-2.7	0.2	-2.6	0.2
Citrate lyase subunit beta (EC 4.1.3.34) (EC 4.1.3.6)	Tricarboxylic acid pathway	*citE*	BN194_20320	K0NBF4	-2.9	0.1	-0.3	0.8	2.6	6.2	-2.3	0.2	-3.0	0.1
Citrate lyase acyl carrier protein (Citrate lyase gamma chain)	Tricarboxylic acid pathway	*citD*	BN194_20330	K0N9Q5	-2.6	0.2	-1.3	0.4	1.4	2.6	-3.4	0.1	-1.6	0.1
Fumarate hydratase class II (Fumarase C) (EC 4.2.1.2)	Tricarboxylic acid pathway	*fumC*	BN194_25340	K0MXL5	0.6	1.5	-1.5	0.4	-2.1	0.2	-0.1	0.9	-0.1	0.5
RNA polymerase sigma factor SigA	RNA polymerase	*rpoD,sigA*	BN194_16920	K0NAV6	0.5	1.4	-5.4	0.0	-5.9	0.0	-2.7	0.2	-0.4	0.8
DNA-directed RNA polymerase subunit omega (RNAP omega subunit) (EC 2.7.7.6) (RNA polymerase omega subunit) (Transcriptase subunit omega)	RNA polymerase	*rpoZ*	BN194_18100	K0N5T7	1.0	2.0	-2.5	0.2	-3.5	0.1	3.5	11.7	-1.2	0.4
DNA-directed RNA polymerase subunit alpha (RNAP subunit alpha) (EC 2.7.7.6) (RNA polymerase subunit alpha) (Transcriptase subunit alpha)	RNA polymerase	*rpoA*	BN194_25960	K0N7E5	-0.1	0.9	-7.6	0.0	-7.5	0.0	-1.1	0.5	-0.7	0.0
DNA-directed RNA polymerase subunit beta' (RNAP subunit beta') (EC 2.7.7.6) (RNA polymerase subunit beta') (Transcriptase subunit beta')	RNA polymerase	*rpoC*	BN194_26330	K0NAN3	0.0	1.0	-7.4	0.0	-7.4	0.0	1.1	2.2	-1.6	0.3

DNA-directed RNA polymerase subunit beta (RNAP subunit beta) (EC 2.7.7.6) (RNA polymerase subunit beta) (Transcriptase subunit beta)	RNA polymerase	*rpoB*	BN194_26340	K0MXV4	0.2	1.1	-4.6	0.0	-4.7	0.0	1.0	2.0	-1.7	0.
Probable DNA-directed RNA polymerase subunit delta (RNAP delta factor)	RNA polymerase	*rpoE*	BN194_26810	K0N7L4	-0.2	0.9	-5.3	0.0	-5.1	0.0	-1.1	0.5	0.3	1.
Transcriptional repressor smtB homolog	Transcriptional regulation	*ziaR*	BN194_01180	K0N4L0	-0.5	0.7	-1.1	0.5	-0.6	0.7	-1.8	0.3	1.2	2.
HTH-type transcriptional regulator iolR	Transcriptional regulation	*iolR*	BN194_02190	K0MS58	-1.6	0.3	-3.5	0.1	-1.8	0.3	-0.4	0.8	0.0	1.
Hex regulon repressor	Transcriptional regulation		BN194_02320	K0N7J9	-1.9	0.3	-2.8	0.1	-0.9	0.5	-1.6	0.3	1.1	2.
Transcriptional regulator lytR	Transcriptional regulation	*lytR*	BN194_02540	K0MS94	-0.5	0.7	0.2	1.1	0.6	1.6	0.9	1.9	4.1	17
HTH-type transcriptional repressor glcR	Transcriptional regulation	*glcR*	BN194_02570	K0N7M8	-0.6	0.7	-3.7	0.1	-3.1	0.1	-2.1	0.2	0.4	1.
HTH-type transcriptional regulator galR	Transcriptional regulation	*galR*	BN194_03780	K0N5G9	-1.0	0.5	-1.3	0.4	-0.3	0.8	-0.7	0.6	4.5	22
Transcriptional regulator, xre family	*Transcriptional regulation*		BN194_05600	K0N260	0.3	1.3	-2.5	0.2	-2.9	0.1	-1.5	0.3	-1.1	0.
Lactose phosphotransferase system repressor	Transcriptional regulation	*lacR*	BN194_07510	K0N2X5	-1.7	0.3	-3.0	0.1	-1.3	0.4	0.2	1.2	-1.0	0.
Transcriptional regulator	*Transcriptional regulation*		BN194_08230	K0N6I4	-0.3	0.8	-4.0	0.1	-3.7	0.1	-0.3	0.8	0.9	1.
Putative transcriptional regulator (DtxR family)	*Transcriptional regulation*		BN194_08410	K0N354	0.3	1.2	-3.4	0.1	-3.7	0.1	-1.1	0.5	-1.5	0.
Uncharacterized protein ytoI	Transcriptional regulation	*ytoI*	BN194_08440	K0MTM0	-0.6	0.7	-4.0	0.1	-3.4	0.1	-0.8	0.6	-0.4	0.
Probable transcription repressor NiaR	Transcriptional regulation	*niaR*	BN194_08730	K0N6L8	-1.9	0.3	-3.3	0.1	-1.4	0.4	-3.5	0.1	0.0	1.
Probable catabolite control protein A	Transcriptional regulation	*ccpA*	BN194_08750	K0N323	0.2	1.1	-8.5	0.0	-8.7	0.0	1.2	2.2	0.7	1.
Xre-like DNA-binding protein	*Transcriptional regulation*		BN194_10050	K0N3E1	2.0	4.1	2.7	6.5	0.7	1.6	1.3	2.5	3.0	8.
Phosphate-specific transport system accessory protein PhoU	Transcriptional regulation	*phoU*	BN194_10290	K0MTZ9	-2.0	0.3	-3.6	0.1	-1.7	0.3	-0.9	0.6	0.7	1.
Putative sporulation transcription regulator WhiA	Transcriptional regulation	*whiA*	BN194_10490	K0MU14	-0.7	0.6	-2.3	0.2	-1.6	0.3	-3.5	0.1	1.0	2.
Organic hydroperoxide resistance transcriptional regulator	Transcriptional regulation	*ohrR*	BN194_10500	K0N3J7	-0.3	0.8	-4.5	0.0	-4.2	0.1	-1.4	0.4	-0.6	0.
Double-stranded beta-helix related protein	*Transcriptional regulation*		BN194_11420	K0N9U8	-1.0	0.5	-1.9	0.3	-1.0	0.5	-1.9	0.3	-0.5	0.
Probable transcriptional regulatory protein BN194_11600	*Transcriptional regulation*		BN194_11600	K0N3Z3	-0.3	0.8	-3.7	0.1	-3.5	0.1	-1.6	0.3	-1.3	0.
Transcriptional regulator, TetR family	*Transcriptional regulation*		BN194_12190	K0MUM1	-0.1	0.9	-4.9	0.0	-4.8	0.0	-1.1	0.5	-1.4	0.
Transcriptional regulator, xre family	*Transcriptional regulation*		BN194_13860	K0N4E8	-0.3	0.8	-4.4	0.0	-4.1	0.1	0.0	1.0	-2.0	0.
Transcriptional regulator	*Transcriptional regulation*		BN194_16100	K0N551	-2.2	0.2	-6.5	0.0	-4.3	0.1	-0.8	0.6	1.9	3.
Transcriptional regulator GltC	Transcriptional regulation	*nac*	BN194_16620	K0NAT7	-0.8	0.6	-2.1	0.2	-1.3	0.4	0.7	1.6	2.2	4.
Putative pyruvate, phosphate dikinase regulatory protein (PPDK regulatory protein) (EC 2.7.11.32) (EC 2.7.4.27)	Transcriptional regulation	*rp2*	BN194_17060	K0N598	0.4	1.3	-2.2	0.2	-2.5	0.2	1.4	2.7	-2.0	0.

Heat-inducible transcription repressor HrcA	Transcriptional regulation	*hrcA*	BN194_17480	K0N915	0.3	1.2	-4.3	0.0	-4.7	0.0	1.5	2.9	-2.3	0.2
HTH-type transcriptional regulator yodB	Transcriptional regulation	*yodB*	BN194_18590	K0MW80	-0.9	0.6	-3.7	0.1	-2.9	0.1	-2.2	0.2	0.0	1.0
Transcriptional repressor NrdR	Transcriptional regulation	*nrdR*	BN194_18900	K0N5Z5	-0.9	0.6	-3.6	0.1	-2.8	0.1	-2.1	0.2	-1.9	0.3
Arginine repressor	Transcriptional regulation	*argR1,argR*	BN194_19110	K0N5R1	0.5	1.4	0.4	1.3	-0.1	1.0	-1.4	0.4	3.3	10
HTH-type transcriptional repressor yvoA	Transcriptional regulation	*yvoA_2*	BN194_19880	K0N9L8	0.7	1.6	-3.2	0.1	-3.8	0.1	-0.7	0.6	2.5	5.6
Transcriptional regulator lytR	Transcriptional regulation	*lytR_3*	BN194_21700	K0N6U3	0.0	1.0	0.0	1.0	-0.1	1.0	0.9	1.9	0.6	1.5
MarR family transcriptional regulator	*Transcriptional regulation*		BN194_22610	K0N6N9	0.1	1.1	-0.5	0.7	-0.6	0.6	-3.0	0.1	-0.9	0.5
Uncharacterized protein	*Transcriptional regulation*		BN194_22670	K0NBT5	0.3	1.3	-3.5	0.1	-3.8	0.1	-0.7	0.6	0.2	1.1
Uncharacterized protein	*Transcriptional regulation*		BN194_22710	K0N6Q3	-0.4	0.7	-1.0	0.5	-0.6	0.7	-0.6	0.7	-0.5	0.7
Transcriptional regulator, xre family	*Transcriptional regulation*		BN194_23510	K0N6Y7	0.2	1.2	-5.4	0.0	-5.6	0.0	-2.0	0.3	-2.0	0.2
Transcriptional regulator lytR	Transcriptional regulation	*lytR_4*	BN194_23780	K0NA85	-0.5	0.7	-0.4	0.7	0.1	1.1	1.4	2.6	4.1	17
Redox-sensing transcriptional repressor Rex	Transcriptional regulation	*rex_2,rex*	BN194_23820	K0NBZ5	-0.1	0.9	-7.0	0.0	-6.9	0.0	-0.9	0.5	-0.9	0.5
Transcriptional repressor CcpN	Transcriptional regulation	*ccpN*	BN194_24740	K0MXH2	-0.2	0.9	-2.2	0.2	-2.0	0.3	-1.7	0.3	0.5	1.4
MerR family transcriptional regulator	*Transcriptional regulation*		BN194_25900	K0N833	-0.2	0.9	-1.3	0.4	-1.1	0.5	-0.8	0.6	-2.7	0.2
Transcriptional regulator, PadR-like family	*Transcriptional regulation*		BN194_26580	K0NAQ3	1.3	2.5	0.2	1.1	-1.2	0.4	1.6	3.0	-0.9	0.6
Pur operon repressor	Transcriptional regulation	*purR_2*	BN194_26960	K0N7M9	-1.3	0.4	-7.5	0.0	-6.2	0.0	0.5	1.4	1.7	3.2
Putative transcriptional regulator, MarR family	*Transcriptional regulation*		BN194_27490	K0MY64	-0.2	0.9	-0.6	0.6	-0.5	0.7	-1.5	0.3	0.3	1.2
Glucitol operon repressor	Transcriptional regulation	*srlR*	BN194_28690	K0MYG3	-0.7	0.6	-3.7	0.1	-3.1	0.1	-1.0	0.5	-2.5	0.2
Transcriptional regulator, XRE family	*Transcriptional regulation*		BN194_30170	K0NDP4	-0.2	0.9	-4.4	0.0	-4.2	0.1	-1.3	0.4	-0.2	0.9
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA*	BN194_08450	K0N309	-0.2	0.9	2.2	4.7	2.5	5.5	-0.7	0.6	-1.9	0.3
Ribonuclease Y (RNase Y) (EC 3.1.-.-)	RNA degradation	*rny*	BN194_10100	K0N3E5	0.0	1.0	-0.1	0.9	-0.1	0.9	-0.5	0.7	-2.2	0.2
Uncharacterized protein	RNA degradation		BN194_11250	K0N3V2	1.3	2.5	2.7	6.6	1.4	2.7	1.3	2.5	-2.5	0.2
Ribonuclease J 1 (EC 3.1.-.-)	RNA degradation	*rnjA*	BN194_15020	K0NAH6	0.0	1.0	-5.5	0.0	-5.5	0.0	-1.3	0.4	0.1	1.1
Uncharacterized protein	RNA degradation		BN194_15290	K0MVC2	-0.5	0.7	-2.3	0.2	-1.7	0.3	-1.5	0.4	-0.2	0.9
3'-5' exoribonuclease yhaM (EC 3.1.-.-)	RNA degradation	*yhaM*	BN194_19070	K0NB84	-0.4	0.7	-4.9	0.0	-4.5	0.0	-1.2	0.4	-3.5	0.2
Bifunctional oligoribonuclease and PAP phosphatase nrnA (EC 3.1.-.-) (EC 3.1.3.7)	RNA degradation	*nrnA_2*	BN194_29210	K0N8B2	1.6	3.0	2.6	5.9	1.0	2.0	1.3	2.5	-2.7	0.2
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA1, greA*	BN194_02150	K0N1G7	2.4	5.1	-0.2	0.9	-2.6	0.2	0.1	1.1	-3.7	0.1

Cold shock protein 1	Transcription-associated proteins	*csp*	BN194_06990	K0MT67	0.9	1.9	1.5	2.8	0.6	1.5	-0.2	0.8	-1.0	0.5
Cold shock-like protein CspLA	Transcription-associated proteins	*cspLA*	BN194_12460	K0N438	-0.4	0.7	0.3	1.3	0.7	1.7	-0.7	0.6	-0.7	0.6
Transcription termination/antitermination protein NusA	Transcription-associated proteins	*nusA*	BN194_17580	K0N927	0.0	1.0	-4.2	0.1	-4.2	0.1	-2.0	0.3	-1.6	0.3
N utilization substance protein B homolog (Protein NusB)	Transcription-associated proteins	*nusB*	BN194_18220	K0NB49	-0.1	0.9	-1.5	0.4	-1.3	0.4	-1.5	0.4	-1.3	0.4
Transcription elongation factor GreA (Transcript cleavage factor GreA)	Transcription-associated proteins	*greA*	BN194_18520	K0NB62	-0.5	0.7	0.1	1.1	0.5	1.5	-2.5	0.2	-2.5	0.2
Transcription termination/antitermination protein NusG	Transcription-associated proteins	*nusG*	BN194_24260	K0N730	0.1	1.1	-3.7	0.1	-3.9	0.1	-0.2	0.8	-0.7	0.6
30S ribosomal protein S6	Ribosomal proteins	*rpsF*	BN194_00100	K0N0Z1	0.0	1.0	-4.4	0.0	-4.4	0.0	-1.2	0.4	-1.8	0.3
30S ribosomal protein S18	Ribosomal proteins	*rpsR*	BN194_00120	K0N6T2	0.1	1.1	-1.7	0.3	-1.8	0.3	-0.6	0.6	-0.5	0.7
50S ribosomal protein L9	Ribosomal proteins	*rplI*	BN194_01130	K0N4K3	-0.1	0.9	-6.7	0.0	-6.5	0.0	-0.1	0.9	2.1	4.2
30S ribosomal protein S14	Ribosomal proteins	*rpsN*	BN194_09950	K0N3D1	3.4	10.7	-1.8	0.3	-5.2	0.0	3.9	15.3	-0.8	0.6
30S ribosomal protein S4	Ribosomal proteins	*rpsD*	BN194_14440	K0MV63	0.0	1.0	-5.2	0.0	-5.2	0.0	-0.3	0.8	-1.8	0.3
30S ribosomal protein S20	Ribosomal proteins	*rpsT*	BN194_15250	K0N4X9	0.1	1.1	-4.4	0.0	-4.6	0.0	-0.6	0.6	0.3	1.2
30S ribosomal protein S15	Ribosomal proteins	*rpsO*	BN194_15260	K0N4Q6	-0.5	0.7	-3.7	0.1	-3.2	0.1	-0.5	0.7	1.0	2.0
50S ribosomal protein L32	Ribosomal proteins	*rpmF*	BN194_15510	K0N4T0	-2.6	0.2	-3.2	0.1	-0.6	0.7	1.3	2.4	10.4	13
30S ribosomal protein S1 homolog	Ribosomal proteins	*ypfD*	BN194_15720	K0NAL9	0.4	1.3	-2.8	0.1	-3.2	0.1	-0.8	0.6	1.1	2.1
30S ribosomal protein S21	Ribosomal proteins	*rpsU*	BN194_17050	K0N5E5	0.6	1.5	-2.7	0.2	-3.2	0.1	-0.5	0.7	2.6	6.1
30S ribosomal protein S2	Ribosomal proteins	*rpsB*	BN194_17680	K0N936	0.1	1.1	-4.9	0.0	-5.0	0.0	-2.2	0.2	-1.3	0.4
50S ribosomal protein L19	Ribosomal proteins	*rplS*	BN194_17770	K0NB12	0.1	1.1	-1.6	0.3	-1.7	0.3	-0.6	0.6	-2.3	0.2
30S ribosomal protein S16	Ribosomal proteins	*rpsP*	BN194_17810	K0N5H1	0.0	1.0	-4.7	0.0	-4.7	0.0	0.6	1.5	2.7	6.5
50S ribosomal protein L27	Ribosomal proteins	*rpmA*	BN194_18270	K0NB51	-0.1	0.9	-5.9	0.0	-5.8	0.0	-0.3	0.8	1.7	3.3
Uncharacterized protein ysxB	Ribosomal proteins	*ysxB*	BN194_18280	K0N9A9	0.0	1.0	-2.2	0.2	-2.2	0.2	-0.5	0.7	-1.8	0.3
50S ribosomal protein L21	Ribosomal proteins	*rplU*	BN194_18290	K0MW61	0.9	1.9	-0.6	0.7	-1.6	0.3	-0.8	0.6	2.2	4.7
50S ribosomal protein L20	Ribosomal proteins	*rplT*	BN194_18800	K0N5Y4	0.6	1.6	-5.6	0.0	-6.2	0.0	0.7	1.6	-1.6	0.3
50S ribosomal protein L35	Ribosomal proteins	*rpmI*	BN194_18810	K0N5P1	0.2	1.1	-5.5	0.0	-5.6	0.0	0.1	1.0	2.9	7.3
50S ribosomal protein L33	Ribosomal proteins	*rpmG*	BN194_20200	K0N697	1.8	3.4	-5.1	0.0	-6.9	0.0	-4.3	0.1	-2.2	0.2
50S ribosomal protein L7/L12	Ribosomal proteins	*rplL*	BN194_24080	K0NA98	0.8	1.7	-0.5	0.7	-1.3	0.4	-0.7	0.6	0.5	1.4
50S ribosomal protein L10	Ribosomal proteins	*rplJ*	BN194_24090	K0MXD8	-0.2	0.9	-4.3	0.1	-4.1	0.1	-0.1	0.9	1.3	2.4

50S ribosomal protein L1	Ribosomal proteins	*rplA*	BN194_24150	K0N7M7	0.1	1.0	-4.6	0.0	-4.6	0.0	-1.7	0.3	-1.7	0.
50S ribosomal protein L11	Ribosomal proteins	*rplK*	BN194_24160	K0N724	-0.3	0.8	-4.1	0.1	-3.8	0.1	-1.9	0.3	-0.7	0.
50S ribosomal protein L33	Ribosomal proteins	*rpmG2,rpmG*	BN194_24280	K0NAA5	0.5	1.4	-1.4	0.4	-1.9	0.3	-1.6	0.3	2.1	4.
30S ribosomal protein S9	Ribosomal proteins	*rpsI*	BN194_25840	K0MXR0	2.0	3.9	-5.3	0.0	-7.2	0.0	-2.1	0.2	-1.1	0.
50S ribosomal protein L13	Ribosomal proteins	*rplM*	BN194_25850	K0N828	0.1	1.1	-4.5	0.0	-4.7	0.0	-2.0	0.2	-0.8	0.
50S ribosomal protein L17	Ribosomal proteins	*rplQ*	BN194_25950	K0N841	0.4	1.3	-4.7	0.0	-5.1	0.0	-1.3	0.4	-0.8	0.
30S ribosomal protein S11	Ribosomal proteins	*rpsK*	BN194_25970	K0NCJ0	-0.1	1.0	-2.9	0.1	-2.8	0.1	-1.0	0.5	-0.9	0.
30S ribosomal protein S13	Ribosomal proteins	*rpsM*	BN194_25980	K0NAK3	0.5	1.4	-4.5	0.0	-5.0	0.0	-2.4	0.2	-1.4	0.
50S ribosomal protein L15	Ribosomal proteins	*rplO*	BN194_26030	K0NAK7	0.1	1.1	-4.7	0.0	-4.9	0.0	-0.2	0.9	1.9	3.
50S ribosomal protein L30	Ribosomal proteins	*rpmD*	BN194_26040	K0MXS6	0.1	1.1	-4.2	0.1	-4.4	0.0	-0.7	0.6	1.5	2.
30S ribosomal protein S5	Ribosomal proteins	*rpsE*	BN194_26050	K0N853	0.1	1.0	-4.7	0.0	-4.8	0.0	0.2	1.2	-0.1	0.
50S ribosomal protein L18	Ribosomal proteins	*rplR*	BN194_26060	K0N7F4	0.2	1.2	-3.5	0.1	-3.7	0.1	0.7	1.6	-0.2	0.
50S ribosomal protein L6	Ribosomal proteins	*rplF*	BN194_26070	K0NCK5	0.2	1.2	-3.4	0.1	-3.6	0.1	-1.5	0.3	-0.2	0.
30S ribosomal protein S8	Ribosomal proteins	*rpsH*	BN194_26080	K0NAL1	0.1	1.1	-5.0	0.0	-5.1	0.0	-2.4	0.2	-0.8	0.
30S ribosomal protein S14 type Z	Ribosomal proteins	*rpsZ,rpsN*	BN194_26090	K0MXS9	-0.4	0.7	-5.2	0.0	-4.8	0.0	-3.1	0.1	-2.5	0.
50S ribosomal protein L5	Ribosomal proteins	*rplE*	BN194_26100	K0N859	0.0	1.0	-5.0	0.0	-5.0	0.0	-1.4	0.4	-1.4	0.
50S ribosomal protein L24	Ribosomal proteins	*rplX*	BN194_26110	K0N7F9	0.3	1.3	-4.0	0.1	-4.3	0.0	0.8	1.7	2.8	6.
50S ribosomal protein L14	Ribosomal proteins	*rplN*	BN194_26120	K0NCL3	-0.1	0.9	-4.4	0.0	-4.3	0.1	-2.3	0.2	-1.3	0.
30S ribosomal protein S17	Ribosomal proteins	*rpsQ*	BN194_26130	K0NAL6	-0.1	0.9	-4.5	0.0	-4.3	0.0	-2.6	0.2	0.4	1.
50S ribosomal protein L29	Ribosomal proteins	*rpmC*	BN194_26140	K0MXT6	0.2	1.1	-5.5	0.0	-5.6	0.0	-0.8	0.6	0.3	1.
50S ribosomal protein L16	Ribosomal proteins	*rplP*	BN194_26150	K0N863	0.2	1.1	-4.1	0.1	-4.3	0.1	-0.1	1.0	2.3	4.
30S ribosomal protein S3	Ribosomal proteins	*rpsC*	BN194_26160	K0N7G5	-0.1	1.0	-3.5	0.1	-3.4	0.1	0.4	1.4	-2.0	0.
50S ribosomal protein L22	Ribosomal proteins	*rplV*	BN194_26170	K0NCM1	-0.1	0.9	-4.2	0.1	-4.1	0.1	-0.5	0.7	0.9	1.
30S ribosomal protein S19	Ribosomal proteins	*rpsS*	BN194_26180	K0NAM1	0.4	1.4	-5.5	0.0	-5.9	0.0	-1.2	0.5	-0.5	0.
50S ribosomal protein L2	Ribosomal proteins	*rplB*	BN194_26190	K0MXU1	-0.2	0.9	-5.3	0.0	-5.1	0.0	0.2	1.1	-1.6	0.
50S ribosomal protein L23	Ribosomal proteins	*rplW*	BN194_26200	K0N869	0.2	1.2	-3.9	0.1	-4.1	0.1	-1.1	0.5	0.0	1.
50S ribosomal protein L4	Ribosomal proteins	*rplD*	BN194_26210	K0N7H0	0.1	1.1	-4.5	0.0	-4.7	0.0	-0.3	0.8	-1.4	0.
50S ribosomal protein L3	Ribosomal proteins	*rplC*	BN194_26220	K0NCN1	0.1	1.1	-4.1	0.1	-4.2	0.1	-1.1	0.5	-1.4	0.
30S ribosomal protein S10	Ribosomal proteins	*rpsJ*	BN194_26230	K0NAM5	0.0	1.0	-4.5	0.0	-4.5	0.0	-1.2	0.4	-0.9	0.

30S ribosomal protein S7	Ribosomal proteins	*rpsG*	BN194_26280	K0NAM9	0.1	1.1	-4.8	0.0	-4.9	0.0	-2.5	0.2	-1.7	0.3
30S ribosomal protein S12	Ribosomal proteins	*rpsL*	BN194_26290	K0MXV0	0.2	1.2	-4.0	0.1	-4.3	0.1	0.2	1.2	-2.5	0.3
50S ribosomal protein L31 type B	Ribosomal proteins	*rpmE2*	BN194_26770	K0NCV4	0.2	1.2	-3.9	0.1	-4.1	0.1	-0.3	0.8	-1.3	0.4
Alanine--tRNA ligase (EC 6.1.1.7) (Alanyl-tRNA synthetase)	tRNA aminoacyl synthesis	*alaS*	BN194_08480	K0N6K2	0.3	1.2	-1.5	0.4	-1.8	0.3	0.0	1.0	-1.7	0.3
Leucine--tRNA ligase (EC 6.1.1.4) (Leucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*leuS*	BN194_09210	K0N3A9	0.9	1.9	2.3	4.8	1.3	2.5	-0.5	0.7	-2.6	0.2
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit C (Asp/Glu-ADT subunit C) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatC*	BN194_11950	K0N436	0.2	1.2	2.1	4.2	1.9	3.6	1.7	3.3	-2.6	0.2
Glutamyl-tRNA(Gln) amidotransferase subunit A (Glu-ADT subunit A) (EC 6.3.5.7)	tRNA aminoacyl synthesis	*gatA*	BN194_11960	K0N3Z6	0.0	1.0	1.9	3.7	1.9	3.8	1.4	2.7	-2.5	0.2
Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B (Asp/Glu-ADT subunit B) (EC 6.3.5.-)	tRNA aminoacyl synthesis	*gatB*	BN194_11970	K0NA01	-0.1	0.9	1.9	3.6	1.9	3.8	1.3	2.4	-2.6	0.2
Valine--tRNA ligase (EC 6.1.1.9) (Valyl-tRNA synthetase)	tRNA aminoacyl synthesis	*valS*	BN194_14510	K0N4J6	0.0	1.0	-0.8	0.6	-0.8	0.6	-0.3	0.8	-2.3	0.2
Isoleucine--tRNA ligase (EC 6.1.1.5) (Isoleucyl-tRNA synthetase)	tRNA aminoacyl synthesis	*ileS*	BN194_14810	K0N4L9	0.2	1.2	-0.4	0.8	-0.6	0.7	-0.8	0.6	-2.1	0.2
Asparagine--tRNA ligase (EC 6.1.1.22) (Asparaginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*asnS*	BN194_16760	K0N569	-0.2	0.8	0.7	1.6	1.0	1.9	-1.2	0.4	-1.8	0.3
Glycine--tRNA ligase beta subunit (EC 6.1.1.14) (Glycyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*glyS*	BN194_16950	K0N5D3	0.7	1.7	2.9	7.2	2.1	4.3	0.1	1.0	-3.0	0.1
Aspartate--tRNA ligase (EC 6.1.1.12)	tRNA aminoacyl synthesis	*aspS*	BN194_17100	K0N5F3	0.6	1.5	0.5	1.4	-0.1	0.9	0.4	1.3	-2.5	0.2
Histidine--tRNA ligase (EC 6.1.1.21) (Histidyl-tRNA synthetase)	tRNA aminoacyl synthesis	*hisS*	BN194_17110	K0N5A0	0.7	1.6	1.1	2.1	0.4	1.3	0.4	1.4	-1.1	0.5
Proline--tRNA ligase (EC 6.1.1.15) (Prolyl-tRNA synthetase)	tRNA aminoacyl synthesis	*proS*	BN194_17610	K0N5E2	0.4	1.4	1.8	3.5	1.4	2.6	-0.4	0.8	-2.4	0.2
Phenylalanine--tRNA ligase beta subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase beta subunit)	tRNA aminoacyl synthesis	*pheT*	BN194_18560	K0N5M4	0.9	1.9	1.4	2.6	0.4	1.3	0.9	1.9	-2.3	0.2
Phenylalanine--tRNA ligase alpha subunit (EC 6.1.1.20) (Phenylalanyl-tRNA synthetase alpha subunit)	tRNA aminoacyl synthesis	*pheS*	BN194_18570	K0NB64	0.8	1.8	1.2	2.3	0.4	1.3	2.1	4.2	-2.2	0.2
Threonine--tRNA ligase (EC 6.1.1.3) (Threonyl-tRNA synthetase)	tRNA aminoacyl synthesis	*thrS*	BN194_18860	K0N5P5	-0.4	0.8	-5.2	0.0	-4.8	0.0	0.8	1.7	-0.6	0.0
Protein hit	tRNA aminoacyl synthesis	*hit*	BN194_19040	K0MWA8	0.6	1.6	2.6	5.9	1.9	3.8	-0.5	0.7	-1.1	0.5
Arginine--tRNA ligase (EC 6.1.1.19) (Arginyl-tRNA synthetase)	tRNA aminoacyl synthesis	*argS*	BN194_19120	K0NB86	-1.0	0.5	-4.0	0.1	-3.0	0.1	-0.9	0.5	-1.4	0.4
Serine--tRNA ligase (EC 6.1.1.11) (Seryl-tRNA synthetase) (Seryl-tRNA(Ser/Sec) synthetase)	tRNA aminoacyl synthesis	*serS*	BN194_20080	K0N9N4	0.0	1.0	2.2	4.5	2.1	4.4	-0.6	0.6	-2.6	0.2
Cysteine--tRNA ligase (EC 6.1.1.16) (Cysteinyl-tRNA synthetase)	tRNA aminoacyl synthesis	*cysS*	BN194_24430	K0NAB2	0.0	1.0	1.1	2.1	1.1	2.2	-1.5	0.4	-5.4	0.0
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	*gltX*	BN194_24470	K0NC38	-0.1	0.9	-2.6	0.2	-2.5	0.2	1.0	1.9	1.7	3.3

Lysine--tRNA ligase (EC 6.1.1.6) (Lysyl-tRNA synthetase)	tRNA aminoacyl synthesis	*lysS*	BN194_26380	K0NAN7	-0.4	0.8	-2.0	0.3	-1.6	0.3	-1.2	0.4	0.9	1.9
Ribosomal RNA small subunit methyltransferase B (EC 2.1.1.-)		*rsmB*	BN194_18040	K0MW45	0.3	1.2	-1.9	0.3	-2.3	0.2	1.0	2.0	-2.1	0.2
Tyrosine--tRNA ligase (EC 6.1.1.1)		*tyrS*	BN194_21510	K0N6A9	0.0	1.0	-1.8	0.3	-1.8	0.3	0.5	1.4	-1.8	0.3
Methionine--tRNA ligase (EC 6.1.1.10)	tRNA aminoacyl synthesis	*metG*	BN194_27130	K0NAU5	0.0	1.0	-1.1	0.5	-1.1	0.5	0.0	1.0	-0.6	0.6
Tryptophan--tRNA ligase (EC 6.1.1.2)	tRNA aminoacyl synthesis	*trpS*	BN194_27360	K0N7S4	0.1	1.1	0.4	1.3	0.3	1.2	0.4	1.3	-2.5	0.2
Translation initiation factor IF-2	Protein translation (initiation)	*infB*	BN194_17550	K0N5K7	0.0	1.0	-4.8	0.0	-4.9	0.0	-3.1	0.1	-0.6	0.6
Methionyl-tRNA formyltransferase (EC 2.1.2.9)	Protein translation (initiation)	*fmt*	BN194_18060	K0N5J2	-1.0	0.5	-0.3	0.8	0.6	1.6	-0.3	0.8	-1.9	0.3
Translation initiation factor IF-3	Protein translation (initiation)	*infC*	BN194_18820	K0NB73	0.5	1.4	-6.1	0.0	-6.5	0.0	-1.1	0.5	1.8	3.5
Translation initiation factor IF-1	Protein translation (initiation)	*infA*	BN194_26000	K0N847	-0.2	0.9	-2.8	0.1	-2.5	0.2	-0.6	0.7	1.3	2.5
GTP-binding protein TypA/BipA homolog	Protein translation (elongation)	*typA*	BN194_15150	K0N4W9	0.5	1.4	-5.2	0.0	-5.6	0.0	0.4	1.3	-1.3	0.4
Elongation factor Tu (EF-Tu)	Protein translation (elongation)	*tuf*	BN194_15310	K0N4R1	-0.3	0.8	-0.7	0.6	-0.4	0.8	-1.0	0.5	-0.9	0.5
Elongation factor 4 (EF-4) (EC 3.6.5.n1) (Ribosomal back-translocase LepA)	Protein translation (elongation)	*lepA*	BN194_17440	K0MVU5	-0.6	0.7	-5.4	0.0	-4.8	0.0	-0.4	0.7	-4.0	0.1
Elongation factor Ts (EF-Ts)	Protein translation (elongation)	*tsf*	BN194_17670	K0NB01	-0.6	0.7	0.4	1.3	0.9	1.9	-2.5	0.2	-1.3	0.4
Elongation factor P	Protein translation (elongation)	*efp*	BN194_18240	K0MW57	-0.6	0.7	-1.0	0.5	-0.4	0.8	-0.6	0.7	1.1	2.1
Elongation factor P	Protein translation (elongation)	*efp_2*	BN194_22050	K0N712	-2.0	0.2	-5.0	0.0	-3.0	0.1	-2.5	0.2	-1.3	0.4
Elongation factor G (EF-G)	Protein translation (elongation)	*fusA*	BN194_26270	K0NCN8	-0.6	0.7	-3.0	0.1	-2.4	0.2	-1.0	0.5	-1.1	0.5
Ribosome-binding ATPase YchF	Protein translation (peptide release)	*engD,ychF*	BN194_02070	K0N7F7	-0.2	0.9	-0.8	0.6	-0.7	0.6	-0.2	0.9	-1.3	0.4
Peptide chain release factor 2 (RF-2)	Protein translation (peptide release)	*prfB*	BN194_10180	K0N6W9	0.1	1.1	-3.9	0.1	-4.1	0.1	-1.8	0.3	-1.8	0.3
Methionine aminopeptidase (MAP) (MetAP) (EC 3.4.11.18) (Peptidase M)	Protein translation (peptide release)	*map*	BN194_12230	K0N7E0	1.7	3.2	-4.5	0.0	-6.2	0.0	1.9	3.8	-1.9	0.3
Peptide chain release factor 1 (RF-1)	Protein translation (peptide release)	*prfA*	BN194_13510	K0N4C6	-0.5	0.7	-4.8	0.0	-4.3	0.0	-2.1	0.2	-1.4	0.4
Peptide deformylase (PDF) (EC 3.5.1.88) (Polypeptide deformylase)	Protein translation (peptide release)	*def*	BN194_15060	K0N4N6	-0.1	0.9	-0.7	0.6	-0.5	0.7	-1.0	0.5	-2.3	0.2
Ribosome-recycling factor (RRF) (Ribosome-releasing factor)	Protein translation (peptide release)	*frr*	BN194_17650	K0N5M3	-1.3	0.4	-3.9	0.1	-2.6	0.2	-0.5	0.7	-1.0	0.5
Peptide chain release factor 3 (RF-3)	Protein translation (peptide release)	*prfC*	BN194_19480	K0N9I7	0.2	1.1	-4.4	0.0	-4.6	0.0	0.1	1.1	-2.6	0.2

41 kDa protein	*repA*	BN194_P0550	K0NBI6	-1.1	0.5	-1.9	0.3	-0.8	0.6	-3.2	0.1	-0.3	0.8
Predicted ORF		BN194_P0560	K0MZ29	-1.2	0.4	-1.4	0.4	-0.2	0.8	-2.0	0.2	1.3	2.5
NAD kinase (EC 2.7.1.23) (ATP-dependent NAD kinase)	*nadK*	ppnK	K0N6U5	0.7	1.7	-0.4	0.7	-1.2	0.5	0.0	1.0	2.4	5.4
Microcin C7 self-immunity protein mccF		BN194_01360	K0N1K5	-0.3	0.8	2.5	5.7	2.9	7.3	0.4	1.3	-4.6	0.6
DNA topoisomerase 4 subunit A (EC 5.99.1.-)	*parC*	BN194_16070	K0NAP8	-0.7	0.6	-3.2	0.1	-2.5	0.2	-2.8	0.1	-0.1	0.9
Coenzyme A biosynthesis bifunctional protein CoaBC (EC 4.1.1.36) (EC 6.3.2.5)	*coaBC*	BN194_18090	K0MW49	-4.0	0.1	-3.8	0.1	0.2	1.2	-2.9	0.1	1.2	2.3
Uridine kinase (EC 2.7.1.48)	*udk*	BN194_18540	K0MW76	-1.4	0.4	-1.7	0.3	-0.2	0.9	-1.3	0.4	0.8	1.8
LPXTG-motif cell wall anchor domain protein		BN194_26300	K0N883	-0.2	0.9	1.4	2.6	1.6	3.0	0.6	1.5	-1.3	0.4
Uncharacterized protein			K0N2Q1;K0MXJ1	2.9	7.6	4.1	16.7	1.1	2.2	1.9	3.7	-2.1	0.2
Glucose-1-phosphate thymidylyltransferase	*rmlA*		K0N699;K0MWW4	-0.6	0.7	1.7	3.3	2.3	4.9	0.6	1.5	-2.1	0.2
Spore coat polysaccharide biosynthesis protein spsK			K0N9X8;K0N6D6	-0.1	0.9	2.1	4.4	2.3	4.8	0.1	1.1	-2.5	0.2

Annexure 09: Proteins highly enriched in LiCl (not regulated, FC LICL 4.5 VS CFE pH 4.5 <2), FC values in the corresponding CFEs are provided to allow direct comparision of regulation in CFEs.

Protein names	Functional Class	Class Code	Function	*Gene*	names	Entry	FC CFE 4.5 Vs CFE 6.5	FC UC pH Vs CFE 6.5	FC UC pH Vs CFE 4.5	FC LiCL pH4.5 Vs LiCL pH 6.5	FC LiCL pH4.5 Vs CFE pH4.5	FC LiCL pH6.5 Vs CFE pH 6.5	FASTA headers
D-alanyl-D-alanine carboxypeptidase dacA (EC 3.4.16.4)	Cell wall biogenesis	1.1	late peptidoglycan biosynthesis	*dacA*	BN194_02140	K0MS53	0.58	0.71	1.22	1.33	2.07	0.91	>tr|K0MS53|K0MS53_LACCA DacA protein OS=Lactobacillus casei W56 GN=dacA PE=3 SV=1
Uncharacterized protein	Cell wall biogenesis	1.1	teichoic acid biosynthesis		BN194_02360	K0N1U1	1.27	0.37	0.30	1.60	15.09	11.98	>tr|K0N1U1|K0N1U1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02360 PE=4 SV=1
UTP--glucose-1-phosphate uridylyltransferase	Cell wall biogenesis	1.1	teichoic acid decoration?, exopolysaccharide biosynthesis?	*cap4C*	BN194_12280	K0N7E3	0.50	0.05	0.09	1.01	3.86	1.92	>tr|K0N7E3|K0N7E3_LACCA UTP--glucose-1-phosphate

(EC 2.7.7.9) (UDP-glucose pyrophosphorylase)													uridylyltransferase OS=Lactobacillus casei W56 GN=cap4C PE=3 SV=1
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227) (Undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase)	Cell wall biogenesis	1.1	late peptidoglycan biosynthesis	*murG*	BN194_14730	K0N819	1.39	0.42	0.30	0.33	2.58	10.79	>tr|K0N819|K0N819_LACCA UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase OS=Lactobacillus casei W56 GN=murG PE=3 SV=1
Penicillin-binding protein 1F	Cell wall biogenesis	1.1	peptidoglycan polymerization	*pbpF*	BN194_08770	K0N987	0.61	0.42	0.70	1.79	8.53	2.90	>tr|K0N987|K0N987_LACCA PbpF protein OS=Lactobacillus casei W56 GN=pbpF PE=4 SV=1
Sortase	Cell wall biogenesis	1.1	cell wall protein sorting/binding		BN194_22780	K0NA48	1.46	0.95	0.65	0.59	5.01	12.38	>tr|K0NA48|K0NA48_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_22780 PE=4 SV=1
dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)	Cell wall biogenesis	1.1	exopolysaccharide biosynthesis	*rmlB_2*	BN194_21770	K0NBN4	0.53	1.09	2.07	1.35	8.53	3.33	>tr|K0NBN4|K0NBN4_LACCA dTDP-glucose 4,6-dehydratase OS=Lactobacillus casei W56 GN=rmlB_2 PE=3 SV=1
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10) (D-alanyl-D-alanine-adding enzyme)	Cell wall biogenesis	1.1	late peptidoglycan biosynthesis	*murF*	BN194_26720	K0NCU5	0.62	0.71	1.16	0.72	4.67	4.01	>tr|K0NCU5|K0NCU5_LACCA UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase OS=Lactobacillus casei W56 GN=murF PE=3 SV=1
Exopolyphosphatase	Membrane bioenergetics	1.4	polyphopshate conversion to/from ATP		BN194_27280	K0NAV4	0.35	0.18	0.53	1.67	5.97	1.24	>tr|K0NAV4|K0NAV4_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_27280 PE=4 SV=1
Polyphosphate kinase (EC 2.7.4.1)	Membrane bioenergetics	1.4	polyphopshate conversion to/from ATP	*ppk*	BN194_27270	K0ND10	0.43	0.06	0.14	0.53	2.79	2.26	>tr|K0ND10|K0ND10_LACCA Polyphosphate kinase

(ATP-polyphosphate phosphotransferase) (Polyphosphoric acid kinase)													OS=Lactobacillus casei W56 GN=ppk PE=3 SV=1
Protein translocase subunit SecY	Protein export	1.6	protein secretion: Sec system (translocon)	*secY*	BN194_26020	K0NCJ6	1.81	1.31	0.72	1.84	2.22	2.18	>tr|K0NCJ6|K0NCJ6_LACCA Protein translocase subunit SecY OS=Lactobacillus casei W56 GN=secY PE=3 SV=1
Segregation and condensation protein B	Cytokinesis	1.7	cell division (chromosomal segegration)	*scpB*	BN194_15640	K0MVE6	0.93	0.24	0.26	0.35	2.03	5.38	>tr|K0MVE6|K0MVE6_LACCA Segregation and condensation protein B OS=Lactobacillus casei W56 GN=scpB PE=3 SV=1
Cell division protein FtsX	Cytokinesis	1.7	cell division; divisome complex	*ftsX*	BN194_10200	K0N3G0	0.64	0.59	0.92	1.68	4.13	1.58	>tr|K0N3G0|K0N3G0_LACCA Cell division protein FtsX OS=Lactobacillus casei W56 GN=ftsX PE=3 SV=1
Cell wall surface anchor family protein	Cell surface proteins/internalins	1.8	unknown function		BN194_05290	K0MSU3	0.48	3.46	7.25	1.78	11.04	2.97	>tr|K0MSU3|K0MSU3_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_05290 PE=4 SV=1
ABC transporter, ATP-binding protein	Cell surface proteins/internalins	1.8	unknown function		BN194_15700	K0N514	0.43	0.48	1.12	0.83	9.18	4.75	>tr|K0N514|K0N514_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_15700 PE=4 SV=1
Aspartate racemase (EC 5.1.1.13)	Amino acid-related metabolism	2.2	metabolism of aspartate		BN194_02170	K0N7H2	0.29	0.11	0.37	1.06	2.58	0.70	>tr|K0N7H2|K0N7H2_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02170 PE=4 SV=1
Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)	Nucleic acid/nucleotide metabolism	2.3	DNA synthesis (keeps dUTP levels low)	*dut*	BN194_24640	K0MXG3	0.44	0.08	0.17	1.22	44.10	16.09	>tr|K0MXG3|K0MXG3_LACCA Dut protein OS=Lactobacillus casei W56 GN=dut PE=4 SV=1
Nucleoside diphosphate kinase (EC 2.7.4.6)	Nucleic acid/nucleotide metabolism	2.3	(deoxy)nucleotide biosynthesis except ATP	*ndk*	BN194_08160	K0N340	0.09	0.02	0.24	0.32	2.39	0.70	>tr|K0N340|K0N340_LACCA Ndk protein OS=Lactobacillus casei W56 GN=ndk PE=3 SV=1
Orotidine 5'-phosphate decarboxylase (EC	Nucleic acid/nucleotide metabolism	2.3	UMP/uridine/uracil biosynthesis	*pyrF*	BN194_16430	K0N8M7	0.30	0.06	0.21	0.88	9.31	3.14	>tr|K0N8M7|K0N8M7_LACCA Orotidine 5-phosphate decarboxylase

4.1.1.23) (OMP decarboxylase)													OS=Lactobacillus casei W56 GN=pyrF PE=3 SV=1
Bifunctional protein BirA (EC 6.3.4.15)	Lipid-related metabolism	2.4	fatty acid biosynthesis	*birA*	BN194_08790	K0MTP3	0.56	1.71	3.04	0.95	2.22	1.31	>tr|K0MTP3|K0MTP3_LACCA BirA protein OS=Lactobacillus casei W56 GN=birA PE=4 SV=1
Isoprenyl transferase (EC 2.5.1.-)	Lipid-related metabolism	2.4	isoprenoid biosynthesis; wall lipid carrier	*uppS*	BN194_17640	K0MVX1	0.85	0.29	0.34	0.84	10.55	10.62	>tr|K0MVX1|K0MVX1_LACCA Isoprenyl transferase OS=Lactobacillus casei W56 GN=uppS PE=3 SV=1
3-oxoacyl-[acyl-carrier-protein] reductase FabG (EC 1.1.1.100)	Lipid-related metabolism	2.4	fatty acid biosynthesis	*fabG*	BN194_22560	K0N6N3	0.46	0.06	0.14	1.00	6.69	3.12	>tr|K0N6N3|K0N6N3_LACCA FabG protein OS=Lactobacillus casei W56 GN=fabG PE=4 SV=1
3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100)	Lipid-related metabolism	2.4	fatty acid biosynthesis	*bkr4*	BN194_22550	K0N799	0.50	0.16	0.31	1.51	15.91	5.25	>tr|K0N799|K0N799_LACCA Bkr4 protein OS=Lactobacillus casei W56 GN=bkr4 PE=4 SV=1
Diphosphomevalonate decarboxylase (EC 4.1.1.33)	Lipid-related metabolism	2.4	mevalonate pathway for isoprenoid backbones	*mvd1*	BN194_16830	K0N8S2	0.30	0.08	0.29	0.89	5.75	1.92	>tr|K0N8S2|K0N8S2_LACCA Mvd1 protein OS=Lactobacillus casei W56 GN=mvd1 PE=4 SV=1
Acyl carrier protein (ACP)	Lipid-related metabolism	2.4	fatty acid biosynthesis	*acpP*	BN194_17930	K0N988	3.07	24.37	7.93	0.35	2.40	21.19	>tr|K0N988|K0N988_LACCA Acyl carrier protein OS=Lactobacillus casei W56 GN=acpP PE=3 SV=1
3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ (EC 4.2.1.59)	Lipid-related metabolism	2.4	fatty acid biosynthesis	*fabZ*	BN194_22520	K0NBS8	0.37	0.06	0.16	1.65	12.06	2.70	>tr|K0NBS8|K0NBS8_LACCA 3-hydroxyacyl-[acyl-carrier-protein] dehydratase FabZ OS=Lactobacillus casei W56 GN=fabZ PE=4 SV=1
(3R)-hydroxymyristoyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.-)	Lipid-related metabolism	2.4	fatty acid biosynthesis	*fabZ_2*	BN194_22620	K0NBT3	0.39	0.03	0.07	1.05	2.05	0.76	>tr|K0NBT3|K0NBT3_LACCA FabZ_2 protein OS=Lactobacillus casei W56 GN=fabZ_2 PE=4 SV=1
Phosphopantetheine adenylyltransferase (EC 2.7.7.3) (Dephospho-CoA pyrophosphorylase) (Pantetheine-phosphate	Cofactor-related metabolism	2.5	pantothenate/CoA biosynthesis	*coaD*	BN194_15200	K0N4X3	0.03	0.02	0.76	1.35	3.06	0.07	>tr|K0N4X3|K0N4X3_LACCA Phosphopantetheine adenylyltransferase OS=Lactobacillus casei W56 GN=coaD PE=3 SV=1

adenylyltransferase)													
DNA-binding protein HU	DNA replication-related	3.1	DNA topology change	*hup*	BN194_15740	K0MVF4	1.58	0.11	0.07	1.31	3.78	4.55	>tr|K0MVF4|K0MVF4_LACCA Hup protein OS=Lactobacillus casei W56 GN=hup PE=3 SV=1
DNA topoisomerase 1 (EC 5.99.1.2) (DNA topoisomerase I)	DNA replication-related	3.1	DNA topological change	*topA*	BN194_15970	K0NAP0	0.12	0.02	0.13	0.31	10.80	4.31	>tr|K0NAP0|K0NAP0_LACCA DNA topoisomerase 1 OS=Lactobacillus casei W56 GN=topA PE=3 SV=1
Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	DNA repair/recombination	3.2	DNA repair (base excision;mismatch; homologous recombination)	*recJ*	BN194_17390	K0MVT7	0.62	0.26	0.42	0.22	2.71	7.58	>tr|K0MVT7|K0MVT7_LACCA RecJ protein OS=Lactobacillus casei W56 GN=recJ PE=4 SV=1
Ribosome maturation factor RimP	tRNA/Ribosome assembly/processing	3.6	ribosome processing (SSU)	*rimP*	BN194_17590	K0MVW3	1.98	0.34	0.17	0.44	3.17	14.15	>tr|K0MVW3|K0MVW3_LACCA Ribosome maturation factor RimP OS=Lactobacillus casei W56 GN=rimP PE=3 SV=1
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	3.6	ribosomal RNA processing (LSU)	*rluB*	BN194_15650	K0N509	1.15	0.65	0.57	0.70	35.31	57.68	>tr|K0N509|K0N509_LACCA Pseudouridine synthase OS=Lactobacillus casei W56 GN=rluB PE=3 SV=1
Uncharacterized tRNA/rRNA methyltransferase YsgA (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	3.6	ribosomal RNA processing (LSU)	*ysgA*	BN194_18610	K0N5M8	0.82	0.39	0.48	1.87	39.11	17.09	>tr|K0N5M8|K0N5M8_LACCA YsgA protein OS=Lactobacillus casei W56 GN=ysgA PE=4 SV=1
tRNA (guanine-N(7)-)-methyltransferase (EC 2.1.1.33) (tRNA (guanine(46)-N(7))-methyltransferase) (tRNA(m7G46)-methyltransferase)	tRNA/Ribosome assembly/processing	3.6	tRNA modification	*trmB*	BN194_19000	K0N606	0.13	0.06	0.50	1.04	8.92	1.09	>tr|K0N606|K0N606_LACCA tRNA (guanine-N(7)-)-methyltransferase OS=Lactobacillus casei W56 GN=trmB PE=3 SV=1
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	3.6	ribosomal RNA processing (SSU)	*ytzG*	BN194_09230	K0N6P7	1.05	0.33	0.31	0.84	9.95	12.49	>tr|K0N6P7|K0N6P7_LACCA Pseudouridine synthase OS=Lactobacillus casei W56 GN=ytzG PE=3 SV=1
Uncharacterized protein yabR	tRNA/Ribosome assembly/processing	3.6	unknown ribosome-associated function	*yabR*	BN194_26500	K0N8A7	2.08	0.11	0.05	0.79	12.67	33.60	>tr|K0N8A7|K0N8A7_LACCA YabR protein OS=Lactobacillus casei W56 GN=yabR PE=4 SV=1

Putative RNA methyltransferase YpsC (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	3.6	ribosomal RNA acetylation?	*ypsC*	BN194_16670	K0NAU0	1.88	0.11	0.06	1.85	2.08	2.12	>tr|K0NAU0|K0NAU0_LACCA YpsC protein OS=Lactobacillus casei W56 GN=ypsC PE=4 SV=1
Putative TrmH family tRNA/rRNA methyltransferase YacO (EC 2.1.1.-)	tRNA/Ribosome assembly/processing	3.6	ribosomal RNA processing (LSU)	*yacO*	BN194_24420	K0NC34	0.82	0.03	0.04	1.09	5.02	3.78	>tr|K0NC34|K0NC34_LACCA YacO protein OS=Lactobacillus casei W56 GN=yacO PE=4 SV=1
Uncharacterized protein yabO	tRNA/Ribosome assembly/processing	3.6	ribosome recycling (LSU); stress response?	*yabO*	BN194_26520	K0NCR8	0.43	0.09	0.22	0.31	24.73	34.13	>tr|K0NCR8|K0NCR8_LACCA YabO protein OS=Lactobacillus casei W56 GN=yabO PE=4 SV=1
Ribonuclease P protein component (RNase P protein) (RNaseP protein) (EC 3.1.26.5) (Protein C5)	tRNA/Ribosome assembly/processing	3.6	tRNA and 4.5S processing	*rnpA*	BN194_30620	K0NDS2	4.84	0.24	0.05	0.96	6.79	34.20	>tr|K0NDS2|K0NDS2_LACCA Ribonuclease P protein component OS=Lactobacillus casei W56 GN=rnpA PE=3 SV=1
SsrA-binding protein (Small protein B)	Posttranslational modification	3.8	defective protein degradation (tagging)	*smpB*	BN194_11110	K0N3S3	1.62	0.44	0.27	0.24	3.76	25.59	>tr|K0N3S3|K0N3S3_LACCA SsrA-binding protein OS=Lactobacillus casei W56 GN=smpB PE=3 SV=1
33 kDa chaperonin (Heat shock protein 33 homolog)	Protein folding/turnover	3.9	protein folding; stress response	*hslO*	BN194_26400	K0N893	0.54	0.07	0.13	0.37	2.51	3.72	>tr|K0N893|K0N893_LACCA 33 kDa chaperonin OS=Lactobacillus casei W56 GN=hslO PE=3 SV=1
Serine protease Do-like HtrA (EC 3.4.21.107)	Protein folding/turnover	3.9	recycling defective proteins; protein folding; stress response	*htrA*	BN194_29460	K0N8D9	0.24	0.37	1.58	0.13	5.55	9.68	>tr|K0N8D9|K0N8D9_LACCA HtrA protein OS=Lactobacillus casei W56 GN=htrA PE=4 SV=1
Carboxy-terminal processing protease CtpA (EC 3.4.21.102)	Protein folding/turnover	3.9	protein activation; recycling defective proteins	*ctpA*	BN194_15880	K0N8G1	2.12	0.85	0.40	0.82	2.87	7.46	>tr|K0N8G1|K0N8G1_LACCA CtpA protein OS=Lactobacillus casei W56 GN=ctpA PE=3 SV=1
Uncharacterized protein	Prophage genome	4.3	phage associated protein (addiction module?)		BN194_09330	K0N6Q4	0.80	0.15	0.18	1.47	5.16	2.80	>tr|K0N6Q4|K0N6Q4_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_09330 PE=4 SV=1
Uncharacterized protein yaaA	General prediction only	5	unknown role (DNA replication and/or repair?)	*yaaA*	BN194_00040	K0MRL5	0.97	0.92	0.95	0.60	27.39	44.33	>tr|K0MRL5|K0MRL5_LACCA YaaA protein OS=Lactobacillus casei W56 GN=yaaA PE=4 SV=1

Putative RNA-binding protein ylmH	General prediction only	5	unknown function (cell division-related?)	*ylmH*	BN194_14790	K0MV84	0.39	0.15	0.40	0.47	4.39	3.58	>tr|K0MV84|K0MV84_LACCA YlmH protein OS=Lactobacillus casei W56 GN=ylmH PE=4 SV=1
Uncharacterized oxidoreductase YcsN (EC 1.-.-.-)	General prediction only	5	unknown function	*ycsN*	BN194_27290	K0MY45	0.44	0.10	0.22	0.52	6.15	5.22	>tr|K0MY45|K0MY45_LACCA YcsN protein OS=Lactobacillus casei W56 GN=ycsN PE=4 SV=1
UPF0337 protein lp_1708	General prediction only	5	stress response (phosphate starvation)?		BN194_05810	K0N2J8	0.06	0.90	15.52	0.10	5.27	3.03	>tr|K0N2J8|K0N2J8_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_05810 PE=4 SV=1
Acetyltransferase	General prediction only	5	unknown function		BN194_08200	K0N2Z8	0.44	2.27	5.11	0.71	2.08	1.31	>tr|K0N2Z8|K0N2Z8_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_08200 PE=4 SV=1
Uncharacterized protein yitL	General prediction only	5	unknown function	*yitL*	BN194_15600	K0N505	0.95	1.16	1.23	1.51	167.10	104.98	>tr|K0N505|K0N505_LACCA YitL protein OS=Lactobacillus casei W56 GN=yitL PE=4 SV=1
Putative nitroreductase HBN1 (EC 1.-.-.-)	General prediction only	5	unknown function	*HBN1*	BN194_16550	K0N597	0.56	5.34	9.56	0.31	2.41	4.37	>tr|K0N597|K0N597_LACCA HBN1 protein OS=Lactobacillus casei W56 GN=HBN1 PE=4 SV=1
UPF0337 protein yhjA	General prediction only	5	stress response (phosphate starvation)?	*yhjA*	BN194_24800	K0N7S1	0.23	75.09	326.62	1.27	12.65	2.30	>tr|K0N7S1|K0N7S1_LACCA YhjA protein OS=Lactobacillus casei W56 GN=yhjA PE=4 SV=1
Queuosine transporter QueT	General prediction only	5	unknown function	*queT*	BN194_21930	K0NA07	0.79	1.20	1.51	1.00	4.55	3.60	>tr|K0NA07|K0NA07_LACCA QueT protein OS=Lactobacillus casei W56 GN=queT PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_01790	K0MS25	0.34	0.31	0.93	1.28	7.24	1.91	>tr|K0MS25|K0MS25_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_01790 PE=4 SV=1
Uncharacterized protein yeaO	Unknown/uncharacterized	6	unknown function	*yeaO*	BN194_08040	K0MTJ2	6.65	0.44	0.07	1.80	4.12	15.24	>tr|K0MTJ2|K0MTJ2_LACCA YeaO protein OS=Lactobacillus casei W56 GN=yeaO PE=4 SV=1
UPF0154 protein BN194_17740	Unknown/uncharacterized	6	unknown function		BN194_17740	K0MVY5	1.50	0.85	0.57	1.81	2.21	1.83	>tr|K0MVY5|K0MVY5_LACCA UPF0154 protein

													BN194_17740 OS=Lactobacillus casei W56 GN=BN194_17740 PE=3 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_23740	K0MXC2	0.50	0.39	0.78	0.66	3.65	2.76	>tr|K0MXC2|K0MXC2_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_23740 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_01760	K0N1N3	0.01	0.01	0.73	0.11	3.34	0.32	>tr|K0N1N3|K0N1N3_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_01760 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_02900	K0N1P1	1.21	0.11	0.10	1.38	10.07	8.84	>tr|K0N1P1|K0N1P1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02900 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_05550	K0N257	0.59	0.23	0.40	1.07	44.76	24.73	>tr|K0N257|K0N257_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_05550 PE=4 SV=1
UPF0297 protein BN194_08510	Unknown/uncharacterized	6	unknown function		BN194_08510	K0N358	0.50	0.07	0.15	1.67	5.23	1.57	>tr|K0N358|K0N358_LACCA UPF0297 protein BN194_08510 OS=Lactobacillus casei W56 GN=BN194_08510 PE=3 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_16650	K0N5A4	1.21	0.51	0.42	0.10	4.38	51.93	>tr|K0N5A4|K0N5A4_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_16650 PE=4 SV=1
Protein dedA	Unknown/uncharacterized	6	unknown function	*dedA*	BN194_08930	K0N6M9	0.33	0.10	0.30	0.57	2.17	1.26	>tr|K0N6M9|K0N6M9_LACCA DedA protein OS=Lactobacillus casei W56 GN=dedA PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_24860	K0N764	0.56	0.02	0.03	0.40	8.90	12.48	>tr|K0N764|K0N764_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_24860 PE=4 SV=1

CBS domain-containing protein	Unknown/uncharacterized	6	unknown function		BN194_26610	K0N7J7	4.24	0.38	0.09	1.94	2.04	4.46	>tr|K0N7J7|K0N7J7_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_26610 PE=4 SV=1
Protein veg	Unknown/uncharacterized	6	unknown function	*veG*	BN194_27010	K0N7N4	2.58	0.61	0.24	0.92	2.16	6.05	>tr|K0N7N4|K0N7N4_LACCA Veg protein OS=Lactobacillus casei W56 GN=veg PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_13680	K0N7T4	1.12	1.27	1.14	0.61	4.74	8.70	>tr|K0N7T4|K0N7T4_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_13680 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_08020	K0N947	0.41	0.24	0.59	1.72	4.00	0.96	>tr|K0N947|K0N947_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_08020 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_21380	K0N9Y1	2.20	0.53	0.24	1.07	13.32	27.29	>tr|K0N9Y1|K0N9Y1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_21380 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_11770	K0N9Y6	1.18	0.30	0.26	1.05	2.54	2.85	>tr|K0N9Y6|K0N9Y6_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_11770 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_23630	K0NA78	0.44	0.36	0.84	0.79	73.16	40.47	>tr|K0NA78|K0NA78_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_23630 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_24780	K0NAC8	0.60	0.13	0.22	0.73	2.21	1.81	>tr|K0NAC8|K0NAC8_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_24780 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	uncharacterised protein		BN194_15370	K0NAJ2	1.77	11.63	6.56	0.39	10.06	45.47	>tr|K0NAJ2|K0NAJ2_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_15370 PE=4 SV=1

UPF0346 protein BN194_15870	Unknown/uncharacterized	6	unknown function		BN194_15870	K0NAN2	0.15	4.10	26.78	0.53	4.98	1.44	>tr|K0NAN2|K0NAN2_LACCA UPF0346 protein BN194_15870 OS=Lactobacillus casei W56 GN=BN194_15870 PE=3 SV=1
Uncharacterized protein M6_Spy0233	Unknown/uncharacterized	6	unknown function		BN194_22970	K0NBV1	1.01	2.79	2.78	1.85	2.06	1.12	>tr|K0NBV1|K0NBV1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_22970 PE=4 SV=1
PTS system beta-glucoside-specific EIIBCA component (EC 2.7.1.-) (EC 2.7.1.69)	Phosphotransferase systems	1.2.1	beta-glucoside uptake	bglP	BN194_06940	K0MT60	1.19	0.40	0.34	1.27	8.69	8.17	>tr|K0MT60|K0MT60_LACCA BglP protein OS=Lactobacillus casei W56 GN=bglP PE=4 SV=1
Sorbose-specific phosphotransferase enzyme IIB component (EC 2.7.1.69)	Phosphotransferase systems	1.2.1	sugar uptake	sorB_2	BN194_29180	K0NB63	0.31	0.71	2.30	0.54	5.36	3.09	>tr|K0NB63|K0NB63_LACCA SorB_2 protein OS=Lactobacillus casei W56 GN=sorB_2 PE=4 SV=1
Oligopeptide-binding protein oppA	ABC-type transporter systems	1.2.2	oligopeptide uptake	*oppA_2*	BN194_20640	K0MWL6	0.03	0.79	24.78	0.31	7.09	0.73	>tr|K0MWL6|K0MWL6_LACCA OppA_2 protein OS=Lactobacillus casei W56 GN=oppA_2 PE=4 SV=1
ABC transporter substrate-binding protein	ABC-type transporter systems	1.2.2	unknown transport		BN194_07700	K0N2V5	0.00	0.00	2.53	0.02	35.03	1.73	>tr|K0N2V5|K0N2V5_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07700 PE=4 SV=1
ABC transporter substrate-binding protein	ABC-type transporter systems	1.2.2	unknown transport		BN194_07710	K0N2Z3	0.05	0.65	11.92	0.05	2.77	3.25	>tr|K0N2Z3|K0N2Z3_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07710 PE=4 SV=1
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	1.2.2	polar amino acid uptake	*glnQ*	BN194_14610	K0N4K4	0.31	0.43	1.39	0.96	22.75	7.29	>tr|K0N4K4|K0N4K4_LACCA GlnQ protein OS=Lactobacillus casei W56 GN=glnQ PE=3 SV=1
Manganese ABC transporter substrate-binding lipoprotein	ABC-type transporter systems	1.2.2	Mn/Zn ion uptake	*fimA*	BN194_25450	K0N7Y2	0.03	0.03	0.90	0.07	3.35	1.46	>tr|K0N7Y2|K0N7Y2_LACCA FimA protein OS=Lactobacillus casei W56 GN=fimA PE=3 SV=1
Glutamine-binding periplasmic protein	ABC-type transporter systems	1.2.2	polar amino acid uptake	*glnH_2*	BN194_29910	K0N8I1	0.49	0.58	1.18	1.08	2.71	1.23	>tr|K0N8I1|K0N8I1_LACCA GlnH_2 protein

													OS=Lactobacillus casei W56 GN=glnH_2 PE=4 SV=1
Glutamine transport ATP-binding protein GlnQ	ABC-type transporter systems	1.2.2	polar amino acid uptake	*glnQ_4*	BN194_29900	K0N971	0.62	0.49	0.79	0.61	2.08	2.11	>tr|K0N971|K0N971_LACCA GlnQ_4 protein OS=Lactobacillus casei W56 GN=glnQ_4 PE=3 SV=1
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	1.2.2	oligopeptide uptake	*oppB_2*	BN194_20630	K0N9S5	0.44	0.20	0.44	0.20	2.40	5.16	>tr|K0N9S5|K0N9S5_LACCA OppB_2 protein OS=Lactobacillus casei W56 GN=oppB_2 PE=3 SV=1
Uncharacterized amino acid permease YfnA	Other transporter proteins	1.2.3	amino acid uptake	*yfnA*	BN194_06960	K0N2T0	0.56	0.62	1.11	0.88	3.03	1.93	>tr|K0N2T0|K0N2T0_LACCA YfnA protein OS=Lactobacillus casei W56 GN=yfnA PE=4 SV=1
Uncharacterized MscS family protein YkuT	Other transporter proteins	1.2.3	osmoregulation	*ykuT*	BN194_08700	K0N322	1.04	0.99	0.95	0.64	2.24	3.63	>tr|K0N322|K0N322_LACCA YkuT protein OS=Lactobacillus casei W56 GN=ykuT PE=4 SV=1
Phosphate acetyltransferase (EC 2.3.1.8)	Carbohydrate-related metabolism	2.1.1	fermentation, end-product formation	*pta*	BN194_11340	K0MU95	0.54	1.55	2.88	0.83	2.27	1.46	>tr|K0MU95|K0MU95_LACCA Pta protein OS=Lactobacillus casei W56 GN=pta PE=4 SV=1
Tagatose-6-phosphate kinase (EC 2.7.1.144)	Carbohydrate-related metabolism	2.1.1	fructose catabolism	*fruK*	BN194_15420	K0NAJ6	1.24	1.24	1.00	1.94	3.47	2.22	>tr|K0NAJ6|K0NAJ6_LACCA Tagatose-6-phosphate kinase OS=Lactobacillus casei W56 GN=fruK PE=3 SV=1
Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	Central glycolytic/intermediary pathways	2.1.2	pentose phosphate pathway	*rpe*	BN194_18000	K0N5T1	0.03	0.02	0.89	0.89	22.05	0.66	>tr|K0N5T1|K0N5T1_LACCA Ribulose-phosphate 3-epimerase OS=Lactobacillus casei W56 GN=rpe PE=3 SV=1
Transcriptional regulator lytR	Transcriptional regulation	3.5.2	unknown regulation	*lytR*	BN194_02540	K0MS94	0.73	1.14	1.56	1.87	17.58	6.86	>tr|K0MS94|K0MS94_LACCA LytR protein OS=Lactobacillus casei W56 GN=lytR PE=4 SV=1
Transcriptional repressor smtB homolog	Transcriptional regulation	3.5.2	regulation of heavy metal efflux	*ziaR*	BN194_01180	K0N4L0	0.72	0.47	0.65	0.28	2.24	5.83	>tr|K0N4L0|K0N4L0_LACCA ZiaR protein OS=Lactobacillus casei W56 GN=ziaR PE=4 SV=1
Transcriptional regulator	Transcriptional regulation	3.5.2	*unknown regulation*		BN194_16100	K0N551	0.22	0.01	0.05	0.57	3.68	1.44	>tr|K0N551|K0N551_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_16100 PE=4 SV=1

HTH-type transcriptional regulator galR	Transcriptional regulation	3.5.2	regulatory role of sugar uptake	*galR*	BN194_03780	K0N5G9	0.49	0.41	0.84	0.63	22.14	17.21	>tr|K0N5G9|K0N5G9_LACCA GalR protein OS=Lactobacillus casei W56 GN=galR PE=4 SV=1
Arginine repressor	Transcriptional regulation	3.5.2	regulation of arginine metabolism genes	*argR1,argR*	BN194_19110	K0N5R1	1.38	1.31	0.95	0.39	10.14	36.28	>tr|K0N5R1|K0N5R1_LACCA Arginine repressor OS=Lactobacillus casei W56 GN=argR1 PE=3 SV=1
Hex regulon repressor	Transcriptional regulation	3.5.2	unknown regulation		BN194_02320	K0N7J9	0.26	0.14	0.53	0.32	2.17	1.79	>tr|K0N7J9|K0N7J9_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02320 PE=4 SV=1
Pur operon repressor	Transcriptional regulation	3.5.2	regulation of purine biosynthesis genes	*purR_2*	BN194_26960	K0N7M9	0.40	0.01	0.01	1.40	3.22	0.93	>tr|K0N7M9|K0N7M9_LACCA PurR_2 protein OS=Lactobacillus casei W56 GN=purR_2 PE=4 SV=1
HTH-type transcriptional repressor yvoA	Transcriptional regulation	3.5.2	regulatory role unknown	*yvoA_2*	BN194_19880	K0N9L8	1.60	0.11	0.07	0.61	5.59	14.75	>tr|K0N9L8|K0N9L8_LACCA YvoA_2 protein OS=Lactobacillus casei W56 GN=yvoA_2 PE=4 SV=1
Transcriptional regulator GltC	Transcriptional regulation	3.5.2	regulatory role (unknown)	*nac*	BN194_16620	K0NAT7	0.56	0.23	0.41	1.62	4.50	1.55	>tr|K0NAT7|K0NAT7_LACCA Nac protein OS=Lactobacillus casei W56 GN=nac PE=4 SV=1
50S ribosomal protein L21	Ribosomal proteins	3.7.1	50S (LSU) ribosome	*rplU*	BN194_18290	K0MW61	1.93	0.65	0.34	0.56	4.68	16.20	>tr|K0MW61|K0MW61_LACCA 50S ribosomal protein L21 OS=Lactobacillus casei W56 GN=rplU PE=3 SV=1
50S ribosomal protein L10	Ribosomal proteins	3.7.1	50S (LSU) ribosome	*rplJ*	BN194_24090	K0MXD8	0.88	0.05	0.06	0.92	2.42	2.31	>tr|K0MXD8|K0MXD8_LACCA 50S ribosomal protein L10 OS=Lactobacillus casei W56 GN=rplJ PE=3 SV=1
50S ribosomal protein L30	Ribosomal proteins	3.7.1	50S (LSU) ribosome	*rpmD*	BN194_26040	K0MXS6	1.09	0.05	0.05	0.63	2.88	4.93	>tr|K0MXS6|K0MXS6_LACCA 50S ribosomal protein L30 OS=Lactobacillus casei W56 GN=rpmD PE=3 SV=1
50S ribosomal protein L9	Ribosomal proteins	3.7.1	50S (LSU) ribosome	*rplI*	BN194_01130	K0N4K3	0.91	0.01	0.01	0.94	4.17	4.05	>tr|K0N4K3|K0N4K3_LACCA 50S ribosomal protein L9 OS=Lactobacillus casei W56 GN=rplI PE=3 SV=1
30S ribosomal protein S21	Ribosomal proteins	3.7.1	30S (SSU) ribosome	*rpsU*	BN194_17050	K0N5E5	1.47	0.16	0.11	0.73	6.09	12.38	>tr|K0N5E5|K0N5E5_LACCA 30S ribosomal protein S21 OS=Lactobacillus casei W56 GN=rpsU PE=3 SV=1

30S ribosomal protein S16	Ribosomal proteins	3.7.1	30S (SSU) ribosome	*rpsP*	BN194_17810	K0N5H1	1.00	0.04	0.04	1.47	6.50	4.40	>tr|K0N5H1|K0N5H1_LACCA 30S ribosomal protein S16 OS=Lactobacillus casei W56 GN=rpsP PE=3 SV=1
50S ribosomal protein L35	Ribosomal proteins	3.7.1	50S (LSU) ribosome	*rpmI*	BN194_18810	K0N5P1	1.13	0.02	0.02	1.04	7.34	7.97	>tr|K0N5P1|K0N5P1_LACCA 50S ribosomal protein L35 OS=Lactobacillus casei W56 GN=rpmI PE=3 SV=1
50S ribosomal protein L24	Ribosomal proteins	3.7.1	50S (LSU) ribosome	*rplX*	BN194_26110	K0N7F9	1.25	0.06	0.05	1.73	6.83	4.96	>tr|K0N7F9|K0N7F9_LACCA 50S ribosomal protein L24 OS=Lactobacillus casei W56 GN=rplX PE=3 SV=1
50S ribosomal protein L16	Ribosomal proteins	3.7.1	50S (LSU) ribosome	*rplP*	BN194_26150	K0N863	1.13	0.06	0.05	0.96	4.88	5.78	>tr|K0N863|K0N863_LACCA 50S ribosomal protein L16 OS=Lactobacillus casei W56 GN=rplP PE=3 SV=1
50S ribosomal protein L33	Ribosomal proteins	3.7.1	50S (LSU) ribosome	*rpmG2,rpmG*	BN194_24280	K0NAA5	1.42	0.38	0.27	0.34	4.28	17.87	>tr|K0NAA5|K0NAA5_LACCA 50S ribosomal protein L33 OS=Lactobacillus casei W56 GN=rpmG2 PE=3 SV=1
50S ribosomal protein L15	Ribosomal proteins	3.7.1	50S (LSU) ribosome	*rplO*	BN194_26030	K0NAK7	1.11	0.04	0.03	0.87	3.64	4.63	>tr|K0NAK7|K0NAK7_LACCA 50S ribosomal protein L15 OS=Lactobacillus casei W56 GN=rplO PE=3 SV=1
30S ribosomal protein S1 homolog	Ribosomal proteins	3.7.1	30S (SSU) ribosome	*ypfD*	BN194_15720	K0NAL9	1.34	0.14	0.11	0.57	2.08	4.89	>tr|K0NAL9|K0NAL9_LACCA YpfD protein OS=Lactobacillus casei W56 GN=ypfD PE=4 SV=1
50S ribosomal protein L27	Ribosomal proteins	3.7.1	50S (LSU) ribosome	*rpmA*	BN194_18270	K0NB51	0.93	0.02	0.02	0.82	3.14	3.59	>tr|K0NB51|K0NB51_LACCA 50S ribosomal protein L27 OS=Lactobacillus casei W56 GN=rpmA PE=3 SV=1
Glutamate--tRNA ligase (EC 6.1.1.17) (Glutamyl-tRNA synthetase)	tRNA aminoacyl synthesis	3.7.2	protein synthesis; tRNA charging	gltX	BN194_24470	K0NC38	0.94	0.17	0.18	1.94	3.28	1.58	>tr|K0NC38|K0NC38_LACCA Glutamate--tRNA ligase OS=Lactobacillus casei W56 GN=gltX PE=3 SV=1
Translation initiation factor IF-1	Protein translation (initiation)	3.7.3	protein synthesis; translation initiation	*infA*	BN194_26000	K0N847	0.85	0.15	0.17	0.65	2.50	3.26	>tr|K0N847|K0N847_LACCA Translation initiation factor IF-1 OS=Lactobacillus casei W56 GN=infA PE=3 SV=1
Translation initiation factor IF-3	Protein translation (initiation)	3.7.3	protein synthesis; translation initiation	*infC*	BN194_18820	K0NB73	1.38	0.02	0.01	0.46	3.47	10.56	>tr|K0NB73|K0NB73_LACCA Translation initiation factor IF-3 OS=Lactobacillus

													casei W56 GN=infC PE=3 SV=1
Elongation factor P	Protein translation (elongation)	3.7.4	protein synthesis; translation elongation	*efp*	BN194_18240	K0MW57	0.66	0.50	0.76	0.68	2.19	2.13	>tr|K0MW57|K0MW57_LACCA Elongation factor P OS=Lactobacillus casei W56 GN=efp PE=3 SV=1
Coenzyme A biosynthesis bifunctional protein CoaBC (EC 4.1.1.36) (EC 6.3.2.5)				*coaBC*	BN194_18090	K0MW49	0.06	0.07	1.19	0.14	2.29	1.05	>tr|K0MW49|K0MW49_LACCA CoaBC protein OS=Lactobacillus casei W56 GN=coaBC PE=4 SV=1
Predicted ORF					BN194_P0560	K0MZ29	0.44	0.37	0.84	0.24	2.48	4.56	>tr|K0MZ29|K0MZ29_LACCA Plasmid pW56, complete sequence OS=Lactobacillus casei W56 GN=BN194_P0560 PE=4 SV=1
Acyltransferase 3			Lipid-related metabolism		BN194_15460	K0N4S6	1.25	0.40	0.32	1.73	4.55	3.30	>tr|K0N4S6|K0N4S6_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_15460 PE=4 SV=1
NAD kinase (EC 2.7.1.23) (ATP-dependent NAD kinase)				*nadK*	ppnK	K0N6U5	1.65	0.74	0.45	0.97	5.37	9.10	>tr|K0N6U5|K0N6U5_LACCA NAD kinase OS=Lactobacillus casei W56 GN=nadK PE=3 SV=1
Uncharacterized protein yeaC	Uncharacterized protein yeaC			*yeaC*	BN194_29960	K0N8I6	0.30	0.10	0.35	0.46	2.00	1.29	>tr|K0N8I6|K0N8I6_LACCA YeaC protein OS=Lactobacillus casei W56 GN=yeaC PE=4 SV=1

Annexure 10: Proteins enriched in LiCl and regulated (fc licl 4.5 vs LiCl pH 6.5 >2), FC values in the corresponding CFEs are provided to allow direct comparision of regulation in CFEs.

Protein names	Functional Class	Class Code	Function	Gene	names	Entry	FC CFE 4.5 Vs CFE 6.5	FC UC pH Vs CFE 6.5	FC UC pH Vs CFE 4.5	FC LiCL pH4.5 Vs LiCL pH 6.5	FC LiCL Ph4.5 Vs CFE pH4.5	FC LiCL pH6.5 Vs CFE pH 6.5	FASTA headers
Possible TrsG protein	Unknown/uncharacterized	6	unknown function		BN194_00240	K0MRM8	1.33	3.19	2.39	10.15	32.73	4.29	>tr|K0MRM8|K0MRM8_LACCA Uncharacterized protein

													OS=Lactobacillus casei W56 GN=BN194_00240 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_11890	K0MUG0	1.11	0.76	0.68	6.44	2.67	0.46	>tr|K0MUG0|K0MUG0_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_11890 PE=4 SV=1
Hypothetical lipoprotein	Unknown/uncharacterized	6	unknown function		BN194_12440	K0MUR1	0.63	0.62	0.99	9.56	3.87	0.25	>tr|K0MUR1|K0MUR1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_12440 PE=4 SV=1
Lipoprotein	ABC-type transporter systems	1.2.2	methionine uptake	*metQ_2*	BN194_13740	K0MV23	6.01	1.92	0.32	10.12	3.05	1.81	>tr|K0MV23|K0MV23_LACCA Lipoprotein OS=Lactobacillus casei W56 GN=metQ_2 PE=3 SV=1
Penicillin-binding protein 1F	Cell wall biogenesis	1.1	peptidoglycan polymerization	*pbpF_2*	BN194_19090	K0MWB2	0.70	0.10	0.14	9.71	35.90	2.60	>tr|K0MWB2|K0MWB2_LACCA PbpF_2 protein OS=Lactobacillus casei W56 GN=pbpF_2 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_20240	K0MWI3	0.91	4.51	4.94	4.33	14.68	3.10	>tr|K0MWI3|K0MWI3_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_20240 PE=4 SV=1
Transaldolase (EC 2.2.1.2)	Central glycolytic/intermediary pathways	2.1.2	pentose phosphate pathway	*fsA*	BN194_28440	K0MYF0	10.21	5.80	0.57	28.78	2.26	0.80	>tr|K0MYF0|K0MYF0_LACCA Transaldolase OS=Lactobacillus casei W56 GN=fsa PE=3 SV=1
4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase) (EC 1.17.1.8)	Amino acid-related metabolism	2.2	L-lysine biosynthesis	*dapB*	BN194_01000	K0N166	0.74	1.05	1.42	4.62	5.81	0.93	>tr|K0N166|K0N166_LACCA 4-hydroxy-tetrahydrodipicolinate reductase OS=Lactobacillus casei W56 GN=dapB PE=3 SV=1
Uncharacterized protein	General prediction only	5	unknown function		BN194_01300	K0N194	1.85	0.25	0.14	2.86	3.87	2.51	>tr|K0N194|K0N194_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_01300 PE=4 SV=1
4-hydroxy-tetrahydrodipicolinate synthase (HTPA synthase) (EC 4.3.3.7)	Amino acid-related metabolism	2.2	L-lysine biosynthesis	*dapA*	BN194_01010	K0N1I2	20.28	22.09	1.09	39.96	3.91	1.98	>tr|K0N1I2|K0N1I2_LACCA 4-hydroxy-tetrahydrodipicolinate synthase OS=Lactobacillus casei W56 GN=dapA PE=3 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function	*yvcC*	BN194_05260	K0N2E5	0.99	2.52	2.54	3.43	17.31	5.01	>tr|K0N2E5|K0N2E5_LACCA YvcC protein OS=Lactobacillus casei W56 GN=yvcC PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_07550	K0N2T9	2.65	89.74	33.83	495.32	103.75	0.56	>tr|K0N2T9|K0N2T9_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_07550 PE=4 SV=1

Gluconate 5-dehydrogenase (EC 1.1.1.69)	General prediction only	5	unknown function	*idnO*	BN194_08150	K0N2Z5	0.85	0.38	0.45	10.95	30.51	2.35	>tr|K0N2Z5|K0N2Z5_LACCA IdnO protein OS=Lactobacillus casei W56 GN=idnO PE=3 SV=1
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	4.2	methylglyoxal removal via acetol	*dkgB*	BN194_08260	K0N347	0.91	0.44	0.48	5.11	3.03	0.54	>tr|K0N347|K0N347_LACCA DkgB protein OS=Lactobacillus casei W56 GN=dkgB PE=4 SV=1
ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136) (ADP-dependent NAD(P)HX dehydratase)	Cofactor-related metabolism	2.5	NAD(P)H metabolism	*nnrD*	BN194_09250	K0N360	3.64	0.79	0.22	3.97	10.68	9.81	>tr|K0N360|K0N360_LACCA ADP-dependent (S)-NAD(P)H-hydrate dehydratase OS=Lactobacillus casei W56 GN=nnrD PE=3 SV=1
Xre-like DNA-binding protein	Transcriptional regulation	3.5.2	regulatory role unknown		BN194_10050	K0N3E1	4.14	6.53	1.58	2.52	7.99	13.12	>tr|K0N3E1|K0N3E1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_10050 PE=4 SV=1
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	3.9	recycling defective proteins; virulence	*clpP_2, clpP*	BN194_10510	K0N3M4	0.34	0.07	0.20	4.25	6.02	0.49	>tr|K0N3M4|K0N3M4_LACCA ATP-dependent Clp protease proteolytic subunit OS=Lactobacillus casei W56 GN=clpP_2 PE=3 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_12100	K0N456	0.94	0.73	0.77	2.92	2.35	0.76	>tr|K0N456|K0N456_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_12100 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_12200	K0N464	0.34	0.21	0.63	6.64	26.06	1.32	>tr|K0N464|K0N464_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_12200 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_01080	K0N4J7	2.09	0.33	0.16	15.49	397.55	53.58	>tr|K0N4J7|K0N4J7_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_01080 PE=4 SV=1
Penicillin-binding protein 2B	Cytokinesis	1.7	cell division; divisome complex	*pbpB*	BN194_14700	K0N4S9	1.22	0.80	0.65	13.42	10.03	0.91	>tr|K0N4S9|K0N4S9_LACCA PbpB protein OS=Lactobacillus casei W56 GN=pbpB PE=4 SV=1
50S ribosomal protein L32	Ribosomal proteins	3.7.1	50S (LSU) ribosome	*rpmF*	BN194_15510	K0N4T0	0.17	0.11	0.68	2.38	1343.80	93.17	>tr|K0N4T0|K0N4T0_LACCA 50S ribosomal protein L32 OS=Lactobacillus casei W56 GN=rpmF PE=3 SV=1
6-phosphogluconate dehydrogenase,	Central glycolytic/intermediary pathways	2.1.2	pentose phosphate pathway	*yqeC*	BN194_02330	K0N532	1.01	1.94	1.93	7.32	9.47	1.30	>tr|K0N532|K0N532_LACCA 6-phosphogluconate dehydrogenase,

decarboxylating (EC 1.1.1.44)													decarboxylating OS=Lactobacillus casei W56 GN=yqeC PE=3 SV=1
Alternansucrase	Cell wall biogenesis	1.1	peptidoglycan turnover		BN194_02430	K0N547	0.15	0.04	0.27	2.26	302.79	20.67	>tr|K0N547|K0N547_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02430 PE=4 SV=1
D-2-hydroxyacid dehydrogenase (EC 1.1.1.-)	General prediction only	5	unknown function	*ddH*	BN194_16660	K0N557	0.46	1.08	2.36	2.59	14.25	2.53	>tr|K0N557|K0N557_LACCA Ddh protein OS=Lactobacillus casei W56 GN=ddh PE=3 SV=1
Putative N-acetylmuramoyl-L-alanine amidase YrvJ (EC 3.5.1.28)	Cytokinesis	1.7	cell division; septum splitting	*yrJ*	BN194_17200	K0N5G4	0.45	0.37	0.82	4.65	110.13	10.66	>tr|K0N5G4|K0N5G4_LACCA YrvJ protein OS=Lactobacillus casei W56 GN=yrvJ PE=4 SV=1
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	1.2.2	oligopeptide uptake	*oppB*	BN194_17900	K0N5S3	3.35	1.80	0.54	2.27	13.87	20.50	>tr|K0N5S3|K0N5S3_LACCA OppB protein OS=Lactobacillus casei W56 GN=oppB PE=3 SV=1
Surface antigen	Cell wall biogenesis	1.1	peptidoglycan turnover		BN194_21500	K0N6S2	2.52	2.85	1.13	19.04	26.32	3.49	>tr|K0N6S2|K0N6S2_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_21500 PE=4 SV=1
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	3.1	DNA replication elongation	*dnaN*	BN194_00020	K0N6S3	1.20	1.52	1.27	2.56	2.44	1.14	>tr|K0N6S3|K0N6S3_LACCA DNA polymerase III subunit beta OS=Lactobacillus casei W56 GN=dnaN PE=4 SV=1
Cytochrome d ubiquinol oxidase subunit 1 (EC 1.10.3.-)	Membrane bioenergetics	1.4	electron transport	*cydA_2*	BN194_23410	K0N6Y2	6.98	8.51	1.22	14.35	3.11	1.51	>tr|K0N6Y2|K0N6Y2_LACCA CydA_2 protein OS=Lactobacillus casei W56 GN=cydA_2 PE=4 SV=1
ABC transporter substrate binding protein	ABC-type transporter systems	1.2.2	metal ion uptake		BN194_25510	K0N7B2	1.30	0.96	0.73	10.10	6.24	0.80	>tr|K0N7B2|K0N7B2_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_25510 PE=4 SV=1
Membrane protein	Unknown/uncharacterized	6	unknown function		BN194_22700	K0N7C6	1.02	0.93	0.92	2.53	3.40	1.36	>tr|K0N7C6|K0N7C6_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_22700 PE=4 SV=1
Putative secreted protein	cell wall biogenesis	1.1	peptidoglycan turnover?		BN194_02820	K0N7S8	5.67	15.90	2.81	18.18	74.69	23.28	>tr|K0N7S8|K0N7S8_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_02820 PE=4 SV=1
Penicillin-binding protein 3	Cell wall biogenesis	1.1	peptidoglycan polymerization	*pbpC*	BN194_03320	K0N7W9	0.91	0.77	0.84	8.80	3.05	0.32	>tr|K0N7W9|K0N7W9_LACCA PbpC protein OS=Lactobacillus casei W56 GN=pbpC PE=4 SV=1

Uncharacterized protein ypuA	Unknown/uncharacterized	6	unknown function	*ypuA*	BN194_27250	K0N8I3	0.58	0.84	1.45	3.46	8.23	1.38	>tr|K0N8I3|K0N8I3_LACCA YpuA protein OS=Lactobacillus casei W56 GN=ypuA PE=4 SV=1
Transcriptional regulator lytR	Transcriptional regulation	3.5.2	regulatory role unknown	*lytR_4*	BN194_23780	K0NA85	0.69	0.74	1.07	2.56	17.45	4.69	>tr|K0NA85|K0NA85_LACCA LytR_4 protein OS=Lactobacillus casei W56 GN=lytR_4 PE=4 SV=1
Dipeptide-binding protein dppE	ABC-type transporter systems	1.2.2	oligopeptide uptake	*dppE_3*	BN194_14020	K0NAD1	2.33	1.09	0.47	8.16	2.29	0.65	>tr|K0NAD1|K0NAD1_LACCA DppE_3 protein OS=Lactobacillus casei W56 GN=dppE_3 PE=4 SV=1
Penicillin-binding protein 1A	Cell wall biogenesis	1.1	cell division; divisome complex; peptidoglycan polymerization	*ponA*	BN194_16720	K0NAU3	1.13	0.98	0.87	5.92	8.66	1.66	>tr|K0NAU3|K0NAU3_LACCA PonA protein OS=Lactobacillus casei W56 GN=ponA PE=4 SV=1
Ribonuclease H (EC 3.1.26.4)	DNA repair/recombination	3.2	DNA repair (ribonucleotide excision)	*rnhA*	BN194_27580	K0NAX8	1.07	0.81	0.76	2.78	45.43	17.57	>tr|K0NAX8|K0NAX8_LACCA RnhA protein OS=Lactobacillus casei W56 GN=rnhA PE=4 SV=1
Inner membrane amino-acid ABC transporter permease protein yecS	ABC-type transporter systems	1.2.2	polar amino acid uptake	*yecS_3*	BN194_29780	K0NB99	0.91	0.79	0.87	28.69	15.42	0.49	>tr|K0NB99|K0NB99_LACCA YecS_3 protein OS=Lactobacillus casei W56 GN=yecS_3 PE=4 SV=1
Uncharacterized protein	Unknown/uncharacterized	6	unknown function		BN194_24220	K0NC21	2.83	0.80	0.28	39.17	9.14	0.66	>tr|K0NC21|K0NC21_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_24220 PE=4 SV=1
Oxidoreductase YdhF (EC 1.-.-.-)	General prediction only	5	unknown function	*ydhF*	BN194_25320	K0NCA1	0.31	0.09	0.29	2.06	2.69	0.40	>tr|K0NCA1|K0NCA1_LACCA YdhF protein OS=Lactobacillus casei W56 GN=ydhF PE=4 SV=1
ErfK family protein	Cell wall biogenesis	1.1	unknown function (peptidoglycan crosslinking?)		BN194_26570	K0NCS1	2.17	0.55	0.25	4.03	4.62	2.48	>tr|K0NCS1|K0NCS1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_26570 PE=4 SV=1
SPFH/Band 7/PHB domain protein	Unknown/uncharacterized	6	unknown function		BN194_29820	K0NDM1	0.93	0.87	0.94	3.02	2.22	0.68	>tr|K0NDM1|K0NDM1_LACCA Uncharacterized protein OS=Lactobacillus casei W56 GN=BN194_29820 PE=4 SV=1

Annexure 11: Protein common in CFE and ECF and their occurrence (acid stress experiment)

PROTEINS COMMON IN CFE AND ECF AND THEIR LABEL FREE QUANTIFICATION (LFQ) INTENSITIES IN REPLICATES						
PROTEINS DETECTED IN ALL GROWTH CONDITIONS (pH 6.5, pH 4.5 and UC pH)						
Protein name or putative annotation	Functional Class	Gene Locus	Entry	Average LFQ		
				pH 4.5	pH 6.5	UC pH
Hup haem-utilization protein, DNA binding	DNA replication-related	BN194_15740	K0MVF4	18	18.5	18.5
DnaK	Protein folding/turnover	BN194_17460	K0N5C7	22	21.8	21.8
GroS	Protein folding/turnover	BN194_23760	K0N700	20	20.0	20.0
PA FMN-binding domain protein sig seq, membrane location	General prediction only	BN194_24320	K0NC29	21	20.8	20.8
ptsH phosphoenolpyruvate-dependent sugar phosphotransferase system	Phosphotransferase systems	BN194_19430	K0N9I2	22	21.7	21.7
OppA, Oligopeptide-binding protein, sig seq	ABC-type transporter systems	BN194_17880	K0N983	17	16.6	16.6
OppA_2, sig. seq., second OppA later	ABC-type transporter systems	BN194_20640	K0MWL6	20	19.5	19.5
L-lactate dehydrogenase	Carbohydrate-related metabolism	BN194_26560	K0N7J5	19	18.9	18.9
Fba_2 protein fructose bisphosphate aldolase	Central glycolytic/intermediary pathways	BN194_05060	K0N2C9	21	21.4	21.4
Gap	Central glycolytic/intermediary pathways	BN194_11010	K0N3R3	23	22.7	22.7
phosphoglycerate kinase	Central glycolytic/intermediary pathways	BN194_11020	K0N9R1	21	21.5	21.5
Enolase	Central glycolytic/intermediary pathways	BN194_11040	K0MU67	24	23.8	23.8
6 phosphofructokinase	Central glycolytic/intermediary pathways	BN194_15570	K0NAK6	22	21.5	21.5
Pyruvate kinase pyk	Central glycolytic/intermediary pathways	BN194_15580	K0N8B6	20	20.3	20.3
2,3-bisphosphoglycerate-dependent phosphoglycerate mutase	Central glycolytic/intermediary pathways	BN194_22740	K0MX58	21	21.4	21.4
csp, DNA binding trans reg	Transcription-associated proteins	BN194_06990	K0MT67	13	12.9	12.9
CspLA protein, RNA chaperone	Transcription-associated proteins	BN194_12460	K0N438	22	22.0	22.0
Elongation factor Tu	Protein translation (elongation)	BN194_15310	K0N4R1	19	19.4	19.4

Elongation factor G	Protein translation (elongation)	BN194_26270	K0NCN8	24	23.5	23.5
Putative secreted protein, sig. seq., Cell wall-associated hydrolase	Uncharacterized	BN194_02820	K0N7S8	24	24.4	24.4
ponA	Uncharacterized	BN194_16720	K0NAU3	19	18.6	18.6
PA surface antigen, sig. seq., PA peptidoglycan hydrolase, cell wall amidase	Uncharacterized	BN194_21500	K0N6S2	23	22.8	22.8
Putative N-acetylmuramoyl-L-alanine amidase YrvJ	Uncharacterized	BN194_17200	K0N5G4	20	20.1	20.1
Cell wall surface anchor family protein, sig. seq., transmembrane	Uncharacterized	BN194_05290	K0MSU3	26	25.7	25.7
PA Serine protease Do-like HtrA, transmembrane	Uncharacterized	BN194_29460	K0N8D9	21	21.4	21.4
possible TgrS, sig seq, coiled coil, Putative peptidoglycan hydrolase, surface antigen	Uncharacterized	BN194_00240	K0MRM8	22	22.5	22.5
YvcC protein, has signal sequence, secreted protein	BN194_05260		K0N2E5	25	25.4	25.4
uncharacterized, sig. seq., 20kDa	Uncharacterized	BN194_20240	K0MWI3	22	22.3	22.3
sig seq, coiled coil, PA = cell wall associated hydrolase	Uncharacterized	BN194_23630	K0NA78	25	24.9	24.9
ABC transporter substrate-binding protein, sig. seq.	Uncharacterized	BN194_07710	K0N2Z3	19	19.2	19.2
LytR protein, transmembrane protein, transcriptional regulator	Uncharacterized	BN194_02540	K0MS94	20	20.4	20.4
LytR_4 transcriptional regulator	Uncharacterized	BN194_23780	K0NA85	21	21.1	21.1
PROTEINS DETECTED IN pH 6.5 AND pH 4.5						
Protein name or putative annotation	Functional Class	Gene Locus	Entry	Average LFQ		
				pH 4.5	pH 6.5	UC pH
D-alanyl-D-alanine carboxypeptidase dacA, sig. seq.	Cell wall biogenesis	BN194_02140	K0MS53	17.5	18.5	0
cytosolic ribosome-associated chaperone	Protein folding/turnover	BN194_15330	K0N884	17.8	20.5	0
PrsA, foldase	Protein folding/turnover	BN194_19060	K0N5Q8	18.5	19.5	0
YpdF 30S ribosomal protein S1 homolog	Ribosomal proteins	BN194_15720	K0NAL9	18.8	20.2	0
PROTEIN DETECTED IN pH 6.5 AND UC pH						
Protein name or putative annotation	Functional Class	Gene Locus	Entry	Average LFQ		
				pH 4.5	pH 6.5	UC pH

Cysteine synthase	Amino acid-related metabolism	BN194_05520	K0N8E6	19.9	12.6	20.43
Elongation factor Ts	Protein translation (elongation)	BN194_17670	K0NB01	0.0	19.0	19.97
PROTEINS DETECTED IN pH 4.5 AND UC pH						
Protein name or putative annotation	Functional Class	Gene Locus	Entry	Average LFQ		
				pH 4.5	pH 6.5	UC pH
GalK galactokinase	Carbohydrate-related metabolism	BN194_07340	K0MTA3	0.0	0.0	20
LacD2 Tagatose 1,6-diphosphate aldolase	Carbohydrate-related metabolism	BN194_27060	K0N7P0	20.9	20.2	6
Triosephosphate isomerase	Central glycolytic/intermediary pathways	BN194_11030	K0N736	18.6	18.5	19
Alternansucrase,sig seq, 100kDa, Lysozyme M1 (1,4-beta-N-acetylmuramidase)	Uncharacterized	BN194_02430	K0N547	22.5	19.3	22
Uncharacterized, Sig. seq.,	Uncharacterized	BN194_21380	K0N9Y1	18.3	0.0	21
YpuA, uncharacterized extracellular protein	Uncharacterized	BN194_21700	K0N8I3	18.9	18.4	21
PROTEIN DETECTED IN pH 4.5 ONLY						
Protein name or putative annotation	Functional Class	Gene Locus	Entry	Average LFQ		
				pH 4.5	pH 6.5	UC pH
LacD2 Tagatose 1,6-diphosphate aldolase	Carbohydrate-related metabolism	BN194_27060	K0N7P0	20.7	6.7	5.7
ItaS1 Lipoteichoic acid synthase 1, transmembran	Uncharacterized	BN194_27250	K0N496	19.2	5.8	0
uncharacterized, sig. seq., 13.7 kDa	Uncharacterized	BN194_01080	K0N4J7	20.5	14.0	0
LytR_3 protein	Uncharacterized	BN194_21700	K0N6U3	20.1	6.6	0
50S ribosomal protein L24	Ribosomal proteins	BN194_26110	K0N7F9	18.7	6.3	0
PROTEIN DETECTED IN UC pH ONLY						
Protein name or putative annotation	Functional Class	Gene Locus	Entry	Average LFQ pH 4.5		
				pH 4.5	pH 6.5	UC pH
GalE	Cell wall biogenesis	BN194_07350	K0N2R3	6.0	0.0	19.2
Glutamine--fructose-6-phosphate aminotransferase	Cell wall biogenesis	BN194_11560	K0N3V9	6.7	6.9	20.8
PepC_2 no signal sequence	Amino acid-related metabolism	BN194_24680	K0NAC2	6.7	0.0	13.4

Threonine--tRNA ligase	tRNA aminoacyl synthesis	BN194_18860	K0N5P5	6.57	0	20.5

Annexure 12: Cell surface proteins detected in LiCl extracts not due to lysis (NaN in all CFE, not detected in ECF)

Protein names	Functional Class	Function	Gene	Mol. weight [kDa] _	Gene locus	FC CFE 4.5 Vs CFE 6.5	FC UC pH Vs CFE 6.5	FC UC pH Vs CFE 4.5	FC LiCL pH 4.5 Vs LiCL pH 6.5	FC LiCL pH 4.5 Vs CFE pH 4.5	FC LiCL pH 6.5 Vs CFE pH 6.5
Uncharacterized protein yaaA	General prediction only	unknown role (DNA replication and/or repair?)	yaaA	7.5	BN194_00040	0.97	0.92	0.95	0.60	27.39	44.33
Membrane protein	Unknown/uncharacterized	unknown function		40.8	BN194_22700	1.02	0.93	0.92	2.53	3.40	1.36
Hypothetical lipoprotein	Unknown/uncharacterized	unknown function		23.3	BN194_12440	0.63	0.62	0.99	9.56	3.87	0.25
Uncharacterized protein	Unknown/uncharacterized	unknown function		8.5	BN194_16650	1.21	0.51	0.42	0.10	4.38	51.93
Queuosine transporter QueT	General prediction only	unknown function	queT	18.3	BN194_21930	0.79	1.20	1.51	1.00	4.55	3.60
Uncharacterized protein	Cell wall biogenesis	teichoic acid biosynthesis		51.1	BN194_02360	1.27	0.37	0.30	1.60	15.09	11.98
Gluconate 5-dehydrogenase (EC 1.1.1.69)	General prediction only	unknown function	idnO	26.6	BN194_08150	0.85	0.38	0.45	10.95	30.51	2.35

Uncharacterized protein yitL	General prediction only	unknown function	yitL	31.9	BN194_15600	0.95	1.16	1.23	1.51	167.10	104.98
Uncharacterized protein	Unknown/uncharacterized	unknown function		11.2	BN194_11770	1.18	0.30	0.26	1.05	2.54	2.85
Protein veg	Unknown/uncharacterized	unknown function	veg	11.4	BN194_27010	2.58	0.61	0.24	0.92	2.16	6.05
Uncharacterized protein	Unknown/uncharacterized	unknown function		10.1	BN194_05550	0.59	0.23	0.40	1.07	44.76	24.73
Arginine repressor	Transcriptional regulation	regulation of arginine metabolism genes	argR1,argR	16.8	BN194_19110	1.38	1.31	0.95	0.39	10.14	36.28
MarR family transcriptional regulator	Transcriptional regulation	regulatory role unknown		19.2	BN194_22610	1.10	0.71	0.64	0.12	0.54	4.76
Transcriptional repressor smtB homolog	Transcriptional regulation	regulation of heavy metal efflux	ziaR	13.0	BN194_01180	0.72	0.47	0.65	0.28	2.24	5.83
Putative transcriptional regulator, MarR family	Transcriptional regulation	regulatory role unknown		15.5	BN194_27490	0.89	0.64	0.72	0.34	1.26	3.26
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	oligopeptide uptake	oppB_2	35.1	BN194_20630	0.44	0.20	0.44	0.20	2.40	5.16
Inner membrane amino-acid ABC transporter permease protein yecS	ABC-type transporter systems	polar amino acid uptake	yecS_3	58.5	BN194_29780	0.91	0.79	0.87	28.69	15.42	0.49
Oligopeptide transport system	ABC-type transporter systems	oligopeptide uptake	oppB	35.7	BN194_17900	3.35	1.80	0.54	2.27	13.87	20.50

permease protein oppB											
Ribosome maturation factor RimP	tRNA/Ribosome assembly/processing	ribosome processing (SSU)	rimP	18.0	BN194_17590	1.98	0.34	0.17	0.44	3.17	14.15
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	ribosomal RNA processing (LSU)	rluB	27.3	BN194_15650	1.15	0.65	0.57	0.70	35.31	57.68
Pseudouridine synthase (EC 5.4.99.-)	tRNA/Ribosome assembly/processing	ribosomal RNA processing (SSU)	ytzG	25.9	BN194_09230	1.05	0.33	0.31	0.84	9.95	12.49
Single-stranded-DNA-specific exonuclease recJ (EC 3.1.-.-)	DNA repair/recombination	DNA repair (base excision;mismatch; homologous recombination)	recJ	87.9	BN194_17390	0.62	0.26	0.42	0.22	2.71	7.58
4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase) (EC 1.17.1.8)	Amino acid-related metabolism	L-lysine biosynthesis	dapB	27.3	BN194_01000	0.74	1.05	1.42	4.62	5.81	0.93
SsrA-binding protein (Small protein B)	Posttranslational modification	defective protein degradation (tagging)	smpB	18.3	BN194_11110	1.62	0.44	0.27	0.24	3.76	25.59
Xanthine permease	Other transporter proteins	xanthine uptake	pbuX	47.3	BN194_12500	0.62	0.70	1.13	0.48	1.95	2.53
50S ribosomal protein L32	Ribosomal proteins	50S (LSU) ribosome	rpmF	7.1	BN194_15510	0.17	0.11	0.68	2.38	1343.80	93.17
ABC transporter, ATP-binding protein	Cell surface proteins/internalins	unknown function		22.1	BN194_15700	0.43	0.48	1.12	0.83	9.18	4.75

NAD kinase (EC 2.7.1.23) (ATP-dependent NAD kinase)	nadK	29.9	ppnK	1.65	0.74	0.45	0.97	5.37	9.10

Annexure 13: Acid regulated (pH 4.5) cell surface proteins (LiCl extracts)

(Note: Yellow highlighted Gene Locus were also found in ECF)

Protein names	**Functional Class**	**Function**	**Gene**	**Mol. weight [kDa]_**	**Gene Locus**	**CFE pH 4.5**	**CFE pH 6.5**	**CFE UC pH**	**LiCl pH 4.5**	**LiCl pH 6.5**	**FC CFE 4.5 Vs CFE 6.5**	**FC UC pH Vs CFE pH 6.5**	**FC UC pH Vs CFE pH 4.5**	**FC LiCL pH 4.5 Vs LiCL pH 6.5**	**FC LiCL pH 4.5 Vs CFE pH 4.5**	**FC LiCL 6.5 Vs CFE pH 6.5**
Surface antigen	Cell wall biogenesis	peptidoglycan turnover		42.7	BN194_21500	Y	Y	Y	Y	Y	2.5	2.9	1.1	19.0	26.3	3.5
Putative secreted protein	cell wall biogenesis	peptidoglycan turnover?		49.7	BN194_02820	Y	Y	Y	Y	Y	5.7	15.9	2.8	18.2	74.7	23.3
Penicillin-binding protein 1F	Cell wall biogenesis	peptidoglycan polymerization	pbpF_2	77.0	BN194_19090	Y	Y	N	Y	Y	0.7	0.1	0.1	9.7	35.9	2.6
Penicillin-binding protein 3	Cell wall biogenesis	peptidoglycan polymerization	pbpC	72.3	BN194_03320	Y	Y	Y	Y	Y	0.9	0.8	0.8	8.8	3.0	0.3
ErfK family protein	Cell wall biogenesis	unknown function (peptidoglycan crosslinking?)		50.4	BN194_26570	Y	Y	N	Y	Y	2.2	0.6	0.3	4.0	4.6	2.5
D-alanine--poly(phosphoribitol) ligase subunit 2 (EC	Cell wall biogenesis	teichoic acid D-alanylation	dltC	8.9	BN194_08610	Y	Y	Y	Y	Y	12.9	55.6	4.3	3.1	1.4	5.7

6.1.1.13) (D-alanyl carrier protein)																
Alternansucrase	Cell wall biogenesis	peptidoglycan turnover		100.6	BN194_02430	Y	Y	Y	Y	Y	0.2	0.0	0.3	2.3	302.8	20.7
Cytochrome d ubiquinol oxidase subunit 1 (EC 1.10.3.-)	Membrane bioenergetics	electron transport	cydA_2	54.8	BN194_23410	Y	Y	Y	Y	Y	7.0	8.5	1.2	14.4	0.6	1.5
Penicillin-binding protein 2B	Cytokinesis	cell division; divisome complex	pbpB	76.8	BN194_14700	Y	Y	Y	Y	Y	1.2	0.8	0.7	13.4	10.0	0.9
Putative N-acetylmuramoyl-L-alanine amidase YrvJ (EC 3.5.1.28)	Cytokinesis	cell division; septum splitting	yrvJ	49.1	BN194_17200	N	Y	Y	Y	Y	0.5	0.4	0.8	4.7	110.1	10.7
4-hydroxy-tetrahydrodipicolinate synthase (HTPA synthase) (EC 4.3.3.7)	Amino acid-related metabolism	L-lysine biosynthesis	dapA	32.1	BN194_01010	Y	Y	Y	Y	Y	20.3	22.1	1.1	40.0	3.9	2.0
4-hydroxy-tetrahydrodipicolinate reductase (HTPA reductase) (EC 1.17.1.8)	Amino acid-related metabolism	L-lysine biosynthesis	dapB	27.3	BN194_01000	N	N	N	Y	Y	0.7	1.1	1.4	4.6	5.8	0.9
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2)	Lipid-related metabolism	fatty acid biosynthesis	accA	28.0	BN194_22470	Y	Y	Y	Y	Y	23.7	1.3	0.1	2.5	0.3	2.3

ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136) (ADP-dependent NAD(P)HX dehydratase)	Cofactor-related metabolism	NAD(P)H metabolism	nnrD	29.6	BN194_09250	Y	N	N	Y	Y	3.6	0.8	0.2	4.0	10.7	9.8
DNA polymerase III subunit beta (EC 2.7.7.7)	DNA replication-related	DNA replication elongation	dnaN	41.5	BN194_00020	Y	Y	Y	Y	Y	1.2	1.5	1.3	2.6	2.4	1.1
Ribonuclease H (EC 3.1.26.4)	DNA repair/recombination	DNA repair (ribonucleotide excision)	rnhA	18.3	BN194_27580	Y	Y	N	Y	Y	1.1	0.8	0.8	2.8	45.4	17.6
ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp)	Protein folding/turnover	recycling defective proteins; virulence	clpP_2, clpP	21.5	BN194_10510	Y	Y	Y	Y	Y	0.3	0.1	0.2	4.2	6.0	0.5
2,5-diketo-D-gluconic acid reductase B (EC 1.1.1.274)	Cell defense/detoxification	methylglyoxal removal via acetol	dkgB	30.9	BN194_08260	Y	Y	Y	Y	Y	0.9	0.4	0.5	5.1	3.0	0.5
Gluconate 5-dehydrogenase (EC 1.1.1.69)	General prediction only	unknown function	idnO	26.6	BN194_08150	N	N	N	Y	Y	0.8	0.4	0.4	11.0	30.5	2.4
Uncharacterized protein	General prediction only	unknown function		53.1	BN194_01300	Y	Y	N	Y	Y	1.9	0.3	0.1	2.9	3.9	2.5
D-2-hydroxyacid dehydrogenase (EC 1.1.1.-)	General prediction only	unknown function	ddh	33.7	BN194_16660	Y	Y	Y	Y	Y	0.5	1.1	2.4	2.6	14.3	2.5

Oxidoreductase YdhF (EC 1.-.-.-)	General prediction only	unknown function	ydhF	36.0	BN194_25320	Y	Y	N	Y	Y	0.3	0.1	0.3	2.1	2.7	0.4
Uncharacterized protein	Unknown/uncharacterized	unknown function		5.4	BN194_07550	Y	N	Y	Y	N	2.7	89.7	33.8	495.3	103.7	0.6
Uncharacterized protein	Unknown/uncharacterized	unknown function		14.0	BN194_24220	Y	N	N	Y	Y	2.8	0.8	0.3	39.2	9.1	0.7
Uncharacterized protein	Unknown/uncharacterized	unknown function		13.7	BN194_01080	Y	N	N	Y	Y	2.1	0.3	0.2	15.5	397.6	53.6
Possible TrsG protein	Unknown/uncharacterized	unknown function		43.4	BN194_00240	Y	Y	Y	Y	Y	1.3	3.2	2.4	10.2	32.7	4.3
Hypothetical lipoprotein	Unknown/uncharacterized	unknown function		23.3	BN194_12440	N	N	N	Y	Y	0.6	0.6	1.0	9.6	3.9	0.3
Uncharacterized protein	Unknown/uncharacterized	unknown function		51.7	BN194_12200	N	Y	N	Y	Y	0.3	0.2	0.6	6.6	26.1	1.3
Uncharacterized protein	Unknown/uncharacterized	unknown function		43.3	BN194_11890	Y	Y	Y	Y	Y	1.1	0.8	0.7	6.4	2.7	0.5
Uncharacterized protein	Unknown/uncharacterized	unknown function		20.0	BN194_20240	Y	Y	Y	Y	Y	0.9	4.5	4.9	4.3	14.7	3.1
Uncharacterized protein	Unknown/uncharacterized	unknown function		18.9	BN194_19210	Y	Y	Y	Y	Y	6.1	6.4	1.0	4.3	1.9	2.7
Uncharacterized protein ypuA	Unknown/uncharacterized	unknown function	ypuA	35.6	BN194_27250	Y	Y	Y	Y	Y	0.6	0.8	1.5	3.5	8.2	1.4
Uncharacterized protein	Unknown/uncharacterized	unknown function	yvcC	63.3	BN194_05260	Y	Y	Y	Y	Y	1.0	2.5	2.5	3.4	17.3	5.0
SPFH/Band 7/PHB domain protein	Unknown/uncharacterized	unknown function		27.3	BN194_29820	N	N	N	Y	Y	0.9	0.9	0.9	3.0	2.2	0.7
Uncharacterized protein	Unknown/uncharacterized	unknown function		13.3	BN194_12100	Y	Y	Y	Y	N	0.9	0.7	0.8	2.9	2.4	0.8
Membrane protein	Unknown/uncharacterized	unknown function		40.8	BN194_22700	N	N	N	Y	Y	1.0	0.9	0.9	2.5	3.4	1.4

Uncharacterized protein ybbP	Unknown/uncharacterized	unknown function	ybbP	32.2	BN194_11530	Y	N	N	Y	Y	8.0	1.9	0.2	2.4	0.7	2.4
Inner membrane amino-acid ABC transporter permease protein yecS	ABC-type transporter systems	polar amino acid uptake	yecS_3	58.5	BN194_29780	N	N	N	Y	Y	0.9	0.8	0.9	28.7	15.4	0.5
Lipoprotein	ABC-type transporter systems	methionine uptake	metQ_2	30.4	BN194_13740	Y	Y	Y	Y	Y	6.0	1.9	0.3	10.1	3.0	1.8
ABC transporter substrate binding protein	ABC-type transporter systems	metal ion uptake		33.3	BN194_25510	Y	Y	Y	Y	Y	1.3	1.0	0.7	10.1	6.2	0.8
Dipeptide-binding protein dppE	ABC-type transporter systems	oligopeptide uptake	dppE_3	63.0	BN194_14020	Y	Y	Y	Y	Y	2.3	1.1	0.5	8.2	2.3	0.7
Oligopeptide transport system permease protein oppB	ABC-type transporter systems	oligopeptide uptake	oppB	35.7	BN194_17900	N	N	N	Y	Y	3.4	1.8	0.5	2.3	13.9	20.5
Transaldolase (EC 2.2.1.2)	Central glycolytic/intermediary pathways	pentose phosphate pathway	fsa	25.1	BN194_28440	Y	Y	Y	Y	Y	10.2	5.8	0.6	28.8	2.3	0.8
6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)	Central glycolytic/intermediary pathways	pentose phosphate pathway	yqeC	32.1	BN194_02330	Y	Y	Y	Y	Y	1.0	1.9	1.9	7.3	9.5	1.3
Transcriptional regulator lytR	Transcriptional regulation	regulatory role unknown	lytR_4	39.0	BN194_23780	Y	Y	Y	Y	Y	0.7	0.7	1.1	2.6	17.5	4.7
Xre-like DNA-binding protein	Transcriptional regulation	regulatory role unknown		33.1	BN194_10050	N	N	Y	Y	Y	4.1	6.5	1.6	2.5	8.0	13.1

50S ribosomal protein L32	Ribosomal proteins	50S (LSU) ribosome	rpmF	7.1	BN194_15510	N	N	N	Y	Y	0.2	0.1	0.7	2.4	1343.8	93.2